GENES AND MEMES

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Preface

This book belongs to a series of online books summarizing the recent state Topological Geometrodynamics (TGD) and its applications. TGD can be regarded as a unified theory of fundamental interactions but is not the kind of unified theory as so called GUTs constructed by graduate students at seventies and eighties using detailed recipes for how to reduce everything to group theory. Nowadays this activity has been completely computerized and it probably takes only a few hours to print out the predictions of this kind of unified theory as an article in the desired format. TGD is something different and I am not ashamed to confess that I have devoted the last 32 years of my life to this enterprise and am still unable to write The Rules.

I got the basic idea of Topological Geometrodynamics (TGD) during autumn 1978, perhaps it was October. What I realized was that the representability of physical space-times as 4-dimensional surfaces of some higher-dimensional space-time obtained by replacing the points of Minkowski space with some very small compact internal space could resolve the conceptual difficulties of general relativity related to the definition of the notion of energy. This belief was too optimistic and only with the advent of what I call zero energy ontology the understanding of the notion of Poincare invariance has become satisfactory.

It soon became clear that the approach leads to a generalization of the notion of space-time with particles being represented by space-time surfaces with finite size so that TGD could be also seen as a generalization of the string model. Much later it became clear that this generalization is consistent with conformal invariance only if space-time is 4-dimensional and the Minkowski space factor of imbedding space is 4-dimensional.

It took some time to discover that also the geometrization of also gauge interactions and elementary particle quantum numbers could be possible in this framework: it took two years to find the unique internal space providing this geometrization involving also the realization that family replication phenomenon for fermions has a natural topological explanation in TGD framework and that the symmetries of the standard model symmetries are much more profound than pragmatic TOE builders have believed them to be. If TGD is correct, main stream particle physics chose the wrong track leading to the recent deep crisis when people decided that quarks and leptons belong to same multiplet of the gauge group implying instability of proton.

There have been also longstanding problems.

- Gravitational energy is well-defined in cosmological models but is not conserved. Hence the conservation of the inertial energy does not seem to be consistent with the Equivalence Principle. Furthermore, the imbeddings of Robertson-Walker cosmologies turned out to be vacuum extremals with respect to the inertial energy. About 25 years was needed to realize that the sign of the inertial energy can be also negative and in cosmological scales the density of inertial energy vanishes: physically acceptable universes are creatable from vacuum. Eventually this led to the notion of zero energy ontology which deviates dramatically from the standard ontology being however consistent with the crossing symmetry of quantum field theories. In this framework the quantum numbers are assigned with zero energy states located at the boundaries of so called causal diamonds defined as intersections of future and past directed light-cones. The notion of energy-momentum becomes length scale dependent since one has a scale hierarchy for causal diamonds. This allows to understand the non-conservation of energy as apparent. Equivalence Principle generalizes and has a formulation in terms of coset representations of Super-Virasoro algebras providing also a justification for p-adic thermodynamics.

- From the beginning it was clear that the theory predicts the presence of long ranged classical electro-weak and color gauge fields and that these fields necessarily accompany classical electromagnetic fields. It took about 26 years to gain the maturity to admit the obvious: these fields are classical correlates for long range color and weak interactions assignable to dark matter. The only possible conclusion is that TGD physics is a fractal consisting of an entire hierarchy of fractal copies of standard model physics. Also the understanding of electro-weak massivation and screening of weak charges has been a long standing problem, and 32 years was needed to discover that what I call weak form of electric-magnetic duality gives a satisfactory solution of the problem and provides also surprisingly powerful insights to the mathematical structure of quantum TGD.

I started the serious attempts to construct quantum TGD after my thesis around 1982. The original optimistic hope was that path integral formalism or canonical quantization might be enough to construct the quantum theory but the first discovery made already during first year of TGD was that these formalisms might be useless due to the extreme non-linearity and enormous vacuum degeneracy of the theory. This turned out to be the case.

- It took some years to discover that the only working approach is based on the generalization of Einstein's program. Quantum physics involves the geometrization of the infinite-dimensional "world of classical worlds" (WCW) identified as 3-dimensional surfaces. Still few years had to pass before I understood that general coordinate invariance leads to a more or less unique solution of the problem and implies that space-time surfaces are analogous to Bohr orbits. Still a coupled of years and I discovered that quantum states of the Universe can be identified as classical spinor fields in WCW. Only quantum jump remains the genuinely quantal aspect of quantum physics.

- During these years TGD led to a rather profound generalization of the space-time concept. Quite general properties of the theory led to the notion of many-sheeted space-time with sheets representing physical subsystems of various sizes. At the beginning of 90s I became dimly aware of the importance of p-adic number fields and soon ended up with the idea that p-adic thermodynamics for a conformally invariant system allows to understand elementary particle massivation with amazingly few input assumptions. The attempts to understand p-adicity from basic principles led gradually to the vision about physics as a generalized number theory as an approach complementary to the physics as an infinite-dimensional spinor geometry of WCW approach. One of its elements was a generalization of the number concept obtained by fusing real numbers and various p-adic numbers along common rationals. The number theoretical trinity involves besides p-adic number fields also quaternions and octonions and the notion of infinite prime.

- TGD inspired theory of consciousness entered the scheme after 1995 as I started to write a book about consciousness. Gradually it became difficult to say where physics ends and consciousness theory begins since consciousness theory could be seen as a generalization of quantum measurement theory by identifying quantum jump as a moment of consciousness and by replacing the observer with the notion of self identified as a system which is conscious as long as it can avoid entanglement with environment. "Everything is conscious and consciousness can be only lost" summarizes the basic philosophy neatly. The idea about p-adic physics as physics of cognition and intentionality emerged also rather naturally and implies perhaps the most dramatic generalization of the space-time concept in which most points of p-adic space-time sheets are infinite in real sense and the projection to the real imbedding space consists of discrete set of points. One of the most fascinating outcomes was the observation that the entropy based on p-adic norm can be negative. This observation led to the vision that life can be regarded as something in the intersection of real and p-adic worlds. Negentropic entanglement has interpretation as a correlate for various positively colored aspects of conscious experience and means also the possibility of strongly correlated states stable under state function reduction and different from the conventional bound states and perhaps playing key role in the energy metabolism of living matter.

- One of the latest threads in the evolution of ideas is only slightly more than six years old. Learning about the paper of Laurent Nottale about the possibility to identify planetary orbits as Bohr orbits with a gigantic value of gravitational Planck constant made once again possible to see the obvious. Dynamical quantized Planck constant is strongly suggested by quantum classical correspondence and the fact that space-time sheets identifiable as quantum coherence regions can have arbitrarily large sizes. During summer 2010 several new insights about the mathematical structure and interpretation of TGD emerged. One of these insights was the realization that the postulated hierarchy of Planck constants might follow from the basic structure of quantum TGD. The point is that due to the extreme non-linearity of the classical action principle the correspondence between canonical momentum densities and time derivatives of the imbedding space coordinates is one-to-many and the natural description of the situation is in terms of local singular covering spaces of the imbedding space. One could speak about effective value of Planck

constant coming as a multiple of its minimal value. The implications of the hierarchy of Planck constants are extremely far reaching so that the significance of the reduction of this hierarchy to the basic mathematical structure distinguishing between TGD and competing theories cannot be under-estimated.

From the point of view of particle physics the ultimate goal is of course a practical construction recipe for the S-matrix of the theory. I have myself regarded this dream as quite too ambitious taking into account how far reaching re-structuring and generalization of the basic mathematical structure of quantum physics is required. It has indeed turned out that the dream about explicit formula is unrealistic before one has understood what happens in quantum jump. Symmetries and general physical principles have turned out to be the proper guide line here. To give some impressions about what is required some highlights are in order.

- With the emergence of zero energy ontology the notion of S-matrix was replaced with M-matrix which can be interpreted as a complex square root of density matrix representable as a diagonal and positive square root of density matrix and unitary S-matrix so that quantum theory in zero energy ontology can be said to define a square root of thermodynamics at least formally.

- A decisive step was the strengthening of the General Coordinate Invariance to the requirement that the formulations of the theory in terms of light-like 3-surfaces identified as 3-surfaces at which the induced metric of space-time surfaces changes its signature and in terms of space-like 3-surfaces are equivalent. This means effective 2-dimensionality in the sense that partonic 2-surfaces defined as intersections of these two kinds of surfaces plus 4-D tangent space data at partonic 2-surfaces code for the physics. Quantum classical correspondence requires the coding of the quantum numbers characterizing quantum states assigned to the partonic 2-surfaces to the geometry of space-time surface. This is achieved by adding to the modified Dirac action a measurement interaction term assigned with light-like 3-surfaces.

- The replacement of strings with light-like 3-surfaces equivalent to space-like 3-surfaces means enormous generalization of the super conformal symmetries of string models. A further generalization of these symmetries to non-local Yangian symmetries generalizing the recently discovered Yangian symmetry of $\mathcal{N} = 4$ supersymmetric Yang-Mills theories is highly suggestive. Here the replacement of point like particles with partonic 2-surfaces means the replacement of conformal symmetry of Minkowski space with infinite-dimensional super-conformal algebras. Yangian symmetry provides also a further refinement to the notion of conserved quantum numbers allowing to define them for bound states using non-local energy conserved currents.

- A further attractive idea is that quantum TGD reduces to almost topological quantum field theory. This is possible if the Kähler action for the preferred extremals defining WCW Kähler function reduces to a 3-D boundary term. This takes place if the conserved currents are so called Beltrami fields with the defining property that the coordinates associated with flow lines extend to single global coordinate variable. This ansatz together with the weak form of electric-magnetic duality reduces the Kähler action to Chern-Simons term with the condition that the 3-surfaces are extremals of Chern-Simons action subject to the constraint force defined by the weak form of electric magnetic duality. It is the latter constraint which prevents the trivialization of the theory to a topological quantum field theory. Also the identification of the Kähler function of WCW as Dirac determinant finds support as well as the description of the scattering amplitudes in terms of braids with interpretation in terms of finite measurement resolution coded to the basic structure of the solutions of field equations.

- In standard QFT Feynman diagrams provide the description of scattering amplitudes. The beauty of Feynman diagrams is that they realize unitarity automatically via the so called Cutkosky rules. In contrast to Feynman's original beliefs, Feynman diagrams and virtual particles are taken only as a convenient mathematical tool in quantum field theories. QFT approach is however plagued by UV and IR divergences and one must keep mind open for the possibility that a genuine progress might mean opening of the black box of the virtual particle.

  In TGD framework this generalization of Feynman diagrams indeed emerges unavoidably. Light-like 3-surfaces replace the lines of Feynman diagrams and vertices are replaced by 2-D partonic

2-surfaces. Zero energy ontology and the interpretation of parton orbits as light-like "wormhole throats" suggests that virtual particle do not differ from on mass shell particles only in that the four- and three- momenta of wormhole throats fail to be parallel. The two throats of the wormhole defining virtual particle would contact carry on mass shell quantum numbers but for virtual particles the four-momenta need not be parallel and can also have opposite signs of energy. Modified Dirac equation suggests a number theoretical quantization of the masses of the virtual particles. The kinematic constraints on the virtual momenta are extremely restrictive and reduce the dimension of the sub-space of virtual momenta and if massless particles are not allowed (IR cutoff provided by zero energy ontology naturally), the number of Feynman diagrams contributing to a particular kind of scattering amplitude is finite and manifestly UV and IR finite and satisfies unitarity constraint in terms of Cutkosky rules. What is remarkable that fermionic propagatos are massless propagators but for on mass shell four-momenta. This gives a connection with the twistor approach and inspires the generalization of the Yangian symmetry to infinite-dimensional super-conformal algebras.

What I have said above is strongly biased view about the recent situation in quantum TGD and I have left all about applications to the introductions of the books whose purpose is to provide a bird's eye of view about TGD as it is now. This vision is single man's view and doomed to contain unrealistic elements as I know from experience. My dream is that young critical readers could take this vision seriously enough to try to demonstrate that some of its basic premises are wrong or to develop an alternative based on these or better premises. I must be however honest and tell that 32 years of TGD is a really vast bundle of thoughts and quite a challenge for anyone who is not able to cheat himself by taking the attitude of a blind believer or a light-hearted debunker trusting on the power of easy rhetoric tricks.

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Neither TGD nor these books would exist without the help and encouragement of many people. The friendship with Heikki and Raija Haila and their family have been kept me in contact with the everyday world and without this friendship I would not have survived through these lonely 32 years most of which I have remained unemployed as a scientific dissident. I am happy that my children have understood my difficult position and like my friends have believed that what I am doing is something valuable although I have not received any official recognition for it.

During last decade Tapio Tammi has helped me quite concretely by providing the necessary computer facilities and being one of the few persons in Finland with whom to discuss about my work. I have had also stimulating discussions with Samuli Penttinen who has also helped to get through the economical situations in which there seemed to be no hope. The continual updating of fifteen online books means quite a heavy bureaucracy at the level of bits and without a systemization one ends up with endless copying and pasting and internal consistency is soon lost. Pekka Rapinoja has offered his help in this respect and I am especially grateful for him for my Python skills. Also Matti Vallinkoski has helped me in computer related problems.

The collaboration with Lian Sidoroff was extremely fruitful and she also helped me to survive economically through the hardest years. The participation to CASYS conferences in Liege has been an important window to the academic world and I am grateful for Daniel Dubois and Peter Marcer for making this participation possible. The discussions and collaboration with Eduardo de Luna and Istvan Dienes stimulated the hope that the communication of new vision might not be a mission impossible after all. Also blog discussions have been very useful. During these years I have received innumerable email contacts from people around the world. In particualr, I am grateful for Mark McWilliams and Ulla Matfolk for providing links to possibly interesting web sites and articles. These contacts have helped me to avoid the depressive feeling of being some kind of Don Quixote of Science and helped me to widen my views: I am grateful for all these people.

In the situation in which the conventional scientific communication channels are strictly closed it is important to have some loop hole through which the information about the work done can at

least in principle leak to the publicity through the iron wall of the academic censorship. Without any exaggeration I can say that without the world wide web I would not have survived as a scientist nor as individual. Homepage and blog are however not enough since only the formally published result is a result in recent day science. Publishing is however impossible without a direct support from power holders- even in archives like arXiv.org.

Situation changed for five years ago as Andrew Adamatsky proposed the writing of a book about TGD when I had already got used to the thought that my work would not be published during my life time. The Prespacetime Journal and two other journals related to quantum biology and consciousness - all of them founded by Huping Hu - have provided this kind of loop holes. In particular, Dainis Zeps, Phil Gibbs, and Arkadiusz Jadczyk deserve my gratitude for their kind help in the preparation of an article series about TGD catalyzing a considerable progress in the understanding of quantum TGD. Also the viXra archive founded by Phil Gibbs and its predecessor Archive Freedom have been of great help: Victor Christianto deserves special thanks for doing the hard work needed to run Archive Freedom. Also the Neuroquantology Journal founded by Sultan Tarlaci deserves a special mention for its publication policy. And last but not least: there are people who experience as a fascinating intellectual challenge to spoil the practical working conditions of a person working with something which might be called unified theory: I am grateful for the people who have helped me to survive through the virus attacks, an activity which has taken roughly one month per year during the last half decade and given a strong hue of grey to my hair.

For a person approaching his sixty year birthday it is somewhat easier to overcome the hard feelings due to the loss of academic human rights than for an inpatient youngster. Unfortunately the economic situation has become increasingly difficult during the twenty years after the economic depression in Finland which in practice meant that Finland ceased to be a constitutional state in the strong sense of the word. It became possible to depose people like me from the society without fear about public reactions and the classification as dropout became a convenient tool of ridicule to circumvent the ethical issues. During last few years when the right wing has held the political power this trend has been steadily strengthening. In this kind of situation the concrete help from individuals has been and will be of utmost importance. Against this background it becomes obvious that this kind of work is not possible without the support from outside and I apologize for not being able to mention all the people who have helped me during these years.

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Chapter 1

Introduction

1.1 Background

T(opological) G(eometro)D(ynamics) is one of the many attempts to find a unified description of basic interactions. The development of the basic ideas of TGD to a relatively stable form took time of about half decade [2]. The great challenge is to construct a mathematical theory around these physically very attractive ideas and I have devoted the last twenty-three years for the realization of this dream and this has resulted in seven online books about TGD and eight online books about TGD inspired theory of consciousness and of quantum biology.

Quantum T(opological) G(eometro)D(ynamics) as a classical spinor geometry for infinite-dimensional configuration space, p-adic numbers and quantum TGD, and TGD inspired theory of consciousness and of quantum biology have been for last decade of the second millenium the basic three strongly interacting threads in the tapestry of quantum TGD.

For few years ago the discussions with Tony Smith initiated a fourth thread which deserves the name 'TGD as a generalized number theory'. The basic observation was that classical number fields might allow a deeper formulation of quantum TGD. The work with Riemann hypothesis made time ripe for realization that the notion of infinite primes could provide, not only a reformulation, but a deep generalization of quantum TGD. This led to a thorough and extremely fruitful revision of the basic views about what the final form and physical content of quantum TGD might be. Together with the vision about the fusion of p-adic and real physics to a larger coherent structure these sub-threads fused to the "physics as generalized number theory" th

A further thread emerged from the realization that by quantum classical correspondence TGD predicts an infinite hierarchy of macroscopic quantum systems with increasing sizes, that it is not at all clear whether standard quantum mechanics can accommodate this hierarchy, and that a dynamical quantized Planck constant might be necessary and certainly possible in TGD framework. The identification of hierarchy of Planck constants whose values TGD "predicts" in terms of dark matter hierarchy would be natural. This also led to a solution of a long standing puzzle: what is the proper interpretation of the predicted fractal hierarchy of long ranged classical electro-weak and color gauge fields. Quantum classical correspondences allows only single answer: there is infinite hierarchy of p-adically scaled up variants of standard model physics and for each of them also dark hierarchy. Thus TGD Universe would be fractal in very abstract and deep sense.

Every updating of the books makes me frustrated as I see how badly the structure of the representation reflects my bird's eye of view as it is at the moment of updating. At this time I realized that the chronology based identification of the threads is quite natural but not logical and it is much more logical to see p-adic physics, the ideas related to classical number fields, and infinite primes as sub-threads of a thread which might be called "physics as a generalized number theory". In the following I adopt this view. This reduces the number of threads to four! I am not even sure about the number of threads! Be patient!

TGD forces the generalization of physics to a quantum theory of consciousness, and represent TGD as a generalized number theory vision leads naturally to the emergence of p-adic physics as physics of cognitive representations. The seven online books [80, 60, 49, 47, 61, 70, 68] about TGD and eight online books about TGD inspired theory of consciousness and of quantum biology [75, 11, 55, 10, 32,

39, 42, 67] are warmly recommended to the interested reader.

1.2 Basic Ideas of TGD

The basic physical picture behind TGD was formed as a fusion of two rather disparate approaches: namely TGD is as a Poincare invariant theory of gravitation and TGD as a generalization of the old-fashioned string model.

1.2.1 TGD as a Poincare invariant theory of gravitation

The first approach was born as an attempt to construct a Poincare invariant theory of gravitation. Space-time, rather than being an abstract manifold endowed with a pseudo-Riemannian structure, is regarded as a surface in the 8-dimensional space $H = M^4_{\times} CP_2$, where M^4 denotes Minkowski space and $CP_2 = SU(3)/U(2)$ is the complex projective space of two complex dimensions [33, 17, 28, 15].

The identification of the space-time as a submanifold [12, 31] of $M^4 \times CP_2$ leads to an exact Poincare invariance and solves the conceptual difficulties related to the definition of the energy-momentum in General Relativity.

It soon however turned out that submanifold geometry, being considerably richer in structure than the abstract manifold geometry, leads to a geometrization of all basic interactions. First, the geometrization of the elementary particle quantum numbers is achieved. The geometry of CP_2 explains electro-weak and color quantum numbers. The different H-chiralities of H-spinors correspond to the conserved baryon and lepton numbers. Secondly, the geometrization of the field concept results. The projections of the CP_2 spinor connection, Killing vector fields of CP_2 and of H-metric to four-surface define classical electro-weak, color gauge fields and metric in X^4.

1.2.2 TGD as a generalization of the hadronic string model

The second approach was based on the generalization of the mesonic string model describing mesons as strings with quarks attached to the ends of the string. In the 3-dimensional generalization 3-surfaces correspond to free particles and the boundaries of the 3- surface correspond to partons in the sense that the quantum numbers of the elementary particles reside on the boundaries. Various boundary topologies (number of handles) correspond to various fermion families so that one obtains an explanation for the known elementary particle quantum numbers. This approach leads also to a natural topological description of the particle reactions as topology changes: for instance, two-particle decay corresponds to a decay of a 3-surface to two disjoint 3-surfaces.

This decay vertex does not however correspond to a direct generalization of trouser vertex of string models. Indeed, the important difference between TGD and string models is that the analogs of string world sheet diagrams do not describe particle decays but the propagation of particles via different routes. Particle reactions are described by generalized Feynman diagrams for which 3-D light-like surface describing particle propagating join along their ends at vertices. As 4-manifolds the space-time surfaces are therefore singular like Feynman diagrams as 1-manifolds.

1.2.3 Fusion of the two approaches via a generalization of the space-time concept

The problem is that the two approaches to TGD seem to be mutually exclusive since the orbit of a particle like 3-surface defines 4-dimensional surface, which differs drastically from the topologically trivial macroscopic space-time of General Relativity. The unification of these approaches forces a considerable generalization of the conventional space-time concept. First, the topologically trivial 3-space of General Relativity is replaced with a "topological condensate" containing matter as particle like 3-surfaces "glued" to the topologically trivial background 3-space by connected sum operation. Secondly, the assumption about connectedness of the 3-space is given up. Besides the "topological condensate" there could be "vapor phase" that is a "gas" of particle like 3-surfaces (counterpart of the "baby universies" of GRT) and the nonconservation of energy in GRT corresponds to the transfer of energy between the topological condensate and vapor phase.

What one obtains is what I have christened as many-sheeted space-time. One particular aspect is topological field quantization meaning that various classical fields assignable to a physical system correspond to space-time sheets representing the classical fields to that particular system. One can speak of the field body of a particular physical system. Field body consists of topological light rays, and electric and magnetic flux quanta. In Maxwell's theory system does not possess this kind of field identity. The notion of magnetic body is one of the key players in TGD inspired theory of consciousness and quantum biology.

This picture became more detailed with the advent of zero energy ontology (ZEO). The basic notion of ZEO is causal diamond (CD) identified as the Cartesian product of CP_2 and of the intersection of future and past directed light-cones and having scale coming as an integer multiple of CP_2 size is fundamental. CDs form a fractal hierarchy and zero energy states decompose to products of positive and negative energy parts assignable to the opposite boundaries of CD defining the ends of the space-time surface. The counterpart of zero energy state in positive energy ontology is in terms of initial and final states of a physical event, say particle reaction.

General Coordinate Invariance allows to identify the basic dynamical objects as space-like 3-surfaces at the ends of space-time surface at boundaries of CD: this means that space-time surface is analogous to Bohr orbit. An alternative identification is as light-like 3-surfaces at which the signature of the induced metric changes from Minkowskian to Euclidian and interpreted as lines of generalized Feynman diagrams. Also the Euclidian 4-D regions would have similar interpretation. The requirement that the two interpretations are equivalent, leads to a strong form of General Coordinate Invariance. The outcome is effective 2-dimensionality stating that the partonic 2-surfaces identified as intersections of the space-like ends of space-time surface and light-like wormhole throats are the fundamental objects. That only effective 2-dimensionality is in question is due to the effects caused by the failure of strict determinism of Kähler action. In finite length scale resolution these effects can be neglected below UV cutoff and above IR cutoff. One can also speak about strong form of holography.

There is a further generalization of the space-time concept inspired by p-adic physics forcing a generalization of the number concept through the fusion of real numbers and various p-adic number fields. Also the hierarchy of Planck constants forces a generalization of the notion of space-time.

A very concise manner to express how TGD differs from Special and General Relativities could be following. Relativity Principle (Poincare Invariance), General Coordinate Invariance, and Equivalence Principle remain true. What is new is the notion of sub-manifold geometry: this allows to realize Poincare Invariance and geometrize gravitation simultaneously. This notion also allows a geometrization of known fundamental interactions and is an essential element of all applications of TGD ranging from Planck length to cosmological scales. Sub-manifold geometry is also crucial in the applications of TGD to biology and consciousness theory.

1.3 The threads in the development of quantum TGD

The development of TGD has involved several strongly interacting threads: physics as infinite-dimensional geometry; TGD as a generalized number theory, the hierarchy of Planck constants interpreted in terms of dark matter hierarchy, and TGD inspired theory of consciousness. In the following these threads are briefly described.

1.3.1 Quantum TGD as spinor geometry of World of Classical Worlds

A turning point in the attempts to formulate a mathematical theory was reached after seven years from the birth of TGD. The great insight was "Do not quantize". The basic ingredients to the new approach have served as the basic philosophy for the attempt to construct Quantum TGD since then and have been the following ones:

1. Quantum theory for extended particles is free(!), classical(!) field theory for a generalized Schrödinger amplitude in the configuration space CH consisting of all possible 3-surfaces in H. "All possible" means that surfaces with arbitrary many disjoint components and with arbitrary internal topology and also singular surfaces topologically intermediate between two different manifold topologies are included. Particle reactions are identified as topology changes [27, 34, 36]. For instance, the decay of a 3-surface to two 3-surfaces corresponds to the decay $A \to B + C$. Classically this corresponds to a path of configuration space leading from 1-particle sector

to 2-particle sector. At quantum level this corresponds to the dispersion of the generalized Schrödinger amplitude localized to 1-particle sector to two-particle sector. All coupling constants should result as predictions of the theory since no nonlinearities are introduced.

2. During years this naive and very rough vision has of course developed a lot and is not anymore quite equivalent with the original insight. In particular, the space-time correlates of Feynman graphs have emerged from theory as Euclidian space-time regions and the strong form of General Coordinate Invariance has led to a rather detailed and in many respects un-expected visions. This picture forces to give up the idea about smooth space-time surfaces and replace space-time surface with a generalization of Feynman diagram in which vertices represent the failure of manifold property. I have also startd introduced the word "world of classical worlds" (WCW) instead of rather formal "configuration space". I hope that "WCW" does not induce despair in the reader having tendency to think about the technicalities involved!

3. WCW is endowed with metric and spinor structure so that one can define various metric related differential operators, say Dirac operator, appearing in the field equations of the theory. The most ambitious dream is that zero energy states correspond to a complete solution basis for the Dirac operator of WCW so that this classical free field theory would dictate M-matrices which form orthonormal rows of what I call U-matrix. Given M-matrix in turn would decompose to a product of a hermitian density matrix and unitary S-matrix.

   M-matrix would define time-like entanglement coefficients between positive and negative energy parts of zero energy states (all net quantum numbers vanish for them) and can be regarded as a hermitian quare root of density matrix multiplied by a unitary S-matrix. Quantum theory would be in well-defined sense a square root of thermodynamics. The orthogonality and hermiticity of the complex square roots of density matrices commuting with S-matrix means that they span infinite-dimensional Lie algebra acting as symmetries of the S-matrix. Therefore quantum TGD would reduce to group theory in well-defined sense: its own symmetries would define the symmetries of the theory. In fact the Lie algebra of Hermitian M-matrices extends to Kac-Moody type algebra obtained by multiplying hermitian square roots of density matrices with powers of the S-matrix. Also the analog of Yangian algebra involving only non-negative powers of S-matrix is possible.

4. By quantum classical correspondence the construction of WCW spinor structure reduces to the second quantization of the induced spinor fields at space-time surface. The basic action is so called modified Dirac action in which gamma matrices are replaced with the modified gamma matrices defined as contractions of the canonical momentum currents with the imbedding space gamma matrices. In this manner one achieves super-conformal symmetry and conservation of fermionic currents among other things and consistent Dirac equation. This modified gamma matrices define as anticommutators effective metric, which might provide geometrization for some basic observables of condensed matter physics. The conjecture is that Dirac determinant for the modified Dirac action gives the exponent of Kähler action for a preferred extremal as vacuum functional so that one might talk about bosonic emergence in accordance with the prediction that the gauge bosons and graviton are expressible in terms of bound states of fermion and antifermion.

The evolution of these basic ideas has been rather slow but has gradually led to a rather beautiful vision. One of the key problems has been the definition of Kähler function. Kähler function is Kähler action for a preferred extremal assignable to a given 3-surface but what this preferred extremal is? The obvious first guess was as absolute minimum of Kähler action but could not be proven to be right or wrong. One big step in the progress was boosted by the idea that TGD should reduce to almost topological QFT in which braids wold replace 3-surfaces in finite measurement resolution, which could be inherent property of the theory itself and imply discretization at partonic 2-surfaces with discrete points carrying fermion number.

1. TGD as almost topological QFT vision suggests that Kähler action for preferred extremals reduces to Chern-Simons term assigned with space-like 3-surfaces at the ends of space-time (recall the notion of causal diamond (CD)) and with the light-like 3-surfaces at which the signature of the induced metric changes from Minkowskian to Euclidian. Minkowskian and

Euclidian regions would give at wormhole throats the same contribution apart from coefficients and in Minkowskian regions the $\sqrt{g_4}$ factor would be imaginary so that one would obtain sum of real term identifiable as Kähler function and imaginary term identifiable as the ordinary action giving rise to interference effects and stationary phase approximation central in both classical and quantum field theory. Imaginary contribution - the presence of which I realized only after 33 years of TGD - could also havetopological interpretation as a Morse function. On physical side the emergence of Euclidian space-time regions is something completely new and leads to a dramatic modification of the ideas about black hole interior.

2. The manner to achieve the reduction to Chern-Simons terms is simple. The vanishing of Coulombic contribution to Kähler action is required and is true for all known extremals if one makes a general ansatz about the form of classical conserved currents. The so called weak form of electric-magnetic duality defines a boundary condition reducing the resulting 3-D terms to Chern-Simons terms. In this manner almost topological QFT results. But only "almost" since the Lagrange multiplier term forcing electric-magnetic duality implies that Chern-Simons action for preferred extremals depends on metric.

3. A further quite recent hypothesis inspired by effective 2-dimensionality is that Chern-Simons terms reduce to a sum of two 2-dimensional terms. An imaginary term proportional to the total area of Minkowskian string world sheets and a real tem proportional to the total area of partonic 2-surfaces or equivalently strings world sheets in Euclidian space-time regions. Also the equality of the total areas of strings world sheets and partonic 2-surfaces is highly suggestive and would realize a duality between these two kinds of objects. String world sheets indeed emerge naturally for the proposed ansatz defining preferred extremals. Therefore Kähler action would have very stringy character apart from effects due to the failure of the strict determinism meaning that radiative corrections break the effective 2-dimensionality.

1.3.2 TGD as a generalized number theory

Quantum T(opological)D(ynamics) as a classical spinor geometry for infinite-dimensional configuration space, p-adic numbers and quantum TGD, and TGD inspired theory of consciousness, have been for last ten years the basic three strongly interacting threads in the tapestry of quantum TGD. The fourth thread deserves the name 'TGD as a generalized number theory'. It involves three separate threads: the fusion of real and various p-adic physics to a single coherent whole by requiring number theoretic universality discussed already, the formulation of quantum TGD in terms of hyper-counterparts of classical number fields identified as sub-spaces of complexified classical number fields with Minkowskian signature of the metric defined by the complexified inner product, and the notion of infinite prime.

p-Adic TGD and fusion of real and p-adiuc physics to single coherent whole

The p-adic thread emerged for roughly ten years ago as a dim hunch that p-adic numbers might be important for TGD. Experimentation with p-adic numbers led to the notion of canonical identification mapping reals to p-adics and vice versa. The breakthrough came with the successful p-adic mass calculations using p-adic thermodynamics for Super-Virasoro representations with the super-Kac-Moody algebra associated with a Lie-group containing standard model gauge group. Although the details of the calculations have varied from year to year, it was clear that p-adic physics reduces not only the ratio of proton and Planck mass, the great mystery number of physics, but all elementary particle mass scales, to number theory if one assumes that primes near prime powers of two are in a physically favored position. Why this is the case, became one of the key puzzless and led to a number of arguments with a common gist: evolution is present already at the elementary particle level and the primes allowed by the p-adic length scale hypothesis are the fittest ones.

It became very soon clear that p-adic topology is not something emerging in Planck length scale as often believed, but that there is an infinite hierarchy of p-adic physics characterized by p-adic length scales varying to even cosmological length scales. The idea about the connection of p-adics with cognition motivated already the first attempts to understand the role of the p-adics and inspired 'Universe as Computer' vision but time was not ripe to develop this idea to anything concrete (p-adic numbers are however in a central role in TGD inspired theory of consciousness). It became however

obvious that the p-adic length scale hierarchy somehow corresponds to a hierarchy of intelligences and that p-adic prime serves as a kind of intelligence quotient. Ironically, the almost obvious idea about p-adic regions as cognitive regions of space-time providing cognitive representations for real regions had to wait for almost a decade for the access into my consciousness.

There were many interpretational and technical questions crying for a definite answer.

1. What is the relationship of p-adic non-determinism to the classical non-determinism of the basic field equations of TGD? Are the p-adic space-time region genuinely p-adic or does p-adic topology only serve as an effective topology? If p-adic physics is direct image of real physics, how the mapping relating them is constructed so that it respects various symmetries? Is the basic physics p-adic or real (also real TGD seems to be free of divergences) or both? If it is both, how should one glue the physics in different number field together to get *The Physics*? Should one perform p-adicization also at the level of the configuration space of 3-surfaces? Certainly the p-adicization at the level of super-conformal representation is necessary for the p-adic mass calculations.

2. Perhaps the most basic and most irritating technical problem was how to precisely define p-adic definite integral which is a crucial element of any variational principle based formulation of the field equations. Here the frustration was not due to the lack of solution but due to the too large number of solutions to the problem, a clear symptom for the sad fact that clever inventions rather than real discoveries might be in question. Quite recently I however learned that the problem of making sense about p-adic integration has been for decades central problem in the frontier of mathematics and a lot of profound work has been done along same intuitive lines as I have proceeded in TGD framework. The basic idea is certainly the notion of algebraic continuation from the world of rationals belonging to the intersection of real world and various p-adic worlds.

Despite these frustrating uncertainties, the number of the applications of the poorly defined p-adic physics growed steadily and the applications turned out to be relatively stable so that it was clear that the solution to these problems must exist. It became only gradually clear that the solution of the problems might require going down to a deeper level than that represented by reals and p-adics.

The key challenge is to fuse various p-adic physics and real physics to single larger structures. This has inspired a proposal for a generalization of the notion of number field by fusing real numbers and various p-adic number fields and their extensions along rationals and possible common algebraic numbers. This leads to a generalization of the notions of imbedding space and space-time concept and one can speak about real and p-adic space-time sheets. The quantum dynamics should be such that it allows quantum transitions transforming space-time sheets belonging to different number fields to each other. The space-time sheets in the intersection of real and p-adic worlds are of special interest and the hypothesis is that living matter resides in this intersection. This leads to surprisingly detailed predictions and far reaching conjectures. For instance, the number theoretic generalization of entropy concept allows negentropic entanglement central for the applications to living matter.

The basic principle is number theoretic universality stating roughly that the physics in various number fields can be obtained as completion of rational number based physics to various number fields. Rational number based physics would in turn describe physics in finite measurement resolution and cognitive resolution. The notion of finite measurement resolution has become one of the basic principles of quantum TGD and leads to the notions of braids as representatives of 3-surfaces and inclusions of hyper-finite factors as a representation for finite measurement resolution.

The role of classical number fields

The vision about the physical role of the classical number fields relies on the notion of number theoretic compactifiction stating that space-time surfaces can be regarded as surfaces of either M^8 or $M^4 \times CP_2$. As surfaces of M^8 identifiable as space of hyper-octonions they are hyper-quaternionic or co-hyper-quaternionic- and thus maximally associative or co-associative. This means that their tangent space is either hyper-quaternionic plane of M^8 or an orthogonal complement of such a plane. These surface can be mapped in natural manner to surfaces in $M^4 \times CP_2$ [73] provided one can assign to each point of tangent space a hyper-complex plane $M^2(x) \subset M^4$. One can also speak about $M^8 - H$ duality.

This vision has very strong predictive power. It predicts that the extremals of Kähler action correspond to either hyper-quaternionic or co-hyper-quaternionic surfaces such that one can assign to tangent space at each point of space-time surface a hyper-complex plane $M^2(x) \subset M^4$. As a consequence, the M^4 projection of space-time surface at each point contains $M^2(x)$ and its orthogonal complement. These distributions are integrable implying that space-time surface allows dual slicings defined by string world sheets Y^2 and partonic 2-surfaces X^2. The existence of this kind of slicing was earlier deduced from the study of extremals of Kähler action and christened as Hamilton-Jacobi structure. The physical interpretation of $M^2(x)$ is as the space of non-physical polarizations and the plane of local 4-momentum.

One can fairly say, that number theoretical compactification is responsible for most of the understanding of quantum TGD that has emerged during last years. This includes the realization of Equivalence Principle at space-time level, dual formulations of TGD as Minkowskian and Euclidian string model type theories, the precise identification of preferred extremals of Kähler action as extremals for which second variation vanishes (at least for deformations representing dynamical symmetries) and thus providing space-time correlate for quantum criticality, the notion of number theoretic braid implied by the basic dynamics of Kähler action and crucial for precise construction of quantum TGD as almost-topological QFT, the construction of configuration space metric and spinor structure in terms of second quantized induced spinor fields with modified Dirac action defined by Kähler action realizing automatically the notion of finite measurement resolution and a connection with inclusions of hyper-finite factors of type II_1 about which Clifford algebra of configuration space represents an example.

The two most important number theoretic conjectures relate to the preferred extremals of Kähler action. The general idea is that classical dynamics for the preferred extremals of Kähler action should reduce to number theory: space-time surfaces should be either associative or co-associative in some sense.

1. The first meaning for associativity (co-associativity) would be that tangent (normal) spaces of space-time surfaces are quaternionic in some sense and thus associative. This can be formulated in terms of octonionic representation of the imbedding space gamma matrices possible in dimension $D = 8$ and states that induced gamma matrices generate quaternionic sub-algebra at each space-time point. It seems that induced rather than modified gamma matrices must be in question.

2. Second meaning for associative (co-associativity) would be following. In the case of complex numbers the vanishing of the real part of real-analytic function defines a 1-D curve. In octnionic case one can decompose octonion to sum of quaternion and quaternion multiplied by an octonionic imaginary unit. Quaternionicity could mean that space-time surfaces correspond to the vanishing of the imaginary part of the octonion real-analytic function. Co-quaternionicity would be defined in an obvious manner. Octonionic real analytic functions form a function field closed also with respect to the composition of functions. Space-time surfaces would form the analog of function field with the composition of functions with all operations realized as algebraic operations for space-time surfaces. Co-associaty could be perhaps seen as an additional feature making the algebra in question also co-algebra.

3. The third conjecture is that these conjectures are equivalent.

Infinite primes

The discovery of the hierarchy of infinite primes and their correspondence with a hierarchy defined by a repeatedly second quantized arithmetic quantum field theory gave a further boost for the speculations about TGD as a generalized number theory. The work with Riemann hypothesis led to further ideas.

After the realization that infinite primes can be mapped to polynomials representable as surfaces geometrically, it was clear how TGD might be formulated as a generalized number theory with infinite primes forming the bridge between classical and quantum such that real numbers, p-adic numbers, and various generalizations of p-adics emerge dynamically from algebraic physics as various completions of the algebraic extensions of rational (hyper-)quaternions and (hyper-)octonions. Complete algebraic, topological and dimensional democracy would characterize the theory.

What is especially satisfying is that p-adic and real regions of the space-time surface could emerge automatically as solutions of the field equations. In the space-time regions where the solutions of field equations give rise to in-admissible complex values of the imbedding space coordinates, p-adic solution can exist for some values of the p-adic prime. The characteristic non-determinism of the p-adic differential equations suggests strongly that p-adic regions correspond to 'mind stuff', the regions of space-time where cognitive representations reside. This interpretation implies that p-adic physics is physics of cognition. Since Nature is probably an extremely brilliant simulator of Nature, the natural idea is to study the p-adic physics of the cognitive representations to derive information about the real physics. This view encouraged by TGD inspired theory of consciousness clarifies difficult interpretational issues and provides a clear interpretation for the predictions of p-adic physics.

1.3.3 Hierarchy of Planck constants and dark matter hierarchy

By quantum classical correspondence space-time sheets can be identified as quantum coherence regions. Hence the fact that they have all possible size scales more or less unavoidably implies that Planck constant must be quantized and have arbitrarily large values. If one accepts this then also the idea about dark matter as a macroscopic quantum phase characterized by an arbitrarily large value of Planck constant emerges naturally as does also the interpretation for the long ranged classical electroweak and color fields predicted by TGD. Rather seldom the evolution of ideas follows simple linear logic, and this was the case also now. In any case, this vision represents the fifth, relatively new thread in the evolution of TGD and the ideas involved are still evolving.

Dark matter as large $\hbar$ phase

D. Da Rocha and Laurent Nottale [10] have proposed that Schrödinger equation with Planck constant $\hbar$ replaced with what might be called gravitational Planck constant $\hbar_{gr} = \frac{GmM}{v_0}$ ($\hbar = c = 1$). v_0 is a velocity parameter having the value $v_0 = 144.7 \pm .7$ km/s giving $v_0/c = 4.6 \times 10^{-4}$. This is rather near to the peak orbital velocity of stars in galactic halos. Also subharmonics and harmonics of v_0 seem to appear. The support for the hypothesis coming from empirical data is impressive.

Nottale and Da Rocha believe that their Schrödinger equation results from a fractal hydrodynamics. Many-sheeted space-time however suggests astrophysical systems are not only quantum systems at larger space-time sheets but correspond to a gigantic value of gravitational Planck constant. The gravitational (ordinary) Schrödinger equation would provide a solution of the black hole collapse (IR catastrophe) problem encountered at the classical level. The resolution of the problem inspired by TGD inspired theory of living matter is that it is the dark matter at larger space-time sheets which is quantum coherent in the required time scale [65] .

TGD predicts correctly the value of the parameter v_0 assuming that cosmic strings and their decay remnants are responsible for the dark matter. The harmonics of v_0 can be understood as corresponding to perturbations replacing cosmic strings with their n-branched coverings so that tension becomes n^2-fold: much like the replacement of a closed orbit with an orbit closing only after n turns. $1/n$-sub-harmonic would result when a magnetic flux tube split into n disjoint magnetic flux tubes. Also a model for the formation of planetary system as a condensation of ordinary matter around quantum coherent dark matter emerges [65] .

The values of Planck constants postulated by Nottale are gigantic and it is natural to assign them to the space-time sheets mediating gravitational interaction and identifiable as magnetic flux tubes (quanta). The magnetic energy of these flux quanta would correspond to dark energy and magnetic tension would give rise to negative "pressure" forcing accelerate cosmological expansion. This leads to a rather detailed vision about the evolution of stars and galaxies identified as bubbles of ordinary and dark matter inside magnetic flux tubes identifiable as dark energy.

Hierarchy of Planck constants from the anomalies of neuroscience biology

The quantal effects of ELF em fields on vertebrate brain have been known since seventies. ELF em fields at frequencies identifiable as cyclotron frequencies in magnetic field whose intensity is about 2/5 times that of Earth for biologically important ions have physiological effects and affect also behavior. What is intriguing that the effects are found only in vertebrates (to my best knowledge). The energies for the photons of ELF em fields are extremely low - about 10^{-10} times lower than thermal energy

at physiological temperatures- so that quantal effects are impossible in the framework of standard quantum theory. The values of Planck constant would be in these situations large but not gigantic.

This inspired the hypothesis that these photons correspond to so large value of Planck constant that the energy of photons is above the thermal energy. The proposed interpretation was as dark photons and the general hypothesis was that dark matter corresponds to ordinary matter with non-standard value of Planck constant. If only particles with the same value of Planck constant can appear in the same vertex of Feynman diagram, the phases with different value of Planck constant are dark relative to each other. The phase transitions changing Planck constant can however make possible interactions between phases with different Planck constant but these interactions do not manifest themselves in particle physics. Also the interactions mediated by classical fields should be possible. Dark matter would not be so dark as we have used to believe.

Also the anomalies of biology support the view that dark matter might be a key player in living matter.

Does the hierarchy of Planck constants reduce to the vacuum degeneracy of Kähler action?

This starting point led gradually to the recent picture in which the hierarchy of Planck constants is postulated to come as integer multiples of the standard value of Planck constant. Given integer multiple $\hbar = n\hbar_0$ of the ordinary Planck constant $\hbar_0$ is assigned with a multiple singular covering of the imbedding space [27]. One ends up to an identification of dark matter as phases with non-standard value of Planck constant having geometric interpretation in terms of these coverings providing generalized imbedding space with a book like structure with pages labelled by Planck constants or integers characterizing Planck constant. The phase transitions changing the value of Planck constant would correspond to leakage between different sectors of the extended imbedding space. The question is whether these coverings must be postulated separately or whether they are only a convenient auxiliary tool.

The simplest option is that the hierarchy of coverings of imbedding space is only effective. Many-sheeted coverings of the imbedding space indeed emerge naturally in TGD framework. The huge vacuum degeneracy of Kähler action implies that the relationship between gradients of the imbedding space coordinates and canonical momentum currents is many-to-one: this was the very fact forcing to give up all the standard quantization recipes and leading to the idea about physics as geometry of the "world of classical worlds". If one allows space-time surfaces for which all sheets corresponding to the same values of the canonical momentum currents are present, one obtains effectively many-sheeted covering of the imbedding space and the contributions from sheets to the Kähler action are identical. If all sheets are treated effectively as one and the same sheet, the value of Planck constant is an integer multiple of the ordinary one. A natural boundary condition would be that at the ends of space-time at future and past boundaries of causal diamond containing the space-time surface, various branches co-incide. This would raise the ends of space-time surface in special physical role.

Dark matter as a source of long ranged weak and color fields

Long ranged classical electro-weak and color gauge fields are unavoidable in TGD framework. The smallness of the parity breaking effects in hadronic, nuclear, and atomic length scales does not however seem to allow long ranged electro-weak gauge fields. The problem disappears if long range classical electro-weak gauge fields are identified as space-time correlates for massless gauge fields created by dark matter. Also scaled up variants of ordinary electro-weak particle spectra are possible. The identification explains chiral selection in living matter and unbroken $U(2)_{ew}$ invariance and free color in bio length scales become characteristics of living matter and of bio-chemistry and bio-nuclear physics. A possible solution of the matter antimatter asymmetry is based on the identification of also antimatter as dark matter.

1.3.4 TGD as a generalization of physics to a theory consciousness

General coordinate invariance forces the identification of quantum jump as quantum jump between entire deterministic quantum histories rather than time=constant snapshots of single history. The new view about quantum jump forces a generalization of quantum measurement theory such that

observer becomes part of the physical system. Thus a general theory of consciousness is unavoidable outcome. This theory is developed in detail in the books [75, 11, 55, 10, 32, 39, 42, 67] .

Quantum jump as a moment of consciousness

The identification of quantum jump between deterministic quantum histories (configuration space spinor fields) as a moment of consciousness defines microscopic theory of consciousness. Quantum jump involves the steps

$$\Psi_i \to U\Psi_i \to \Psi_f \ ,$$

where U is informational "time development" operator, which is unitary like the S-matrix characterizing the unitary time evolution of quantum mechanics. U is however only formally analogous to Schrödinger time evolution of infinite duration although there is *no* real time evolution involved. It is not however clear whether one should regard U-matrix and S-matrix as two different things or not: U-matrix is a completely universal object characterizing the dynamics of evolution by self-organization whereas S-matrix is a highly context dependent concept in wave mechanics and in quantum field theories where it at least formally represents unitary time translation operator at the limit of an infinitely long interaction time. The S-matrix understood in the spirit of superstring models is however something very different and could correspond to U-matrix.

The requirement that quantum jump corresponds to a measurement in the sense of quantum field theories implies that each quantum jump involves localization in zero modes which parameterize also the possible choices of the quantization axes. Thus the selection of the quantization axes performed by the Cartesian outsider becomes now a part of quantum theory. Together these requirements imply that the final states of quantum jump correspond to quantum superpositions of space-time surfaces which are macroscopically equivalent. Hence the world of conscious experience looks classical. At least formally quantum jump can be interpreted also as a quantum computation in which matrix U represents unitary quantum computation which is however not identifiable as unitary translation in time direction and cannot be 'engineered'.

The notion of self

The concept of self is absolutely essential for the understanding of the macroscopic and macro-temporal aspects of consciousness. Self corresponds to a subsystem able to remain un-entangled under the sequential informational 'time evolutions' U. Exactly vanishing entanglement is practically impossible in ordinary quantum mechanics and it might be that 'vanishing entanglement' in the condition for self-property should be replaced with 'subcritical entanglement'. On the other hand, if space-time decomposes into p-adic and real regions, and if entanglement between regions representing physics in different number fields vanishes, space-time indeed decomposes into selves in a natural manner.

It is assumed that the experiences of the self after the last 'wake-up' sum up to single average experience. This means that subjective memory is identifiable as conscious, immediate short term memory. Selves form an infinite hierarchy with the entire Universe at the top. Self can be also interpreted as mental images: our mental images are selves having mental images and also we represent mental images of a higher level self. A natural hypothesis is that self S experiences the experiences of its subselves as kind of abstracted experience: the experiences of subselves S_i are not experienced as such but represent kind of averages $\langle S_{ij} \rangle$ of sub-subselves S_{ij}. Entanglement between selves, most naturally realized by the formation of join along boundaries bonds between cognitive or material space-time sheets, provides a possible a mechanism for the fusion of selves to larger selves (for instance, the fusion of the mental images representing separate right and left visual fields to single visual field) and forms wholes from parts at the level of mental images.

An attractive possibility suggested by zero energy ontology is that the notions of self and quantum jump reduce to each other and that a fractal hierarchy of quantum jumps within quantum jumps is enough. CDs would serve as imbedding space correlates of selves and quantum jumps would be followed by cascades of state function reductions beginning from given CD and proceeding downwards to the smaller scales (smaller CDs). State function reduction cascades could also take place in parallel branches of the quantum state. One ends up with concrete ideas about how the arrow of geometric time is induced from that of subjective time defined by the experiences induced by the sequences of quantum jumps for sub-selves of self. One ends also ends up with concrete ideas about how the

localization of the contents of sensory experience and cognition to the upper boundaries of CD could take place.

Relationship to quantum measurement theory

The third basic element relates TGD inspired theory of consciousness to quantum measurement theory. The assumption that localization occurs in zero modes in each quantum jump implies that the world of conscious experience looks classical. It also implies the state function reduction of the standard quantum measurement theory as the following arguments demonstrate (it took incredibly long time to realize this almost obvious fact!).

1. The standard quantum measurement theory a la von Neumann involves the interaction of brain with the measurement apparatus. If this interaction corresponds to entanglement between microscopic degrees of freedom m with the macroscopic effectively classical degrees of freedom M characterizing the reading of the measurement apparatus coded to brain state, then the reduction of this entanglement in quantum jump reproduces standard quantum measurement theory provide the unitary time evolution operator U acts as flow in zero mode degrees of freedom and correlates completely some orthonormal basis of configuration space spinor fields in non-zero modes with the values of the zero modes. The flow property guarantees that the localization is consistent with unitarity: it also means 1-1 mapping of quantum state basis to classical variables (say, spin direction of the electron to its orbit in the external magnetic field).

2. Since zero modes represent classical information about the geometry of space-time surface (shape, size, classical Kähler field,...), they have interpretation as effectively classical degrees of freedom and are the TGD counterpart of the degrees of freedom M representing the reading of the measurement apparatus. The entanglement between quantum fluctuating non-zero modes and zero modes is the TGD counterpart for the $m-M$ entanglement. Therefore the localization in zero modes is equivalent with a quantum jump leading to a final state where the measurement apparatus gives a definite reading.

This simple prediction is of utmost theoretical importance since the black box of the quantum measurement theory is reduced to a fundamental quantum theory. This reduction is implied by the replacement of the notion of a point like particle with particle as a 3-surface. Also the infinite-dimensionality of the zero mode sector of the configuration space of 3-surfaces is absolutely essential. Therefore the reduction is a triumph for quantum TGD and favors TGD against string models.

Standard quantum measurement theory involves also the notion of state preparation which reduces to the notion of self measurement. Each localization in zero modes is followed by a cascade of self measurements leading to a product state. This process is obviously equivalent with the state preparation process. Self measurement is governed by the so called Negentropy Maximization Principle (NMP) stating that the information content of conscious experience is maximized. In the self measurement the density matrix of some subsystem of a given self localized in zero modes (after ordinary quantum measurement) is measured. The self measurement takes place for that subsystem of self for which the reduction of the entanglement entropy is maximal in the measurement. In p-adic context NMP can be regarded as the variational principle defining the dynamics of cognition. In real context self measurement could be seen as a repair mechanism allowing the system to fight against quantum thermalization by reducing the entanglement for the subsystem for which it is largest (fill the largest hole first in a leaking boat).

Selves self-organize

The fourth basic element is quantum theory of self-organization based on the identification of quantum jump as the basic step of self-organization [62] . Quantum entanglement gives rise to the generation of long range order and the emergence of longer p-adic length scales corresponds to the emergence of larger and larger coherent dynamical units and generation of a slaving hierarchy. Energy (and quantum entanglement) feed implying entropy feed is a necessary prerequisite for quantum self-organization. Zero modes represent fundamental order parameters and localization in zero modes implies that the sequence of quantum jumps can be regarded as hopping in the zero modes so that Haken's classical theory of self organization applies almost as such. Spin glass analogy is a further important element:

self-organization of self leads to some characteristic pattern selected by dissipation as some valley of the "energy" landscape.

Dissipation can be regarded as the ultimate Darwinian selector of both memes and genes. The mathematically ugly irreversible dissipative dynamics obtained by adding phenomenological dissipation terms to the reversible fundamental dynamical equations derivable from an action principle can be understood as a phenomenological description replacing in a well defined sense the series of reversible quantum histories with its envelope.

Classical non-determinism of Kähler action

The fifth basic element are the concepts of association sequence and cognitive space-time sheet. The huge vacuum degeneracy of the Kähler action suggests strongly that the absolute minimum space-time is not always unique. For instance, a sequence of bifurcations can occur so that a given space-time branch can be fixed only by selecting a finite number of 3-surfaces with time like(!) separations on the orbit of 3-surface. Quantum classical correspondence suggest an alternative formulation. Space-time surface decomposes into maximal deterministic regions and their temporal sequences have interpretation a space-time correlate for a sequence of quantum states defined by the initial (or final) states of quantum jumps. This is consistent with the fact that the variational principle selects preferred extremals of Kähler action as generalized Bohr orbits.

In the case that non-determinism is located to a finite time interval and is microscopic, this sequence of 3-surfaces has interpretation as a simulation of a classical history, a geometric correlate for contents of consciousness. When non-determinism has long lasting and macroscopic effect one can identify it as volitional non-determinism associated with our choices. Association sequences relate closely with the cognitive space-time sheets defined as space-time sheets having finite time duration and psychological time can be identified as a temporal center of mass coordinate of the cognitive space-time sheet. The gradual drift of the cognitive space-time sheets to the direction of future force by the geometry of the future light cone explains the arrow of psychological time.

p-Adic physics as physics of cognition and intentionality

The sixth basic element adds a physical theory of cognition to this vision. TGD space-time decomposes into regions obeying real and p-adic topologies labelled by primes $p = 2, 3, 5, ...$ p-Adic regions obey the same field equations as the real regions but are characterized by p-adic non-determinism since the functions having vanishing p-adic derivative are pseudo constants which are piecewise constant functions. Pseudo constants depend on a finite number of positive pinary digits of arguments just like numerical predictions of any theory always involve decimal cutoff. This means that p-adic space-time regions are obtained by gluing together regions for which integration constants are genuine constants. The natural interpretation of the p-adic regions is as cognitive representations of real physics. The freedom of imagination is due to the p-adic non-determinism. p-Adic regions perform mimicry and make possible for the Universe to form cognitive representations about itself. p-Adic physics space-time sheets serve also as correlates for intentional action.

A more more precise formulation of this vision requires a generalization of the number concept obtained by fusing reals and p-adic number fields along common rationals (in the case of algebraic extensions among common algebraic numbers). This picture is discussed in [72] . The application this notion at the level of the imbedding space implies that imbedding space has a book like structure with various variants of the imbedding space glued together along common rationals (algebraics). The implication is that genuinely p-adic numbers (non-rationals) are strictly infinite as real numbers so that most points of p-adic space-time sheets are at real infinity, outside the cosmos, and that the projection to the real imbedding space is discrete set of rationals (algebraics). Hence cognition and intentionality are almost completely outside the real cosmos and touch it at a discrete set of points only.

This view implies also that purely local p-adic physics codes for the p-adic fractality characterizing long range real physics and provides an explanation for p-adic length scale hypothesis stating that the primes $p \simeq 2^k$, k integer are especially interesting. It also explains the long range correlations and short term chaos characterizing intentional behavior and explains why the physical realizations of cognition are always discrete (say in the case of numerical computations). Furthermore, a concrete quantum model for how intentions are transformed to actions emerges.

The discrete real projections of p-adic space-time sheets serve also space-time correlate for a logical thought. It is very natural to assign to p-adic pinary digits a p-valued logic but as such this kind of logic does not have any reasonable identification. p-Adic length scale hypothesis suggest that the $p = 2^k - n$ pinary digits represent a Boolean logic B^k with k elementary statements (the points of the k-element set in the set theoretic realization) with n taboos which are constrained to be identically true.

p-Adic and dark matter hierarchies and hierarchy of moments of consciousness

Dark matter hierarchy assigned to a spectrum of Planck constant having arbitrarily large values brings additional elements to the TGD inspired theory of consciousness.

1. Macroscopic quantum coherence can be understood since a particle with a given mass can in principle appear as arbitrarily large scaled up copies (Compton length scales as $\hbar$). The phase transition to this kind of phase implies that space-time sheets of particles overlap and this makes possible macroscopic quantum coherence.

2. The space-time sheets with large Planck constant can be in thermal equilibrium with ordinary ones without the loss of quantum coherence. For instance, the cyclotron energy scale associated with EEG turns out to be above thermal energy at room temperature for the level of dark matter hierarchy corresponding to magnetic flux quanta of the Earth's magnetic field with the size scale of Earth and a successful quantitative model for EEG results [23] .

Dark matter hierarchy leads to detailed quantitative view about quantum biology with several testable predictions [23] . The general prediction is that Universe is a kind of inverted Mandelbrot fractal for which each bird's eye of view reveals new structures in long length and time scales representing scaled down copies of standard physics and their dark variants. These structures would correspond to higher levels in self hierarchy. This prediction is consistent with the belief that 75 per cent of matter in the universe is dark.

1. Living matter and dark matter

Living matter as ordinary matter quantum controlled by the dark matter hierarchy has turned out to be a particularly successful idea. The hypothesis has led to models for EEG predicting correctly the band structure and even individual resonance bands and also generalizing the notion of EEG [23] . Also a generalization of the notion of genetic code emerges resolving the paradoxes related to the standard dogma [41, 23] . A particularly fascinating implication is the possibility to identify great leaps in evolution as phase transitions in which new higher level of dark matter emerges [23] .

It seems safe to conclude that the dark matter hierarchy with levels labelled by the values of Planck constants explains the macroscopic and macro-temporal quantum coherence naturally. That this explanation is consistent with the explanation based on spin glass degeneracy is suggested by following observations. First, the argument supporting spin glass degeneracy as an explanation of the macro-temporal quantum coherence does not involve the value of $\hbar$ at all. Secondly, the failure of the perturbation theory assumed to lead to the increase of Planck constant and formation of macroscopic quantum phases could be precisely due to the emergence of a large number of new degrees of freedom due to spin glass degeneracy. Thirdly, the phase transition increasing Planck constant has concrete topological interpretation in terms of many-sheeted space-time consistent with the spin glass degeneracy.

2. Dark matter hierarchy and the notion of self

The vision about dark matter hierarchy leads to a more refined view about self hierarchy and hierarchy of moments of consciousness [22, 23] . The larger the value of Planck constant, the longer the subjectively experienced duration and the average geometric duration $T(k) \propto \hbar$ of the quantum jump.

Quantum jumps form also a hierarchy with respect to p-adic and dark hierarchies and the geometric durations of quantum jumps scale like $\hbar$. Dark matter hierarchy suggests also a slight modification of the notion of self. Each self involves a hierarchy of dark matter levels, and one is led to ask whether the highest level in this hierarchy corresponds to single quantum jump rather than a sequence of quantum jumps. The averaging of conscious experience over quantum jumps would occur only for

sub-selves at lower levels of dark matter hierarchy and these mental images would be ordered, and single moment of consciousness would be experienced as a history of events. The quantum parallel dissipation at the lower levels would give rise to the experience of flow of time. For instance, hadron as a macro-temporal quantum system in the characteristic time scale of hadron is a dissipating system at quark and gluon level corresponding to shorter p-adic time scales. One can ask whether even entire life cycle could be regarded as a single quantum jump at the highest level so that consciousness would not be completely lost even during deep sleep. This would allow to understand why we seem to know directly that this biological body of mine existed yesterday.

The fact that we can remember phone numbers with 5 to 9 digits supports the view that self corresponds at the highest dark matter level to single moment of consciousness. Self would experience the average over the sequence of moments of consciousness associated with each sub-self but there would be no averaging over the separate mental images of this kind, be their parallel or serial. These mental images correspond to sub-selves having shorter wake-up periods than self and would be experienced as being time ordered. Hence the digits in the phone number are experienced as separate mental images and ordered with respect to experienced time.

3. The time span of long term memories as signature for the level of dark matter hierarchy

The basic question is what time scale can one assign to the geometric duration of quantum jump measured naturally as the size scale of the space-time region about which quantum jump gives conscious information. This scale is naturally the size scale in which the non-determinism of quantum jump is localized. During years I have made several guesses about this time scales but zero energy ontology and the vision about fractal hierarchy of quantum jumps within quantum jumps leads to a unique identification.

Causal diamond as an imbedding space correlate of self defines the time scale τ for the space-time region about which the consciousness experience is about. The temporal distances between the tips of CD as come as integer multiples of CP_2 length scales and for prime multiples correspond to what I have christened as secondary p-adic time scales. A reasonable guess is that secondary p-adic time scales are selected during evolution and the primes near powers of two are especially favored. For electron, which corresponds to Mersenne prime $M_{127} = 2^{127} - 1$ this scale corresponds to .1 seconds defining the fundamental time scale of living matter via 10 Hz biorhythm (alpha rhythm). The unexpected prediction is that all elementary particles correspond to time scales possibly relevant to living matter.

Dark matter hierarchy brings additional finesse. For the higher levels of dark matter hierarchy τ is scaled up by $\hbar/\hbar_0$. One could understand evolutionary leaps as the emergence of higher levels at the level of individual organism making possible intentionality and memory in the time scale defined τ.

Higher levels of dark matter hierarchy provide a neat quantitative view about self hierarchy and its evolution. Various levels of dark matter hierarchy would naturally correspond to higher levels in the hierarchy of consciousness and the typical duration of life cycle would give an idea about the level in question. The level would determine also the time span of long term memories as discussed in [23] . The emergence of these levels must have meant evolutionary leap since long term memory is also accompanied by ability to anticipate future in the same time scale. This picture would suggest that the basic difference between us and our cousins is not at the level of genome as it is usually understood but at the level of the hierarchy of magnetic bodies [41, 23]. In fact, higher levels of dark matter hierarchy motivate the introduction of the notions of super-genome and hyper-genome. The genomes of entire organ can join to form super-genome expressing genes coherently. Hyper-genomes would result from the fusion of genomes of different organisms and collective levels of consciousness would express themselves via hyper-genome and make possible social rules and moral.

1.4 Bird's eye of view about the topics of the book

The topics of this book relate to DNA and genetic code in several manners.

1. The oldest layers in the stratigraphy are the vision about DNA inspired by the notion of many-sheeted space-time and the model of genetic code inspired by the notion of Combinatorial Hierarchy predicting also the existence of what I have called memetic code. Additional number

theoretical models of genetic code based on p-adic thermodynamics for small p-adic primes and maximization of entropy or negentropy emerged much later. One must however admit that although these models reproduce the genetic code they fail to predict it. Models also fail also to make interesting predictions.

2. The almost exact symmetries of the code table with respect to the first letter lead to the proposal that the genetic code could has evolved from a simpler code involving only two letters and this leads to concrete suggestion about how the genetic code might have evolved as a fusion of two letter code and single letter code. These symmetries were also an essential element of number theoretical models.

3. The work with a model of topological quantum computation inspired by the vision about dark matter hierarchy and the idea that genome and cell membrane act as topological quantum computer generated several new chapters. The magnetic flux tubes as carriers of dark matter characterized by a large value of Planck constant would make living matter a macroscopic quantum system. DNA nucleotides and lipids of the cell membrane would be connected by magnetic flux tubes and the flow of the 2-D liquid formed by lipids induces braiding of flux tubes providing both temporal dynamics defining topological quantum computation and a storage of the program to memory by the braiding of flux tubes in the final state.

4. This model led to a cascade of ideas about quantum control in living matter. Quite generally, magnetic flux tubes would make living matter kind of Indra's net explaining the strange features of gel phase. For instance, the phase transitions changing Planck constant inducing a contraction or lengthening of the flux tubes would explain why bio-molecules are able to find each other extremely selectively in the dense soup of bio-molecules inside cell. The anomalies related to ionic currents find an explanation and a model of nerve pulse and EEG emerges along these lines.

5. The discoveries of Peter Gariaev about the interaction of ordinary and laser light with genome combined with the ideas about dark matter and water memory led to a concrete model for the interaction of photons with DNA. One prediction is that it is possible to "see" dark matter by allowing ordinary matter interaction with DNA and Peter Gariaev might have already done this. In this process ordinary photons would transform to dark ones, scatter from dark matter, transform back to ordinary photons and arrive at camera. A second discovery - certainly one of the greatest surprises of my professional life - was an end product of an attempt to understand the mechanism behind water memory for which rather strong support exists now. The idea was that dark nuclei which sizes zoomed up to atomic size scale could provide a representation of genes. It indeed turned out that the model for dark nucleon consisting of three quarks predicts counterparts of 64 DNAs and RNAs and 20 aminoacids and allows to identify genetic code as a natural mapping of DNA type states to aminoacid type states. The numbers of DNAs mapped to a given aminoacid are same as for the vertebrate genetic code. This would mean that genetic code would be realized at the level of elementary particle physics and chemical realization would be only one of the many. In fact, the quite recent experimental discoveries suggest that this kind of representation must exist besides the representation based on the temporal patterns of polarization direction discovered by Gariaev.

The topics of the book are organized as follows.

1. In the first part of the book I will discuss the new physics relevant to biology suggested by TGD and consider a general model for how TGD Universe could act as topological quantum computer.

2. In the second part of the book the idea that there exists a hierarchy of codes based on the notion of Combinatorial Hierarchy is discussed. The hierarchy would contain at least three levels including predecessor of genetic code, genetic code, and what I have coined as memetic code. The chapter devoted to the notion of many-sheeted DNA represents rather old contributions. The remaining chapters are devoted to the model of DNA as topological quantum computer and the ideas inspired by this work. This includes a model of protein folding and biocatalysis, a model for evolution in many-sheeted space-time, and a model for the above mentioned Gariaev's

findings. The model for nucleon predicting correctly vertebrate genetic code is certainly the most fascinating predictions of this line of approach.

3. The third part of the book is devoted to the number theoretical models of the genetic code.

The seven online books about TGD [80, 60, 49, 47, 61, 70, 68] and eight online books about TGD inspired theory of consciousness and quantum biology [75, 11, 55, 10, 32, 39, 42, 67] are warmly recommended for the reader willing to get overall view about what is involved.

1.5 The contents of the book

1.5.1 PART I: SOME PHYSICAL AND MATHEMATICAL BACKGROUND

About the New Physics Behind Qualia

This chapter was originally about the new physics behind qualia. The model of qualia indeed involves a lot of new physics: many-sheeted space-time; massless extremals; exotic Super Virasoro representations associated with discrete qualia; magnetic and cyclotron phase transitions associated with quantum critical quantum spin glass phases of exotic super conductors at cellular space-time sheets; classical color and electro-weak gauge fields in macroscopic length scales, to name the most important ingredients. Gradually the chapter however expanded so that it touches practically all new physics possibly relevant to TGD inspired quantum biology. Various physical mechanisms are discussed in exploratory spirit rather than restricting the consideration to those ideas which seem to be the final word about quantum biology or qualia just at this moment.

Topological Quantum Computation in TGD Universe

Topological quantum computation (TQC) is one of the most promising approaches to quantum computation. The coding of logical qubits to the entanglement of topological quantum numbers promises to solve the de-coherence problem whereas the S-matrices of topological field theories (modular functors) providing unitary representations for braids provide a realization of quantum computer programs with gates represented as simple braiding operations. Because of their effective 2-dimensionality anyon systems are the best candidates for realizing the representations of braid groups.

TGD allows several new insights related to quantum computation. TGD predicts new information measures as number theoretical negative valued entanglement entropies defined for systems having extended rational entanglement and characterizes bound state entanglement as bound state entanglement. Negentropy Maximization Principle and p-adic length scale hierarchy of space-time sheets encourage to believe that Universe itself might do its best to resolve the de-coherence problem. The new view about quantum jump suggests strongly the notion of quantum parallel dissipation so that thermalization in shorter length scales would guarantee coherence in longer length scales. The possibility of negative energies and communications to geometric future in turn might trivialize the problems caused by long computation times: computation could be iterated again and again by turning the computer on in the geometric past and TGD inspired theory of consciousness predicts that something like this occurs routinely in living matter.

The absolute minimization of Kähler action is the basic variational principle of classical TGD and predicts extremely complex but non-chaotic magnetic flux tube structures, which can get knotted and linked. The dimension of CP_2 projection for these structures is $D = 3$. These structures are the corner stone of TGD inspired theory of living matter and provide the braid structures needed by TQC.

Anyons are the key actors of TQC and TGD leads to detailed model of anyons as systems consisting of track of a periodically moving charged particle realized as a flux tube containing the particle inside it. This track would be a space-time correlate for the outcome of dissipative processes producing the asymptotic self-organization pattern. These tracks in general carry vacuum Kähler charge which is topologized when the CP_2 projection of space-time sheet is $D = 3$. This explains charge fractionization predicted to occur also for other charged particles. When a system approaches chaos periodic orbits become slightly aperiodic and the correlate is flux tube which rotates N times before closing. This gives rise to Z_N valued topological quantum number crucial for TQC using anyons ($N = 4$ holds true in this case). Non-Abelian anyons are needed by TQC, and the existence of long range classical electro-weak fields predicted by TGD is an essential prerequisite of non-Abelianity.

Negative energies and zero energy states are of crucial importance of TQC in TGD. The possibility of phase conjugation for fermions would resolve the puzzle of matter-antimatter asymmetry in an elegant manner. Anti-fermions would be present but have negative energies. Quite generally, it is possible to interpret scattering as a creation of pair of positive and negative energy states, the latter representing the final state. One can characterize precisely the deviations of this Eastern world view with respect to the Western world view assuming an objective reality with a positive definite energy and understand why the Western illusion apparently works. In the case of TQC the initial *resp.* final state of braided anyon system would correspond to positive *resp.* negative energy state.

The light-like boundaries of magnetic flux tubes are ideal for TQC. The point is that 3-dimensional light-like quantum states can be interpreted as representations for the time evolution of a two-dimensional system and thus represented self-reflective states being "about something". The light-likeness (no geometric time flow) is a space-time correlate for the ceasing of subjective time flow during macro-temporal quantum coherence. The S-matrices of TQC can be coded to these light-like states such that each elementary braid operation corresponds to positive energy anyons near the boundary of the magnetic flux tube A and negative energy anyons with opposite topological charges residing near the boundary of flux tube B and connected by braided threads representing the quantum gate. Light-like boundaries also force Chern-Simons action as the only possible general coordinate invariant action since the vanishing of the metric determinant does not allow any other candidate. Chern-Simons action indeed defines the modular functor for braid coding for a TQC program.

The comparison of the concrete model for TQC in terms of magnetic flux tubes with the structure of DNA gives tantalizing hints that DNA double strand is a topological quantum computer. Strand *resp.* conjugate strand would carry positive *resp.* negative energy anyon systems. The knotting and linking of DNA double strand would code for 2-gates realized as a unique maximally entangling Yang-Baxter matrix R for 2-state system. The pairs A-T, T-A, C-G, G-C in active state would code for the four braid operations of 3-braid group in 1-qubit Temperley Lieb representation associated with quantum group $SL(2)_q$. On basis of this picture one can identify N-O hydrogen bonds between DNA strands as structural correlates of 3-braids responsible for the nontrivial 1-gates whereas N-N hydrogen bonds would be correlates for the return gates acting as identity gates. Depending on whether the nucleotide is active or not it codes for nontrivial 1-gate or for identity gate so that DNA strand can program itself or be programmed dynamically.

1.5.2 PART II: PHYSICS INSPIRED MODELS FOR GENOME AND EVOLUTION OF GENETIC CODE

Genes and Memes

In this article basic TGD inspired ideas about genetic code are discussed.

1. Genetic and memetic code from the model of abstraction process

The basic numbers of genetic code are probably not accidental. This led for more than ten years ago to an attempt to construct a model for abstraction process reproducing the basic numbers of the genetic code. The simplest model for an abstraction process is based on a repeated formation of statements about statements starting from two basic statements. If one drops at each step of the construction the statement corresponding to empty set in the set theoretic realization of Boolean algebra, one obtains a hierarchy allowing to understand the basic numbers of genetic code, including the number of amino-acids. What one obtains is so called Combinatorial Hierarchy consisting of the Mersenne numbers $2, M(1) = 3, 7$,$127, 2^{127} - 1, ..$ constructed using the rule $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$. The explicitly listed ones are known to be primes. Combinatorial Hierarchy emerges from a model of abstraction process as subsequent transitions from level to meta level by forming Boolean statements about Boolean statements of level n and dropping one statement away.

The infinite hierarchy of possible genetic codes suggests the possibility of an infinite hierarchy of increasingly complex life-forms. The natural question is whether a counterpart of the genetic code could make sense for our ideas, memes. Combinatorial Hierarchy model for abstraction process predicts that memetic code should correspond to the level M_{127} of the hierarchy. This leads to a precise realization of the memetic code in terms of binary sequences. Codewords, counterparts of mRNA, correspond to 126-bit sequences. Also almost-127-bit code with $2^{127} - 1$ codons is possible.

2. Frequency and pulse representations of codes

p-Adic length scale hypothesis and identification of codes as special cases of a hierarchy of p-adic

cognitive codes allows quantitative predictions. The most general assumption assigns to any prime $p \simeq 2^k$, k integer, a hierarchy of cognitive codes with codeword having a duration equal to n-ary p-adic time scale $T_p(n)$ such that the number of bits is factor k_1 of k. Codewords could be realized either as k_1 harmonics of the fundamental frequency $f_p(n) = 1/T_p(n)$ or as temporal sequences of bits of duration $\tau = T_p(n)/k_1$ represented as pulses of maximal duration τ. Pulse-frequency dichotomy corresponds to dichotomies like particle-wave, nerve pulse-EEG, and talking left brain-singing right brain.

Genetic code would correspond to $k = 2^7 - 1 = 127$ and have 6 bits (64 DNA triplets). These codewords could be realized dynamically as temporal field patterns. For genetic code primes $p \simeq 2^k$, $k = 6 \times n$ define candidates for the duration of the genetic code word if all factors of k are assumed to define a possible number of bits of the code word. The time scales come as powers of 8 so that they cover the entire range of biologically relevant time scales down to CP_2 length scale, and genetic code could appear as fractally scaled versions unlike memetic code and perhaps also outside the biological context. $k = 2 \times 126 = 2 \times 6 \times 21 = 252$ allows the representation of both 126-bit memetic codeword, 6-bit genetic codeword, and almost-7-bit genetic code word. For pulse representation genetic codon would have a duration of 50 ms whereas the bit would have duration of 8.3 ms so that the realization using nerve pulse patterns is in principle possible. Frequency representation would be realized as 6 first harmonics of the fundamental frequency $f_1 = 2^n \times 20$ Hz, where $f_1 = 20$ Hz defines the lower end of audible frequency range and also the rate for the translation of mRNA triplets to amino-acids. 126-bit memetic code allows a representation as sequence of 21 nerve pulses of duration 2.4 ms each of them accompanied by 6-bit genetic codon realized at the microtubular level (this representation of genetic code has been suggested by Koruga).

The secondary p-adic time scale associated with M_{127} is .1 seconds and defines the duration of the almost 127-bit memetic codeword. For frequency representation is realized as 127 first harmonics of $f_1 = 10$ Hz and the duration of the bit for pulse representation is .8 ms which is shorter than the duration of nerve pulse. The duration .1 seconds of code word might be identified as the minimal duration of cortical mental images, and the so called features introduced by Walter Freeman could define pulse representation of memetic code words of 127 bits. The highest frequency in the frequency representation is 1270 Hz and could define the frequency responsible for synchronous neuronal firing known to be about 1 kHz. Various numerical co-incidences suggest that language corresponds to a particular realization of memetic and genetic codes closely related to their realization at DNA level.

3. Model for the evolution of genetic code from the symmetries of the code

TGD leads to a model for the evolution of the genetic code motivated by the observation that the genetic code possesses an exact A-G and almost exact T-C permutation symmetry with respect to the third nucleotide of the DNA triplet. This leads to the hypothesis that genetic code has evolved as a fusion of doublet and singlet codes accompanied by a small breaking of the product symmetry. The hypothesis is highly predictive, and it is possible to reproduce genetic code and its variants by this mechanism in a natural manner. The mechanism has deep implications for the models of the bio-chemical evolution before genetic code: in particular a detailed model for the evolution of genetic code and pre-biotic evolution emerges.

4. Mapping memetic code to 169-bit micro-tubular code

169-bit micro-tubular code words is excellent candidate for a representation of long term memories as a temporal list of activated memes. The model for the mapping of memetic code to 169-bit microtubular code is dictated by the general ideas about realization of intentions and p-adic cognitive codes. When combined with general number theoretical arguments and physical considerations the model becomes highly unique. The prediction for the intronic representation of the memetic codon involving 9 DNA triplets as parity bits is readily testable, and also the prediction for the microtubular electric field pattern is in principle testable.

5. Genes, memes, and universal language

Also static representations of the memetic code are possible and intronic DNA could provide representation of memetic codewords as sequences of 21 DNA triplets. At DNA level memes and genes should relate like computer software and hardware. In the case of language the rules producing a given linguistic expression can be seen as the high level software, main programs, whereas words can be seen as hardware-like lower level subprograms. This leads to the idea that memetic codewords define the basic program modules producing linguistic expressions by activating genes which express themselves in terms of field patterns generating nerv pulse patterns generating words or word sequences very much analogous to proteins.

Time mirror mechanism and the structure of the computer language LISP inspire a concrete model for memes as intronic programs initiated from magnetic body and calling genes as subprograms in turn calling other genes as subprograms and generating at the lowest level field patterns generating nerve pulses patterns giving rise to the motor action producing speech. Phonemes could directly correspond to DNA triplets and define the basic building blocks of language having as such no meaning. If this view is correct, the development of spoken and written language would mean basically the emergence of a higher level of intentionality, which utilizes an already existing repertoire of memes expressed in many other manners. This would in turn suggest that animals and even plants possess some kind of languages realized at cellular level, and that even inter-species communications using common memetic grammar and genetic vocabulary.

6. Corals and men

A strong support for the idea of interspecies communications come from the sensational finding that the genome of corals, known to be the most primitive animals having nervous system, share a large number of common genes with vertebrates whereas they share much less common genes with flies and worms. This finding challenges profoundly the existing view about the evolution of animals and adds a further mystery to the halo of mysteries surrounding Cambrian explosion.

Since corals are usually regarded as relatively simple creatures, the most obvious questions concern the function of the complex genome. The TGD inspired answer is that the common genes provide a common vocabulary making possible communications between corals and vertebrates such as fishes. The genes express themselves in terms of electromagnetic field patterns and cyclotron transitions of Ca_{++} ions giving rise to primitive EEG are crucially involved. The calcium containing skeleton possessed by both corals and vertebrates could amplify the field patterns representing genes and make possible interspecies communications.

Coral reefs can be also seen as super organisms with cells replaced by double cell layers forming the corals. This forces to consider the possibility that coral reefs are super-organisms perhaps even possessing super-neural system consisting of super-neurons defined by differentiated corals. Accordingly, in TGD Universe coral reefs could be seen as descendants of higher level intra-terrestrial life forms which boosted Cambrian explosion by horizontal transfer of genes to much simpler life forms and providing also them with a nervous system.

7. Does ontogeny recapitulate also the future phylogeny at the level of genes and memes?

Ontogeny recapitulates phylogeny means that the morphogenesis of the embryo repeats the evolutionary steps leading to the organism. One might ask whether and how this process is realized at the level of genes and memes (introns expressing themselves electromagnetically): this could provide further understanding of the mysterious "junk DNA". Combining this question with some recent puzzling findings leads to a rather radical revision of the view about evolution proceeding through random mutations.

a) The second strange finding besides coral genome reported in New Scientist (5 June, 2004) was that the removal of large portions of conserved intronic DNA from mice has no detectable effects on the basic biological functions. Conserved parts of DNA are usually thought as being an outcome of a long selection process and far from genetic trash. This could be understood if the conserved introns have been radiated from corals and the selection process has occurred already before the Cambrian explosion induced by the emergence of the corals and leading to the sudden emergence of new highly developed life forms. That mouse introns did not have any identifiable function could mean that they are still waiting for time to become ripe for their expression.

b) A third strange discovery relates to morphogenesis and is known as Ciba Geigy effect. Chemists Guido Ebner and Guido Schuerch exposed germs, seeds, and eggs to an electric field with strength in the range .5-2 kV/m. For instance, the resulting trouts appeared to resemble their ancient predecessors. The leaves of certain plants represented a series of snapshots from evolution with the oldest leaves dating back to 300 million years. This suggests that the memone and genome represent ontogeny recapitulates phylogeny principle quite concretely, and that static electric fields could provide the practical manner to activate and study the ancient morphologies. Even partial transmutation of life forms to each other might be possible (beautiful swan to ugly duckling at least!). The activation of morphologies not yet realized is probably more difficult: new memetic programs require new genetic hardware.

The resulting vision about evolution of higher organisms would be as the activation of conserved memes and genes basically inherited from corals rather than by the emergence of new genes by random mutations. Very much like learning new features of a text processing program. The explosive

evolution of human civilization could correspond to a rapid shift of the activated portion of memone and genome. The fact that 95 per cent of our DNA consists of introns suggests that an enormous evolutionary potential exists also at the level of personal evolution during single life cycle. TGD view about space-time as a 4-dimensional living organism would mean that this personal evolution continues after the biological death since the 4-body of geometric past does not disappear in the biological death.

Many-Sheeted DNA

The problems of how genes code information about the morphology of organism and how this information is expressed, belong to the great puzzles of the developmental biology. A closely related mystery is the differentiation of cells. The notion of the genetic program is far from precise and it is not clear how close the analogy with a computer program is. There are also several problems which challenge the basic dogmas of genetics.

a) Only 1 per cent of DNA of human genome actually codes polypeptides. Eukaryote genes contain intron sequences which are transcribed into hnRNA but snipped of when hnRNA is transformed mRNA in process called slicing. The higher the evolutionary level of organism, the higher the fraction of introns is. Molecular Darwinists see introns as "junk DNA" but there is evidence that introns are far from junk. For instance, the splicing of intron contribution from hnRNA to give mRNA can give several different outcomes depending on the stage of development of the organism and introns are crucial for the effectiveness of immune system. Hence one can wonder whether intronic mRNA and protein mRNA could both form the real output of gene subprograms serving in some sense as input for other gene subprograms. This interpretation obviously conflicts with "gene-single protein" dogma in its basic form.

b) There are large amounts of highly repetitive DNA which is silent. One can wonder whether there is some fundamental mis-understanding involved. Could it be that this DNA is analogous to control DNA not transcribed to RNA and therefore not all useless. There is also active repetitive DNA.

c) There is large amount of silent DNA in control sections between genes. Could it be that this silent DNA expresses itself in some nonchemical manner? Chemical expression is very slow, translation rate being twenty aminoacids per second, and one can wonder whether life might have invented faster modes of gene expression and control of gene expression.

d) Plant genome is often by a factor of hundred longer than human genome. One could argue that the complexity of organism is measured by the length of the shortest program coding the organism. It is however not at all obvious how the genome of plants could be more redundant than human genome since repetitive sequences common to all animals are present. Introns are in fact more frequent in human genome. This suggests that some new unidentified degrees of freedom giving rise to complexity might be present and that the chemistry of DNA in the sense of standard physics is perhaps not all that is needed to understand genetic program.

e) Various self-organization process such as self-assembly and de-assembly are very frequent in living systems. The problem how genes give rise to morphology of the organism is poorly understood. This forces to challenge the dogma of genetic determinism. One should be able to understand what is determined by genes and what is determined by self-organization and whether the genes of the standard physics are enough.

The reason why the above mentioned problems have turned out to be so untractable might be due to a wrong view about space-time. Many-sheeted space-time concept of TGD might be absolutely crucial for the expression of genetic code. Gene itself might be many-sheeted space-time structure coding faithfully the topology of the expression domain of gene. This many-sheeted structure of DNA could allow to understand the miraculous looking features of DNA replication and cell differentiation. TGD based view of evolution as p-adic evolution implied by the basic quantum theory, should be a crucial element of the picture. Together with p-adic length scale hypothesis, with Combinatorial Hierarchy model for genetic code allowing to interpret genes as Boolean statements, and general vision about quantum control and coordination based on a hierarchy of weakly coupled super conductors, the notion of many-sheeted DNA leads to precise quantitative predictions and a general model for genetic program. In particular, one can understand the mystery of introns. What interesting from the point of view of our consciousness is that it might be possible to interpret the Boolean statements represented by the exon and intron parts of genes as a physical representation for our belief system.

Thus genes would code both matter– and mind like hardware of the living system.

The notion of magnetic body is central in the TGD inspired theory of living matter. Every system possesses magnetic body and there are strong reasons to believe that the magnetic body associated with human body is of order Earth size and that there could be hierarchy of these bodies with even much larger sizes. Therefore the question arises what distinguishes between the magnetic bodies of Earth and human body.

The vision about dark matter hierarchy labelled partially by a hierarchy of values of Planck constant coming as $\hbar(k_d) = \lambda^{k_d}\hbar_0$, $\lambda \simeq 2^{11}$, leads to a rather concrete view about the hierarchy of magnetic bodies and implies a natural generalization leading to the notion of super- and hyper genes.

Super genes consist of genes in different cell nuclei arranged to threads along magnetic flux sheets like text lines on the page of book whereas hyper genes traverse through genomes of different organisms. Super and hyper genes provide an enormous representative capacity and together with the dark matter hierarchy allows to resolve the paradox created by the observation that human genome does not differ appreciably in size from that of wheat.

DNA as Topological Quantum Computer

The chapter represents a vision about how DNA might act as a topological quantum computer (tqc). Tqc means that the braidings of braid strands define tqc programs and M-matrix (generalization of S-matrix in zero energy ontology) defining the entanglement between states assignable to the end points of strands define the tqc usually coded as unitary time evolution for Schrödinger equation.

Before a representation of the model of tqc general vision about what happens in quantum jump, which at least in formal sense can be regarded as quantum computation, is represented. Included is also a section about modification of thermodynamics required by the possibility of negentropic entanglement. The modification corresponds simply to the replacement $S \to S - N$ for the entropy in standard thermodynamics. The implications of this replacement are however highly non-trivial. The generalization of the second law allows to understand the thermodynamical aspect of topological quantum computation. One can understand why living matter is so effective entropy producer as compared to inanimate matter and also the characteristic decomposition of living systems to highly negentropic and entropic parts as a consequence of generalized second law. ADP-ATP process of metabolism provides a concrete application for the generalized thermodynamics and allows to see this process as a transfer of negentropic entanglement. Also DNA double strand for which sugar-phosphate backbone consists of XMPs, X= A,T,C,G containing negentropy carrying phosphate bonds can be seen as analogous to conscious brain with DNA strands representing right and left hemispheres.

One can end up to the model of topological quantum computation in the following manner.

1. Darwinian selection for which the standard theory of self-organization provides a model, should apply also to tqc programs. Tqc programs should correspond to asymptotic self-organization patterns selected by dissipation in the presence of metabolic energy feed. The spatial and temporal pattern of the metabolic energy feed characterizes the tqc program - or equivalently - sub-program call.

2. Since braiding characterizes the tqc program, the self-organization pattern should correspond to a hydrodynamical flow or a pattern of magnetic field inducing the braiding. Braid strands must correspond to magnetic flux tubes of the magnetic body of DNA. If each nucleotide is transversal magnetic dipole it gives rise to transversal flux tubes, which can also connect to the genome of another cell. As a matter fact, the flux tubes would correspond to what I call wormhole magnetic fields having pairs of space-time sheets carrying opposite magnetic fluxes.

3. The output of tqc sub-program is probability distribution for the outcomes of state function reduction so that the sub-program must be repeated very many times. It is represented as four-dimensional patterns for various rates (chemical rates, nerve pulse patterns, EEG power distributions,...) having also identification as temporal densities of zero energy states in various scales. By the fractality of TGD Universe there is a hierarchy of tqcs corresponding to p-adic and dark matter hierarchies. Programs (space-time sheets defining coherence regions) call programs in shorter scale. If the self-organizing system has a periodic behavior each tqc module defines a large number of almost copies of itself asymptotically. Generalized EEG could naturally define

this periodic pattern and each period of EEG would correspond to an initiation and halting of tqc. This brings in mind the periodically occurring sol-gel phase transition inside cell near the cell membrane. There is also a connection with hologram idea: EEG rhythm corresponds to reference wave and nerve pulse patters to the wave carrying the information and interfering with the reference wave.

4. Fluid flow must induce the braiding which requires that the ends of braid strands must be anchored to the fluid flow. Recalling that lipid mono-layers of the cell membrane are liquid crystals and lipids of interior mono-layer have hydrophilic ends pointing towards cell interior, it is easy to guess that DNA nucleotides are connected to lipids by magnetic flux tubes and hydrophilic lipid ends are stuck to the flow.

5. The topology of the braid traversing cell membrane cannot be affected by the hydrodynamical flow. Hence braid strands must be split during tqc. This also induces the desired magnetic isolation from the environment. Halting of tqc reconnects them and make possible the communication of the outcome of tqc.

There are several problems related to the details of the realization.

1. How nucleotides A,T,C,G are coded to the strand color and what this color corresponds to physically? There are two options which could be characterized as fermionic and bosonic.

   i) Magnetic flux tubes having quark and anti-quark at their ends with u,d and u_c, d_c coding for A,G and T,C. CP conjugation would correspond to conjugation for DNA nucleotides.

   ii) Wormhole magnetic flux tubes having wormhole contact and its CP conjugate at its ends with wormhole contact carrying quark and anti-quark at its throats. The latter are predicted to appear in all length scales in TGD Universe.

2. How to split the braid strands in a controlled manner? High T_c super conductivity provides a possible mechanism: braid strand can be split only if the supra current flowing through it vanishes. A suitable voltage pulse induces the supra-current and its negative cancels it. The conformation of the lipid controls whether it it can follow the flow or not.

3. How magnetic flux tubes can be cut without breaking the conservation of the magnetic flux? The notion of wormhole magnetic field could save the situation now: after the splitting the flux returns back along the second space-time sheet of wormhole magnetic field. An alternative solution is based on reconnection of flux tubes. Since only flux tubes of same color can reconnect this process can induce transfer of color: "color inheritance": when applied at the level of amino-acids this leads to a successful model of protein folding. Reconnection makes possible breaking of flux tube connection for both the ordinary magnetic flux tubes and wormhole magnetic flux tubes.

4. How magnetic flux tubes are realized? The interpretation of flux tubes as correlates of directed attention at molecular level leads to concrete picture. Hydrogen bonds are by their asymmetry natural correlates for a directed attention at molecular level. Also flux tubes between acceptors of hydrogen bonds must be allowed and acceptors can be seen as the subjects of directed attention and donors as objects. Examples of acceptors are aromatic rings of nucleotides, O = atoms of phosphates, etc.. A connection with metabolism is obtained if it is assumed that various phosphates XMP, XDP, XTP, $X = A, T, G, C$ act as fundamental acceptors and plugs in the connection lines. The basic metabolic process $ATP \to ADP + P_i$ allows an interpretation as a reconnection splitting flux tube connection, and the basic function of phosphorylating enzymes would be to build flux tube connections as also of breathing and photosynthesis.

The rest of the article represents a more concrete vision about how DNA might act as a topological quantum computer (tqc). The topics discussed are following.

1. How the basic gates are realized concretely. Gates can be identified as basic braid operations so that the question reduces to how braidings of magnetic flux tubes represent gates and what kind of particles represent the quantum states. The identification of the particles is in terms of quarks: TGD indeed predicts a hierarchy of scaled variants of hadron physics.

2. How the braiding is realized concretely? What do braid strands identified as magnetic flux tubes look like? How the braiding operation is induced? The tentative answer is that color magnetic flux tubes connecting DNA nucleotides to the lipids of nuclear and cell membrane define braid strands and that braiding operations are induced by hydrodynamic flow around membrane generating 2-D flow of liquid crystal defined by the lipids. Also nerve pulse propagation can induced this kind of 2-D flow.

3. How magnetic flux tubes are realized? The interpretation of flux tubes as correlates of directed attention at molecular level leads to concrete picture. Hydrogen bonds are by their asymmetry natural correlates for a directed attention at molecular level. Also flux tubes between acceptors of hydrogen bonds must be allowed and acceptors can be seen as the subjects of directed attention and donors as objects. Examples of acceptors are aromatic rings of nucleotides, O = atoms of phosphates, etc.. A connection with metabolism is obtained if it is assumed that various phosphates XMP, XDP, XTP, $X = A, T, G, C$ act as fundamental acceptors and plugs in the connection lines. The basic metabolic process $ATP \to ADP + P_i$ allows an interpretation as a reconnection splitting flux tube connection, and the basic function of phosphorylating enzymes would be to build flux tube connections as also of breathing and photosynthesis.

The model is certainly very speculative and heavily relies on the new physics predicted by TGD. The model makes however strong predictions and is therefore testable.

1. The model makes several testable predictions about DNA itself. In particular, matter-antimatter asymmetry and slightly broken isospin symmetry have counterparts at DNA level induced from the breaking of these symmetries for quarks and antiquarks associated with the flux tubes. DNA cell membrane system is not the only possible system that could perform tqc like activities and store memories in braidings: flux tubes could connect biomolecules and the braiding could provide an almost definition for what it is to be living. Even water memory might reduce to braidings.

2. The model leads also to an improved understanding of other roles of the magnetic flux tubes containing dark matter. Phase transitions changing the value of Planck constant for the magnetic flux tubes could be key element of bio-catalysis and electromagnetic long distance communications in living matter. For instance, one ends up to what might be called code for protein folding and bio-catalysis. There is also a fascinating connection with Peter Gariaev's work suggesting that the phase transitions changing Planck constant have been observed and wormhole magnetic flux tubes containing dark matter have been photographed in his experiments.

3. In the proposed vision genes define the hardware and tqc programs the software responsible for what becomes cultural evolution at the higher levels of evolutionary hierarchy. This vision explains also the mystery of introns. The quite recent findings challenging genetic determinism expressed using the term "genetic dark matter" provide support for an existence of new information carrying level at the level of genome identifiable in terms of tqc programs.

The Notion of Wave-Genome and DNA as Topological Quantum Computer

Peter Gariaev and collaborators have reported several strange effects of laser light and also ordinary light on DNA. These findings include the rotation of polarization plane of laser light by DNA, phantom DNA effect, the transformation of laser light to radio-wave photons having biological effects, the coding of DNA sequences to the modulated polarization plane of laser light and the ability of this kind of light to induce gene expression in another organisms provided the modulated polarization pattern corresponds to an "address" characterizing the organism, and the formation of images of what is believed to be DNA sample itself and of the objects of environment by DNA sample in a cell irradiated by ordinary light in UV-IR range. In this chapter a TGD based model for these effects is discussed. A speculative picture proposing a connection between homeopathy, water memory, and phantom DNA effect is discussed and on basis of this connection a vision about how the tqc hardware represented by the genome is actively developed by subjecting it to evolutionary pressures represented by a virtual world representation of the physical environment. The speculation inspired by this vision is that genetic code as well as DNA-, RNA- and amino-acid sequences should have representation in terms of nuclear strings. The model for dark baryons indeed leads to an identification of these analogs

and the basic numbers of genetic code including also the numbers of aminoacids coded by a given number of codons are predicted correctly. Hence it seems that genetic code is universal rather than being an accidental outcome of the biological evolution.

Model for the Findings about Hologram Generating Properties of DNA

A TGD inspired model for the strange replica structures observed when DNA sample is radiated by red, IR, and UV light using two methods by Peter Gariaev and collaborators. The first method produces what is tentatively interpreted as replica images of either DNA sample or of five red lamps used to irradiate the sample. Second method produce replica image of environment with replication in horizontal direction but only at the right hand side of the apparatus. Also a white phantom variant of the replica trajectory observed in the first experiment is observed and has in vertical direction the size scale of the apparatus.

The model is developed in order to explain the characteristic features of the replica patterns. The basic notions are magnetic body, massless extremal (topological light ray), the existence of Bose-Einstein condensates of Cooper pairs at magnetic flux tubes, and dark photons with large value of Planck constant for which macroscopic quantum coherence is possible. The hypothesis is that the first method makes part of the magnetic body of DNA sample visible whereas method II would produce replica hologram of environment using dark photons and produce also a phantom image of the magnetic tubes becoming visible by method I. Replicas would result as mirror hall effect in the sense that the dark photons would move back and forth between the part of magnetic body becoming visible by method I and serving as a mirror and the objects of environment serving also as mirrors. What is however required is that not only the outer boundaries of objects visible via ordinary reflection act as mirrors but also the parts of the outer boundary not usually visible perform mirror function so that an essentially 3-D vision providing information about the geometry of the entire object would be in question. Many-sheeted space-time allows this.

The presence of the hologram image for method II requires the self-sustainment of the reference beam only whereas the presence of phantom DNA image for method I requires the self-sustainment of both beams. Non-linear dynamics for the energy feed from DNA to the magnetic body could make possible self-sustainment for both beams simultaneously. Non-linear dynamics for beams themselves could allow for the self-sustainment of reference beam and/or reflected beam. The latter option is favored by data.

Evolution in Many-Sheeted Space-Time

The topics of the chapter has been restricted to those, which seem to represent the most well-established ideas. There are many other, more speculative, ideas such as the strong form of the hypothesis that plasmoid like life forms molecular life forms has evolved in "Mother Gaia's womb", maybe even in the hot environment defined by the boundary of mantle and core.

1. Basic facts about and TGD based model for pre-biotic evolution are discussed.

2. A model for the ATP-ADP process based on DNA as topological quantum computer vision, the identification of universal metabolic energy quanta in terms of zero point kinetic energies, and the notion of remote metabolism is discussed.

3. A model for the evolution of the recent genetic code (3-codons) as a fusion of codes for which codons are nucleotides (1-codons) and di-nucleotides (2-codons) is discussed. The symmetries of the genetic code, the observation that tRNA can be seen as a fusion of two hairpin like DNA molecules, and the finding that the first nucleotides of 3-codon code for the reaction path leading from a precursors of the aminoacid to aminoacids for hydrophobic/hydrohilic dichotomy, serve as motivations of the model. 1- and 2-codes corresponding to the two forms of RNA (the exotic $2' - 5'$ RNA and the usual $3' - 5'$ RNA) would have prevailed in RNA world. Aminoacids would have served as catalysts for the copying of RNA on one hand, and RNA molecules would have catalyzed the formation of aminoacids from their precursors on one hand, meaning the presence of a positive feedback loop. In the transition to DNA-aminoacid era RNA began to be translated to aminoacid sequences.

4. Cambrian explosion represents a rather mysterious period in biology: new highly developed phylas emerged out of nowhere. A second strange finding is that continents would fit together to form single super-continent covering entire Earth's surface at time of Cambrian explosion if the radius of Earth would have been one half of its recent value. This finding has inspired Expanding Earth theories but it has not been possible to identify the mechanism causing the expansion. The success of the standard tectonic plate theory requires that possible expansion must have occurred in relatively short geological time scale. The hierarchy of Planck constants implies that cosmic expansion has occurred in quantum leaps increasing the value of $\hbar$ and thus of quantum scales by factors which tend to be powers of 2. Cosmic expansion would have occurred as jerks even in the case of planets. In the proposed model Cambrian explosion would have accompanied the expansion of the Earth's radius by a factor of 2: during this period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place.

5. The last section of the chapter compares TGD based view about the evolution of genetic code to the views of McFadden. This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding.

6. A vision about biological evolution and evolution of brain is discussed on basis of the wisdom gained from the construction of the models of sensory receptor and generalized EEG.

Expanding Earth model and pre-Cambrian evolution of continents, climate, and life

TGD inspired quantum cosmology predicts that astrophysical objects do not follow cosmic expansion except in jerk-wise quantum leaps increasing the gigantic value of the gravitational Planck constant characterizing space-time mediating gravitational interactions between two masses or gravitational self interactions. This assumption provides explanation for the apparent cosmological constant.

Also planets are predicted to expand in a stepwise manner. This provides a new version of Expanding Earth theory originally postulated to explain the intriguing findings suggesting that continents have once formed a connected continent covering almost the entire surface of Earth but with radius which was one half of the recent one.

This leads also to a rather fascinating vision about biology. The mysterious Cambrian Explosion in which a large number of new species emerged suddenly (realized already Darwin as the strongest objection against his theory) could be understood if the life would have gone to underground lakes and seas formed during the expansion period as fractures were formed and the underground cavities expanded and were filled with water. This would have allowed the life to escape cosmic radiation, meteoric bombardment, and the extremely cold climate during Proterozoic period preceding the Cambrian Explosion and migrate back as highly developed life forms as the period of glaciations ended.

Before the Proterozoic era the radius of Earth would have been one half of its recent value and started to grow with gradually accelerating rate. This forces to rewrite the entire geological and climate history of Earth during the Proterozoic period.

1. The postulated physically implausible cyclic appearance of single connected super-continent containing all land mass can be given up and replaced with a single continent containing large inland seas. There is no need to postulate the existence of series of super-oceans whose ocean floor would have subduced totally so that no direct information about them would exist nowadays.

2. The dominating model for pre-Cambrian climate is so called Snowball Earth model inspired by the finding that signatures of glaciations have been found at regions of Earth, which should have been near Equator during the Proterozoic. Snowball model has several difficulties: in particular, there is a lot of evidence that a series of ordinary glaciations was in question. For $R/2$ option the regions located to Equator would have actually been near North Pole so that the glaciations would have indeed been ordinary glaciations proceeding from the poles. A killer prediction is the existence of non-glaciated regions at apparent southern latitudes around about 45 degrees and there is evidence for these indeed exists! The model makes also testable paleomagnetic killer predictions. In particular, during periods when the magnetic dipole in the direction of rotation

axis the directions of the magnetic fields for $R/2$ model are predicted to be same at South Pole and apparent Equator and opposite for the standard option.

A Model for Protein Folding and Bio-catalysis

The model for the evolution of genetic code leads to the idea that the folding of proteins obeys a folding code inherited from the genetic code. The flux connections between molecules containing dark matter in macroscopic quantum phase and characterized by two integers are the basic new physics element of the model.

After some trials one ends up with a general conceptualization of the situation with the identification o magnetic flux tubes as correlates of attention at molecular level so that a direct connection with TGD inspired theory of consciousness emerges at quantitative level. This allows a far reaching generalization of the DNA as topological quantum computer paradigm and makes it much more detailed. By their asymmetric character hydrogen bonds are excellent candidates for contracted magnetic flux tubes serving as correlates of attention at molecular level.

One can consider two models. For the first model the flux tubes between amino-acids are assumed to determine the protein folding.

1. The constant part of free amino-acid containing $O-H$, $O=$, and NH_2 would correspond to the codon XYZ in the sense that the flux tubes would carry the "color" representing the four nucleotides in terms of quark pairs. Color inheritance by flux tube reconnection makes this possible. For the amino-adics inside protein $O=$ and $N-H$ would correspond to YZ. Also flux tubes connecting the acceptor atoms of hydrogen bonds are required by the model of DNA as topological quantum computer. The long flux tubes between $O=$ atoms and their length reduction in a phase transition reducing Planck constant could be essential in protein-ligand interaction.

2. The model predicts a code for protein folding: depending on whether also $=O-O=$ flux tubes are allowed or not, $Y=Z$ or $Y=Z_c$ condition is satisfied by the amino-acids having $N-H--O=$ hydrogen bond. For $=O-O=$ bonds $Y-Y_c$ pairing holds true. If one identifies hydrogen bond with flux tube ($Y(n)=Z(n+k)$) the model works badly for both options. If one assumes only that the presence of a flux tube connecting amino-acids in either direction ($Y(n)=Z(n+k)$ or $Z(n)=Y(n+k)$) is a prerequisite for the formation of hydrogen bond, the model works. $Y=Z_c$ option predicts the average length of alpha bonds correctly. $Y=Z$ rule is however favored by the study of alpha helices for four enzymes: the possible average length of alpha helix is considerably longer than the average length of alpha helix if gene is the unique gene allowing to satisfy $Y=Z$ rule. The explicit study of alpha helices for four enzymes demonstrates that the failure to satisfy the condition for the existence of hydrogen bond fails rarely and at most for two amino-acids (for 2 amino-acids in single case only). For beta sheets there ar no failures for $Y=Z$ option.

3. The information apparently lost in the many-to-one character of the codon-amino-acid correspondence would code for the folding of the protein and similar amino-acid sequences could give rise to different foldings. Also catalyst action would reduce to effective base pairing and one can speak about catalyst code. The DNA sequences associated with alpha helices and beta sheets are completely predictable unless one assumes a quantum counterpart of wobble base pairing meaning that $N-H$ flux tubes are before hydrogen bonding in quantum superpositions of braid colors associated with the third nucleotides Z of codons XYZ coding for amino-acid. Only the latter option works. The outcome is very simple quantitative model for folding and catalyst action based on minimization of energy and predicting as its solutions alpha helices and beta strands.

Second model represents a diametrical opposite of the first model in the sense in that it assumes flux tube connections only between amino-acids and water molecules. These flux tubes mediate an attractive (repulsive) interaction in the case of hydrophily (hydrophoby) due to the behavior of magnetic (presumably) interaction energy as a function of Planck constant (or integers characterizing the level of dark matter) assignable to the flux tube. For hydrophoby (hydrophily) the interaction energy is minimized for long (short) flux tubes. The interaction between amino-acids is induced by this

interaction in a manner analogous to how the interaction between electrons and ions induces secondary interaction between the members of a Cooper pair. The model explains the basic qualitative aspects of protein folding and the quantitative model of folding based on amino-acid-amino-acid flux tubes allows a generalization which is however discussed at numerical level.

Three new physics realizations of the genetic code and the role of dark matter in biosystems

TGD inspired quantum biology leads naturally to the idea that several realizations of genetic code exist. Besides the realizations based on temporal patterns of electromagnetic fields I have considered three different new physics realizations of the genetic code based the notions of many-sheeted spacetime, magnetic body, and the hierarchy of Planck constants explaining dark matter in TGD framework.

1. The first realization - proposed in the model for DNA as topological quantum computer (tqc) - maps the nucleotides A,G and T,C to dark quarks u,d and their anti-quarks assignable to the ends of magnetic flux tubes representing braid strands and connecting nucleotides to lipids of cell membrane.

2. Second realization was discovered in the model of dark nuclei as strings of dark baryons. Dark baryons realize codons in terms of quantum entanglement and without decomposition to letters. Dark baryons are strings of 3 quarks connected by two color flux tubes. The neutral states of the dark baryon predicted by the model are in 1-1 correspondence with DNA, RNA, aminoacids. Candidates for the counterparts of tRNA anticodons are also obtained if one accepts that genetic code actually decomposes to 2 steps $64 \to 40 \to 20$ such that there are 40 dark baryon counterparts for tRNA anticodons. The amazing finding is that vertebrate genetic code comes out correctly.

3. The third realization is a physical realization for the divisor code proposed by Khrennikov and Nilsson. The realization relies on two integers labeling magnetic flux tubes containing dark matter. The dark magnetic flux tubes assignable to DNA codons and amino-acids could be labeled by these integers providing a representation of the genetic code consistent with the divisor code. Also a physical mechanism implying the physical equivalence of the dark baryon code and divisor code can be imagined.

The basic proposal is that dark baryon counterparts of basic bio-molecules and genetic code were present from beginning and gave rise to pre-biotic life at the magnetic flux tubes so that the evolution of biological life meant the development of translation and transcription mechanisms allowing to transform dark baryon variants of the codons to their chemical variants. These mechanisms would be still at work inside the living cell and allow the living matter to perform genetic engineering. This proposal is consistent with recent findings about large variations of genomes inside organism.

There is a strange experimental finding giving support for this picture. A water solution containing human cells infected by bacteria is sterilized by a filtering procedure and healthy cells are added to the filtrate. Within few weeks the infected cells re-appear. A possible explanation is that dark baryon variant of the bacterial genome realized as nano-sized particles remains in the solution despite the filtering.

The codes are discussed from the point of view of DNA as tqc hypothesis and the model for protein folding and bio-catalysis. The basic selection rules of bio-catalysis could be based on the two integers assignable to the dark magnetic flux tubes. Only bio-molecules whose dark magnetic bodies contain a layer characterized by same integers can be connected by dark magnetic flux tubes. The reconnection of the dark magnetic flux tubes selecting the bio-molecules participating the catalytic reaction and the contraction of these flux tubes induced by a phase transition reducing Planck constant and forcing the bio-molecules near to each other would represent basic mechanisms of bio-catalysis.

1.5.3 PART III: NUMBER THEORETICAL MODELS FOR GENETIC CODE AND ITS EVOLUTION

Could Genetic Code Be Understood Number Theoretically?

The number of DNA triplets is 64. This inspires the idea that DNA sequence could be interpreted as an expansion of an integer using 64 as the base. Hence given DNA triplet would represent some

integer in {0,1....,63} (sequences of I Ching symbols give a beautiful realization of these sequences).

The observation which puts bells ringing is that the number of primes smaller than 64 is 18. Together with 0, and 1 this makes 20: the number of aminoacids!

1. Questions

The finding just described stimulates a whole series of questions.

Do aminoacids correspond to integers in the set $S = \{primes < 64\} \cup \{0, 1\}$. Does aminoacid sequence have an interpretation as a representation as a sequence of integers consisting of 0, 1 and products of primes $p = 2, ..., 61$? Does the aminoacid representing 0 have an interpretation as kind of period separating from each other structural units analogous to genes representing integers in the sequence so that we would quite literally consists of sequences of integers? Do 0 and 1 have some special biological properties, say the property of being biologically inert both at the level of DNA and aminoacids?

Does genetic code mediate a map from integers 0,...,63 to set S such that 0 and 1 are mapped to 0 and 1? If so then three integers $2 \leq n \leq 63$ must correspond to stopping sign codons rather than primes. What stopping sign codon property means at the level of integers? How the map from integers 2,...,61 to the primes $p = 2, ..., 61$ is determined?

2. The chain of arguments leading to a number theoretical model for the genetic code

The following chain of arguments induced to large part by concrete numerical experimentation leads to a model providing a partial answer to many of these questions.

a) The partitions of any positive integer n can be interpreted in terms of number theoretical many boson states. The partitions for which a given integer appears at most once have interpretation in terms of fermion states. These states could be identified as bosonic and fermionic states of Super Virasoro representation with given conformal weight n.

b) The generalization of Shannon entropy by replacing logarithms of probabilities with the logarithms of p-adic norms of probabilities allows to have systems with negative entropy and thus positive negentropy. The natural requirement is that n corresponds to such prime $p \leq 61$ that the negentropy assigned to n is maximal in some number theoretic thermodynamics. The resulting correspondence $n \to p(n)$ naturally determined the genetic code.

c) One can assign to the bosonic and fermionic partitions a number theoretic thermodynamics defined by a Hamiltonian. Purely bosonic and fermionic thermodynamics are defined by corresponding partition functions Z_B and Z_F whereas supersymmetric option is defined by the product $Z_B \times Z_F$. Supersymmetric option turns out to be the most realistic one.

d) The simplest option is that Hamiltonian depends only on the number r of the integers in the partition. The dynamics would be in a well defined sense local and would not depend on the sizes of summands at all. The thermodynamical states would be degenerate with degeneracy factors given by total numbers $d_I(n, r)$ of partitions of type $I = B, F$. The invariants known as rank and crank define alternative candidates for the basic building blocks of Hamiltonian.

e) Ordinary exponential thermodynamics based on, say $e^{-H/T} = q_0^{r-1}$, q_0 a rational number, produces typically unrealistic genetic codes for which most integers are mapped to small primes $p \leq 11$ and many primes are not coded at all. The idea that realistic code could result at some critical temperature fails also.

f) Quantum criticality and fractality of TGD Universe inspire the idea that the criticality is an inherent property of Hamiltonian rather than only thermodynamical state. Hence Hamiltonian can depend only weakly on the character of the partition so that all partitions contribute with almost equal weights to the partition function. Fractality is achieved if Boltzmann factors are given by $e^{-H/T} = (r+r_0)^{n_0}$ so that $H(r) = log(r+r_0)$ serves as Hamiltonian and n_0 corresponds to the inverse temperature. The super-symmetric variant of this Hamiltonian yields the most realistic candidates for the genetic code and there are good hopes that a number theoretically small perturbation not changing the divisors $p \leq 61$ of partition function but affecting the probabilities could give correct degeneracies.

Numerical experimentation suggests however that this might not be the case and that simple analytic form of Hamiltonian is too much to hope for. A simple argument however shows that $e^{-H/T} = f(r)$ could be in quantum critical case be deduced from the genetic code by fixing the 62 values of $f(r)$ so that the desired 62 correspondences $n \to p(n)$ result. The idea about almost universality of

the genetic code would be replaced with the idea that quantum criticality allows to engineer a genetic code maximizing the total negentropy associated with DNA triplet-aminoacid pair.

A natural guess is that the map of codons to integers is given as a small deformation of the map induced by the map of DNA codons to integers induced by the identification of nucleotides with 4-digits 0,1,2, 3 (this identification depends on whether first, second, or third nucleotide is in question). This map predicts approximate $p(n) = p(n+1)$ symmetry having also a number theoretical justification. One can deduce codon-integer and aminoacid-prime correspondences and at (at least) two Boltzmann weight distributions $f(n)$ consistent with the genetic code and Negentropy Maximization Principle constrained by the degeneracies of the genetic code.

Unification of Four Approaches to the Genetic Code

A proposal unifying four approaches to genetic code is discussed.

The first approach is introduced by Pitkänen and is geometric: genetic code is interpreted as an imbedding of the aminoacid space to DNA space possessing a fiber bundle like structure with DNAs coding for a given aminoacid forming a discrete fiber with a varying number of points. Also Khrennikov has proposed an analogous approach based on the identification of DNAs coding for a given aminoacid as an orbit a discrete flow defined by iteration of a map of DNA space to itself.

Second approach starts from the 5-adic approach of Dragovich and Dragovich. Codons are labelled by 5-adic integers n which have no non-vanishing 5-digits so that the n is in the range $[31, 124]$. The number of primes in the range $[31, 124]$ is 20. This suggests the labelling of aminoacids by these primes. This inspires an additional condition on the geometric code: if possible, one of the integers n projected to p equals to $p(n)$. This condition fails only for the primes 53,79,101,103 for which some of 5-digits vanishing in 5-ary expansion.

The third approach is based on the generalization of the basic idea of the so called divisor code proposed by Khrennikov and Nilsson. The requirement is that the number of factors for integer n labelling one of DNAs, call it n_d coding for a given aminoacid is the total number of codons coding for the aminoacid, its degeneracy. Therefore a given aminoacid labelled by prime p with no non-vanishing 5-digits is coded by DNAs labelled by p itself and by n_d. A group theoretic and physical interpretation for the origin of the divisor code is proposed.

The fourth approach is a modification of the earlier 4-adic number theoretic thermodynamics approach of Pitkänen.

a) 5-adic thermodynamics involving a maximization of number theoretic negentropy $N_p(n) = -S_p(n) > 0(!)$ as a function of p-adic prime p labelling aminoacids assigns a unique prime to the codon. If no prime in the range divides S_p, the codon is identified as a stopping codon.

b) The number theoretic thermodynamics is assigned with the partitions P of the integer $n_{2)}$ determined by the first two letters of the codon (16 integers belonging to the range $[6, 24]$). The integer valued number theoretic Hamiltonian $h(P) \in Z_{25}$ appearing in the Boltzmann weight $5^{h(P)/T_5}$ is assumed to depend on the number r of summands for the partition only. $h(r)$ is assumed to be tailored by evolution so that it reproduces the code.

c) The effect of the third nucleotide is described in terms of 5-adic temperature $T_5 = 1/n$, $n \in [0, 24]$: the variation of T_5 explains the existence of variants of genetic code and its temporal variation the observed context sensitivity of the codon-aminoacid correspondence for some variants of the code.

A numerical calculation scanning over $N \sim 10^{30}$ candidates for $h(r)$ allows only 11 Hamiltonians and with single additional symmetry inspired condition there are 2 solutions which differ only for 5 largest values of r. Due to the limited computational resources available only 24 percent of the available candidates have been scanned and the naive expectation is that the total number of Hamiltonians is about about 45 unless one poses additional conditions.

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Part I

SOME PHYSICAL AND MATHEMATICAL BACKGROUND

Chapter 2

About the New Physics Behind Qualia

2.1 Introduction

As the title expresses, this chapter was originally about the new physics behind qualia. The model of qualia indeed involves a lot of new physics: many-sheeted space-time; massless extremals; exotic Super Virasoro representations associated with discrete qualia; magnetic and cyclotron phase transitions associated with quantum critical quantum spin glass phases of exotic super conductors at cellular space-time sheets; classical color and electro-weak gauge fields in macroscopic length scales, to name the most important ingredients. Gradually the chapter however expanded so that it touches practically all new physics possibly relevant to TGD inspired quantum biology. Various physical mechanisms are discussed in exploratory spirit rather than restricting the consideration to those ideas which seem to be the final word about quantum biology or qualia just at this moment.

2.1.1 Living matter and dark matter

Dark matter is identified as a macroscopic quantum phase with large $\hbar$. Also living matter would involve in in an essential manner matter with a large value of $\hbar$ and hence dark, and form conformally confined (in the sense that the net conformal weight of the state is real) blobs behaving like single units with extremely quantal properties, including free will and intentional action in time scales familiar to us. Dark matter would be responsible for the mysterious vital force.

Any system for which some interaction becomes so strong that perturbation theory does not work, gives rise to this kind of system in a phase transition in which $\hbar$ increases to not lose perturbativity gives rise to this kind of "super-quantal" matter. In this sense emergence corresponds to strong coupling. One must however remember that emergence is actually much more and involves the notion of quantum jump. Dark matter made possible by dynamical $\hbar$ is necessary for macroscopic and macro-temporal quantum coherence and is thus prerequisite for emergence.

Physically large $\hbar$ means a larger unit for quantum numbers and this requires that single particle states form larger particle like units. This kind of collective states with weak mutual interactions are of course very natural in strongly interacting systems. At the level of quantum jumps quantum jumps integrate effectively to single quantum jump and longer moments of consciousness result. Conformal confinement guarantees all this. Entire hierarchy of size scales for conformally confined blobs is predicted corresponding to values of $\hbar$ related to Beraha numbers [83, 81] but there would be only single value corresponding to very large $\hbar$ for given values of system parameters (gravitational masses, charges,...). The larger the value of $\hbar$ the longer the characteristic time scale of consciousness and of a typical life cycle.

The notion of field body means that dark matter at the magnetic flux tubes would serve as an intentional agent using biological body as a motor instrument and sensory receptor. Dark matter would be the miraculous substance that living systems are fighting for, and perhaps the most important substance in metabolic cycle.

2.1.2 Macroscopic quantum phases in many-sheeted space-time

The crucial empirical ingredient turned out to be the observations about the effects of oscillating ELF electromagnetic fields on central nervous system, endocrine system and immune system made after sixties [16, 18] . The largest effects are obtained at odd multiples of cyclotron frequencies of various biologically important ions like Ca_{++} in Earth's magnetic field. Also amplitude modulation of RF and MW fields by these frequencies has effects. This leads to a surprising conclusion in violent conflict with standard physics view about world. Magnetically confined states of ions in Earth's magnetic field having minimal size of order cell size and energy scale of order 10^{-14} eV would be in question if ordinary quantum theory would be the final word. Dark matter hierarchy with the spectrum of Planck constants given by $\hbar = r\hbar_0$ with the favore values or r given by ruler and compass hypothesis or by Mersenne hypothesis, resolves the paradox [23] . For $k_d = 41$ level of the dark matter hierarchy the energies $E = \hbar\omega$ of ELF photons are above thermal threshold for $f \geq 1$ Hz.

The notion of many-sheeted ionic equilibrium brings in in the mechanism with which supra-currents at the magnetic flux tubes control the matter at atomic space-time sheets. The strange anomalies challenging the notions of ionic channels and pumps [196] provide support for the resulting general vision.

2.1.3 Mind like space-time sheets as massless extremals

Mind like space-time sheets are the geometric correlates of selves. So called massless extremals (MEs) [50] provide ideal and unique candidates for mind like space-time sheets. MEs give rise to hologram like cognitive representations. The assumption that they serve as Josephson junctions allows to understand the amplitude windows associated with the interaction of ELF em fields with brain tissue. The properties of MEs inspire the hypothesis that they give rise to an infinite hierarchy of electromagnetic life forms living in symbiosis with each other and bio-matter. EEG can be interpreted as associated with ELF MEs which is one important level in this hierarchy responsible for the cultural aspects of consciousness.

Our mental images propagating in neural circuits should correspond to microwave (MW) MEs with wavelengths below .3 meters. The communications between quantum antennae associated with ELF and RF MEs provides an elegant model for the formation and recall of long term memories and realize hologrammic cognitive representations. Self hierarchy has as a particular dynamical correlate the hierarchy of Josephson currents modulated by Josephson currents modulated by... having magnetic transition frequencies as their basic frequencies. Josephson currents flow along join along boundaries bonds connecting space-time sheets belonging at various levels of the hierarchy ('biofeedback').

2.1.4 Classical color and electro-weak fields in macroscopic length scales

One can say that the basic physics of standard model without symmetry breaking and color magnetic confinement is realized at classical level on cellular space-time sheets. Classical Z^0 fields, W fields and gluon fields unavoidably accompany non-orthogonal electric and magnetic fields. The proper interpretation of this prediction is in terms of a p-adic and dark fractal hierarchies of standard model physics with scaled down mass scales making possible long range weak and color interactions in arbitrarily long length scales.

This prediction forces to modify even the model of nuclei [69] . Nucleons carry exotic color and form nuclear strings consisting of color bonds with exotic quark q and antiquark $\overline{q}$ at their ends. These exotic quarks correspond to $k = 127$ level of dark matter hierarchy. Also dark variants of ordinary quarks with size of about atom are possible. It is also possible to have $u\overline{d}$ and $\overline{u}d$ type color bonds which carry em and weak charge and this means exotic nuclear ionization. Tetraneutron [3, 1] would represent one particular example of this kind of exotically ionized nucleus [69] . Exotic nuclear physics would have also implications for the ordinary condensed matter physics and could be involved with the very low compressibility of liquid phase and the anomalous behavior of water [24] .

Exotic ionization is the key element in the quantum model for the control action of the magnetic body on biological body. Exotic ionization induces dark plasma oscillations which in turn generate via classical em fields ordinary ohmic currents at the level of the ordinary matter. Nerve pulse patterns [57] and Ca^{2+} waves [34, 37] would represent examples of physiological correlates of this quantum control.

2.1.5 Mersenne hypothesis

The generalization of the imbedding space means a book like structure for which the pages are products of singular coverings or factor spaces of CD (causal diamond defined as intersection of future and past directed light-cones) and of CP_2 [27] . This predicts that Planck constants are rationals and that given value of Planck constant corresponds to an infinite number of different pages of the Big Book, which might be seen as a drawback. If only singular covering spaces are allowed the values of Planck constant are products of integers and given value of Planck constant corresponds to a finite number of pages given by the number of decompositions of the integer to two different integers.

TGD inspired quantum biology and number theoretical considerations suggest preferred values for $r = \hbar/\hbar_0$. For the most general option the values of $\hbar$ are products and ratios of two integers n_a and n_b. Ruler and compass integers defined by the products of distinct Fermat primes and power of two are number theoretically favored values for these integers because the phases $exp(i2\pi/n_i)$, $i \in \{a, b\}$, in this case are number theoretically very simple and should have emerged first in the number theoretical evolution via algebraic extensions of p-adics and of rationals. p-Adic length scale hypothesis favors powers of two as values of r.

One can however ask whether a more precise characterization of preferred Mersennes could exist and whether there could exists a stronger correlation betweeen hierarchies of p-adic length scales and Planck constants. Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1 + i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ are expected to be physically highly interesting and up to $k = 127$ indeed correspond to elementary particles. The number theoretical miracle is that all the four p-adic length scales with $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm). The question has been whether these define scaled up copies of electro-weak and QCD type physics with ordinary value of $\hbar$. The proposal that this is the case and that these physics are in a well-defined sense induced by the dark scaled up variants of corresponding lower level physics leads to a prediction for the preferred values of $r = 2^{k_d}$, $k_d = k_i - k_j$.

What induction means is that dark variant of exotic nuclear physics induces exotic physics with ordinary value of Planck constant in the new scale in a resonant manner: dark gauge bosons transform to their ordinary variants with the same Compton length. This transformation is natural since in length scales below the Compton length the gauge bosons behave as massless and free particles. As a consequence, lighter variants of weak bosons emerge and QCD confinement scale becomes longer.

This proposal will be referred to as Mersenne hypothesis. It leads to strong predictions about EEG [23] since it predicts a spectrum of preferred Josephson frequencies for a given value of membrane potential and also assigns to a given value of $\hbar$ a fixed size scale having interpretation as the size scale of the body part or magnetic body. Also a vision about evolution of life emerges. Mersenne hypothesis is especially interesting as far as new physics in condensed matter length scales is considered: this includes exotic scaled up variants of the ordinary nuclear physics and their dark variants. Even dark nucleons are possible and this gives justification for the model of dark nucleons predicting the counterparts of DNA,RNA, tRNa, and aminoacids as well as realization of vertebrate genetic code [78] .

These exotic nuclear physics with ordinary value of Planck constant could correspond to ground states that are almost vacuum extremals corresponding to homologically trivial geodesic sphere of CP_2 near criticality to a phase transition changing Planck constant. Ordinary nuclear physics would correspond to homologically non-trivial geodesic sphere and far from vacuum extremal property. For vacuum extremals of this kind classical Z^0 field proportional to electromagnetic field is present and this modifies dramatically the view about cell membrane as Josephson junction. The model for cell membrane as almost vacuum extremal indeed led to a quantitative breakthrough in TGD inspired model of EEG and is therefore something to be taken seriously. The safest option concerning empirical facts is that the copies of electro-weak and color physics with ordinary value of Planck constant are possible only for almost vacuum extremals - that is at criticality against phase transition changing Planck constant.

2.1.6 p-Adic-to-real transitions as transformation of intentions to actions

Hearing and cognition are very closely relatedone could even argue that we think using language. The view that p-adic physics is physics of intention and cognition leads to the vision that the transformation of thoughts to actions and sensory inputs to thoughts correspond to real–p-adic phase transitions for

space-time sheets. For a long time the question how p-adic space-time sheets relate to the real ones lacked a precise answer, and therefore also the question what the transformation of p-adic space-time sheet to real ones really means. The advances in the understanding the precise relationship between p-adic and real space-time sheets discussed in [72] led however to a definite progress in this respect [48] .

The transformation of p-adic space-time sheets to real ones must respect the conservation of quantum numbers: this requires that the real system either receives or sends energy when the p-adic-to-real transitions realizing the intention occurs. If p-adic ME is transformed to a negative energy ME in the process, real system must make a transition to a higher energy state. This kind of transitions cannot occur spontaneously so that the outcome is a precisely targeted realization of intention. The additional bonus is that buy now-let others pay mechanism makes possible extreme flexibility. There are reasons to expect that the energies involves cannot be too high however.

The model of intentional action as a quantum transition for which the probabilities for various intention-action pairs should in principle be deducible from S-matrix is discussed in [72] using the vision about physics as a generalized number theory as a guide line. This model leads to fresh insights about the construction of the ordinary S-matrix and essentially the same kind of general expressions for S-matrix elements result as in the case of ordinary scattering.

2.1.7 Exotic super-Virasoro representations

A further piece of new physics of qualia are super-symplectic and super-conformal algebras associated with the light-like M^4_+ projections of the light-like boundaries MEs. p-Adic considerations suggest that $L_0 = 0$ condition might be replaced by a weaker condition $L_0 \ mod \ p^n = 0$ in the p-adic context. The interpretation would be in terms of continuous scaling invariance broken to discrete scalings by powers of p: the analogy with lattice systems of condensed matter is obvious. The general condition $a^{L_0} \ mod \ p = 1$, a positive integer, stating invariance under scalings is by Fermat's little theorem satisfied $L_0 \ mod \ p = 0$ and would state that these scalings act like translations by multiples of lattice vector in lattice.

$p \simeq 2^k$ would guarantee approximately the conditions for $a = 2$. For Mersenne primes, which are in an exceptional role physically, these conditions are satisfied in excellent approximation. The so called Gaussian Mersennes allow also to satisfy these conditions in somewhat more general sense and, rather remarkably, there are four Gaussian Mersennes in the length scale range between cell membrane thickness and cell size.

The model for how local p-adic physics codes for the p-adic fractality of the real physics and for intentional action as a quantum jump transforming p-adic space-time sheet to a real one leads to a rather detailed view about the p-adic fractals possibly giving rise to exotic Super Virasoro representations [72, 48] .

The degeneracy of states for exotic representations (number of states with same L_0) is enormous for the physically interesting values of p-adic prime p. This means that these states provide huge negentropy resources. Thus exotic super-symplectic representations be interpreted as quantum level articulation for the statement that TGD Universe is quantum critical quantum spin glass. Exotic super-symplectic representations clearly provide an excellent candidate for an infinite hierarchy of life forms. These life forms would come in two classes.

1. The representatives of the first class labelled by three integers (k, m, n) if one assumes that physically interesting primes correspond to $p \simeq 2^{k^m}$, k prime and m are integers: n is the power appearing in $L_0 \propto p^n$.

2. The representatives of the second class are labelled by the integers k $L_0 \propto 2^k$, such that $2^k - 1$ is Mersenne prime or $(1 + i)^k - 1$ is Gaussian Mersenne.

It is tempting to assume that it is these life forms emerge already in elementary particle length scales and become increasingly complex when the p-adic length scale increases. Life could perhaps be regarded as a symbiosis of these life forms with super-conducting magnetic flux tubes and ordinary matter at atomic space-time sheets. These life forms ('mind') interact with each other, super-conducting magnetic flux tubes and ordinary matter via the classical gauge fields associated with MEs. A natural hypothesis is that the quantum phase transitions of the macroscopic quantum phases

for the particles of the exotic super-symplectic representations formed in classical fields of MEs (mind like space-time sheets) give rise to some (but not all) qualia.

2.2 Dark matter and living matter

In the sequel general ideas about the role of dark matter in condensed matter physics are described.

2.2.1 Hierarchy of Planck constants and the generalization of the notion of imbedding space

In the following the recent view about structure of imbedding space forced by the quantization of Planck constant is summarized. The question is whether it might be possible in some sense to replace H or its Cartesian factors by their necessarily singular multiple coverings and factor spaces. One can consider two options: either M^4 or the causal diamond CD. The latter one is the more plausible option from the point of view of WCW geometry.

The evolution of physical ideas about hierarchy of Planck constants

The evolution of the physical ideas related to the hierarchy of Planck constants and dark matter as a hierarchy of phases of matter with non-standard value of Planck constants was much faster than the evolution of mathematical ideas and quite a number of applications have been developed during last five years.

1. The starting point was the proposal of Nottale [10] that the orbits of inner planets correspond to Bohr orbits with Planck constant $\hbar_{gr} = GMm/v_0$ and outer planets with Planck constant $\hbar_{gr} = 5GMm/v_0$, $v_0/c \simeq 2^{-11}$. The basic proposal [65] was that ordinary matter condenses around dark matter which is a phase of matter characterized by a non-standard value of Planck constant whose value is gigantic for the space-time sheets mediating gravitational interaction. The interpretation of these space-time sheets could be as magnetic flux quanta or as massless extremals assignable to gravitons.

2. Ordinary particles possibly residing at these space-time sheet have enormous value of Compton length meaning that the density of matter at these space-time sheets must be very slowly varying. The string tension of string like objects implies effective negative pressure characterizing dark energy so that the interpretation in terms of dark energy might make sense [66] . TGD predicted a one-parameter family of Robertson-Walker cosmologies with critical or over-critical mass density and the "pressure" associated with these cosmologies is negative.

3. The quantization of Planck constant does not make sense unless one modifies the view about standard space-time is. Particles with different Planck constant must belong to different worlds in the sense local interactions of particles with different values of $\hbar$ are not possible. This inspires the idea about the book like structure of the imbedding space obtained by gluing almost copies of H together along common "back" and partially labeled by different values of Planck constant.

4. Darkness is a relative notion in this framework and due to the fact that particles at different pages of the book like structure cannot appear in the same vertex of the generalized Feynman diagram. The phase transitions in which partonic 2-surface X^2 during its travel along X^3_l leaks to another page of book are however possible and change Planck constant. Particle (say photon -) exchanges of this kind allow particles at different pages to interact. The interactions are strongly constrained by charge fractionization and are essentially phase transitions involving many particles. Classical interactions are also possible. It might be that we are actually observing dark matter via classical fields all the time and perhaps have even photographed it [77] .

5. The realization that non-standard values of Planck constant give rise to charge and spin fractionization and anyonization led to the precise identification of the prerequisites of anyonic phase [54] . If the partonic 2-surface, which can have even astrophysical size, surrounds the tip of CD, the matter at the surface is anyonic and particles are confined at this surface. Dark matter could

be confined inside this kind of light-like 3-surfaces around which ordinary matter condenses. If the radii of the basic pieces of these nearly spherical anyonic surfaces - glued to a connected structure by flux tubes mediating gravitational interaction - are given by Bohr rules, the findings of Nottale [10] can be understood. Dark matter would resemble to a high degree matter in black holes replaced in TGD framework by light-like partonic 2-surfaces with a minimum size of order Schwartschild radius r_S of order scaled up Planck length $l_{Pl} = \sqrt{\hbar_{gr} G} = GM$. Black hole entropy is inversely proportional to $\hbar$ and predicted to be of order unity so that dramatic modification of the picture about black holes is implied.

6. Perhaps the most fascinating applications are in biology. The anomalous behavior ionic currents through cell membrane (low dissipation, quantal character, no change when the membrane is replaced with artificial one) has a natural explanation in terms of dark supra currents. This leads to a vision about how dark matter and phase transitions changing the value of Planck constant could relate to the basic functions of cell, functioning of DNA and aminoacids, and to the mysteries of bio-catalysis. This leads also a model for EEG interpreted as a communication and control tool of magnetic body containing dark matter and using biological body as motor instrument and sensory receptor. One especially amazing outcome is the emergence of genetic code of vertebrates from the model of dark nuclei as nuclear strings [1, 77] , [1] .

The most general option for the generalized imbedding space

Simple physical arguments pose constraints on the choice of the most general form of the imbedding space.

1. The fundamental group of the space for which one constructs a non-singular covering space or factor space should be non-trivial. This is certainly not possible for M^4, CD, CP_2, or H. One can however construct singular covering spaces. The fixing of the quantization axes implies a selection of the sub-space $H_4 = M^2 \times S^2 \subset M^4 \times CP_2$, where S^2 is geodesic sphere of CP_2. $\hat{M}^4 = M^4 \backslash M^2$ and $\hat{CP}_2 = CP_2 \backslash S^2$ have fundamental group Z since the codimension of the excluded sub-manifold is equal to two and homotopically the situation is like that for a punctured plane. The exclusion of these sub-manifolds defined by the choice of quantization axes could naturally give rise to the desired situation.

2. CP_2 allows two geodesic spheres which left invariant by $U(2$ *resp.* $SO(3)$. The first one is homologically non-trivial. For homologically non-trivial geodesic sphere $H_4 = M^2 \times S^2$ represents a straight cosmic string which is non-vacuum extremal of Kähler action (not necessarily preferred extremal). One can argue that the many-valuedness of $\hbar$ is un-acceptable for non-vacuum extremals so that only homologically trivial geodesic sphere S^2 would be acceptable. One could go even further. If the extremals in $M^2 \times CP_2$ can be preferred non-vacuum extremals, the singular coverings of M^4 are not possible. Therefore only the singular coverings and factor spaces of CP_2 over the homologically trivial geodesic sphere S^2 would be possible. This however looks a non-physical outcome.

   (a) The situation changes if the extremals of type $M^2 \times Y^2$, Y^2 a holomorphic surface of CP_3, fail to be hyperquaternionic. The tangent space M^2 represents hypercomplex sub-space and the product of the modified gamma matrices associated with the tangent spaces of Y^2 should belong to M^2 algebra. This need not be the case in general.

   (b) The situation changes also if one reinterprets the gluing procedure by introducing scaled up coordinates for M^4 so that metric is continuous at $M^2 \times CP_2$ but CDs with different size have different sizes differing by the ratio of Planck constants and would thus have only piece of lower or upper boundary in common.

3. For the more general option one would have four different options corresponding to the Cartesian products of singular coverings and factor spaces. These options can be denoted by $C-C$, $C-F$, $F-C$, and $F-F$, where C (F) signifies for covering (factor space) and first (second) letter signifies for CD (CP_2) and correspond to the spaces $(\hat{CD} \hat{\times} G_a) \times (\hat{CP_2} \hat{\times} G_b)$, $(\hat{CD} \hat{\times} G_a) \times \hat{CP_2}/G_b$, $\hat{CD}/G_a \times (\hat{CP_2} \hat{\times} G_b)$, and $\hat{CD}/G_a \times \hat{CP_2}/G_b$.

4. The groups G_i could correspond to cyclic groups Z_n. One can also consider an extension by replacing M^2 and S^2 with its orbit under more general group G (say tedrahedral, octahedral, or icosahedral group). One expects that the discrete subgroups of $SU(2)$ emerge naturally in this framework if one allows the action of these groups on the singular sub-manifolds M^2 or S^2. This would replace the singular manifold with a set of its rotated copies in the case that the subgroups have genuinely 3-dimensional action (the subgroups which corresponds to exceptional groups in the ADE correspondence). For instance, in the case of M^2 the quantization axes for angular momentum would be replaced by the set of quantization axes going through the vertices of tedrahedron, octahedron, or icosahedron. This would bring non-commutative homotopy groups into the picture in a natural manner.

About the phase transitions changing Planck constant

There are several non-trivial questions related to the details of the gluing procedure and phase transition as motion of partonic 2-surface from one sector of the imbedding space to another one.

1. How the gluing of copies of imbedding space at $M^2 \times CP_2$ takes place? It would seem that the covariant metric of CD factor proportional to $\hbar^2$ must be discontinuous at the singular manifold since only in this manner the idea about different scaling factor of CD metric can make sense. On the other hand, one can always scale the M^4 coordinates so that the metric is continuous but the sizes of CDs with different Planck constants differ by the ratio of the Planck constants.

2. One might worry whether the phase transition changing Planck constant means an instantaneous change of the size of partonic 2-surface in M^4 degrees of freedom. This is not the case. Light-likeness in $M^2 \times S^2$ makes sense only for surfaces $X^1 \times D^2 \subset M^2 \times S^2$, where X^1 is light-like geodesic. The requirement that the partonic 2-surface X^2 moving from one sector of H to another one is light-like at $M^2 \times S^2$ irrespective of the value of Planck constant requires that X^2 has single point of M^2 as M^2 projection. Hence no sudden change of the size X^2 occurs.

3. A natural question is whether the phase transition changing the value of Planck constant can occur purely classically or whether it is analogous to quantum tunneling. Classical non-vacuum extremals of Chern-Simons action have two-dimensional CP_2 projection to homologically non-trivial geodesic sphere S^2_I. The deformation of the entire S^2_I to homologically trivial geodesic sphere S^2_{II} is not possible so that only combinations of partonic 2-surfaces with vanishing total homology charge (Kähler magnetic charge) can in principle move from sector to another one, and this process involves fusion of these 2-surfaces such that CP_2 projection becomes single homologically trivial 2-surface. A piece of a non-trivial geodesic sphere S^2_I of CP_2 can be deformed to that of S^2_{II} using 2-dimensional homotopy flattening the piece of S^2 to curve. If this homotopy cannot be chosen to be light-like, the phase transitions changing Planck constant take place only via quantum tunnelling. Obviously the notions of light-like homotopies (cobordisms) are very relevant for the understanding of phase transitions changing Planck constant.

How one could fix the spectrum of Planck constants?

The question how the observed Planck constant relates to the integers n_a and n_b defining the covering and factors spaces, is far from trivial and I have considered several options. The basic physical inputs are the condition that scaling of Planck constant must correspond to the scaling of the metric of CD (that is Compton lengths) on one hand and the scaling of the gauge coupling strength $g^2/4\pi\hbar$ on the other hand.

1. One can assign to Planck constant to both CD and CP_2 by assuming that it appears in the commutation relations of corresponding symmetry algebras. Algebraist would argue that Planck constants $\hbar(CD)$ and $\hbar(CP_2)$ must define a homomorphism respecting multiplication and division (when possible) by G_i. This requires $r(X) = \hbar(X)\hbar_0 = n$ for covering and $r(X) = 1/n$ for factor space or vice versa.

2. If one assumes that $\hbar^2(X)$, $X = M^4$, CP_2 corresponds to the scaling of the covariant metric tensor g_{ij} and performs an over-all scaling of H-metric allowed by the Weyl invariance of Kähler action by dividing metric with $\hbar^2(CP_2)$, one obtains the scaling of M^4 covariant metric by $r^2 \equiv \hbar^2/\hbar_0^2 = \hbar^2(M^4)/\hbar^2(CP_2)$ whereas CP_2 metric is not scaled at all.

3. The condition that $\hbar$ scales as n_a is guaranteed if one has $\hbar(CD) = n_a\hbar_0$. This does not fix the dependence of $\hbar(CP_2)$ on n_b and one could have $\hbar(CP_2) = n_b\hbar_0$ or $\hbar(CP_2) = \hbar_0/n_b$. The intuitive picture is that n_b- fold covering gives in good approximation rise to n_an_b sheets and multiplies YM action action by n_an_b which is equivalent with the $\hbar = n_an_b\hbar_0$ if one effectively compresses the covering to $CD \times CP_2$. One would have $\hbar(CP_2) = \hbar_0/n_b$ and $\hbar = n_an_b\hbar_0$. Note that the descriptions using ordinary Planck constant and coverings and scaled Planck constant but contracting the covering would be alternative descriptions.

   This gives the following formulas $r \equiv \hbar/\hbar_0 = r(M^4)/r(CP_2)$ in various cases.

	$C-C$	$F-C$	$C-F$	$F-F$
r	n_an_b	$\frac{n_a}{n_b}$	$\frac{n_b}{n_a}$	$\frac{1}{n_an_b}$

Preferred values of Planck constants

Number theoretic considerations favor the hypothesis that the integers corresponding to Fermat polygons constructible using only ruler and compass and given as products $n_F = 2^k \prod_s F_s$, where $F_s = 2^{2^s} + 1$ are distinct Fermat primes, are favored. The reason would be that quantum phase $q = exp(i\pi/n)$ is in this case expressible using only iterated square root operation by starting from rationals. The known Fermat primes correspond to $s = 0, 1, 2, 3, 4$ so that the hypothesis is very strong and predicts that p-adic length scales have satellite length scales given as multiples of n_F of fundamental p-adic length scale. $n_F = 2^{11}$ corresponds in TGD framework to a fundamental constant expressible as a combination of Kähler coupling strength, CP_2 radius and Planck length appearing in the expression for the tension of cosmic strings, and the powers of 2^{11} was proposed to define favored as values of n_a in living matter [23] .

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1+i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that all the four p-adic length scales sith $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm) define scaled up copies of electro-weak and QCD type physics with ordinary value of $\hbar$ and that these physics are induced by dark variants of corresponding lower level physics leads to a prediction for the preferred values of $r = 2^{k_d}$, $k_d = k_i - k_j$, and the resulting picture finds support from the ensuing models for biological evolution and for EEG [23] . This hypothesis - to be referred to as Mersenne hypothesis - replaces the rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant.

How Planck constants are visible in Kähler action?

$\hbar(M^4)$ and $\hbar(CP_2)$ appear in the commutation and anticommutation relations of various superconformal algebras. Only the ratio of M^4 and CP_2 Planck constants appears in Kähler action and is due to the fact that the M^4 and CP_2 metrics of the imbedding space sector with given values of Planck constants are proportional to the corresponding Planck. This implies that Kähler function codes for radiative corrections to the classical action, which makes possible to consider the possibility that higher order radiative corrections to functional integral vanish as one might expect at quantum criticality. For a given p-adic length scale space-time sheets with all allowed values of Planck constants are possible. Hence the spectrum of quantum critical fluctuations could in the ideal case correspond to the spectrum of $\hbar$ coding for the scaled up values of Compton lengths and other quantal lengths and times. If so, large $\hbar$ phases could be crucial for understanding of quantum critical superconductors, in particular high T_c superconductors.

A simple model for fractional quantum Hall effect

The generalization of the imbedding space suggests that it could possible to understand fractional quantum Hall effect [1] at the level of basic quantum TGD as integer QHE for non-standard value of Planck constant.

The formula for the quantized Hall conductance is given by

$$\begin{aligned} \sigma &= \nu \times \frac{e^2}{h} \ , \\ \nu &= \frac{n}{m} \ . \end{aligned} \tag{2.2.1}$$

Series of fractions in $\nu = 1/3, 2/5, 3/7, 4/9, 5/11, 6/13, 7/15...$, $2/3, 3/5, 4/7, 5/9, 6/11, 7/13...$, $5/3, 8/5, 11/7, 14/9...4/3, 7/5, 10/7, 13/9...$, $1/5, 2/9, 3/13...$, $2/7, 3/11...$, $1/7....$ with odd denominator have been observed as are also $\nu = 1/2$ and $\nu = 5/2$ states with even denominator [1] .

The model of Laughlin [16] cannot explain all aspects of FQHE. The best existing model proposed originally by Jain is based on composite fermions resulting as bound states of electron and even number of magnetic flux quanta [13] . Electrons remain integer charged but due to the effective magnetic field electrons appear to have fractional charges. Composite fermion picture predicts all the observed fractions and also their relative intensities and the order in which they appear as the quality of sample improves.

Before proposing the TGD based model of FQHE as IQHE with non-standard value of Planck constant, it is good to represent a simple explanation of IQHE effect. Choose the coordinates of the current currying slab so that x varies in the direction of Hall current and y in the direction of the main current. For IQHE the value of Hall conductivity is given by $\sigma = j_y/E_x = n_e ev/vB = n_e e/B = Ne^2/hBS = Ne^2/mh$, were m characterizes the value of magnetized flux and N is the total number of electrons in the current. In the Landau gauge $A_y = xB$ one can assume that energy eigenstates are momentum eigenstates in the direction of current and harmonic oscillator Gaussians in x-direction in which Hall current runs. This gives

$$\Psi \propto exp(iky) H_n(x + kl^2) exp(-\frac{(x+kl^2)^2}{2l^2}) \ , \quad l^2 = \frac{\hbar}{eB} \ . \tag{2.2.2}$$

Only the states for which the oscillator Gaussian differs considerably from zero inside slab are important so that the momentum eigenvalues are in good approximation in the range $0 \leq k \leq k_{max} = L_x/l^2$. Using $N = (L_y/2\pi) \int_0^{k_{max}} dk$ one obtains that the total number of momentum eigenstates associated with the given value of n is $N = eBdL_xL_y/h = n$. If ν Landau states are filled, the value of σ is $\sigma = \nu e^2/h$.

The interpretation of FQHE as IQHE with non standard value of Planck constant could explain also the fractionization of charge, spin, and electron number. There are $2 \times 2 = 4$ combinations of covering and factor spaces of CP_2 and three of them can lead to the increase or at least fractionization of the Planck constant required by FQHE.

1. The prediction for the filling fraction in FQHE would be

$$\nu = \nu_0 \frac{\hbar_0}{\hbar} \ , \quad \nu_0 = 1, 2, ... \ . \tag{2.2.3}$$

   ν_0 denotes the number of filled Landau levels.

2. Let us denote the options as C-C, C-F, F-C, F-F, where the first (second) letter tells whether a singular covering or factor space of CD (CP_2) is in question. The observed filling fractions are consistent with options C-C, C-F, and F-C for which CD or CP_2 or both correspond to a singular covering space. The values of ν in various cases are given by the following table.

Option	$C-C$	$C-F$	$F-C$
ν	$\frac{\nu_0}{n_a n_b}$	$\frac{\nu_0 n_b}{n_a}$	$\frac{\nu_0 n_a}{n_b}$

(2.2.4)

   There is a complete symmetry under the exchange of CD and CP_2 as far as values of ν are considered.

3. All three options are consistent with observations. Charge fractionization allows only the options $C-C$ and $F-C$. If one believes the general arguments stating that also spin is fractionized in FQHE then only the option $C-C$, for which charge and spin units are equal to $1/n_b$ and $1/n_a$ respectively, remains. For $C-C$ option one must allow $\nu_0 > 1$.

4. Both $\nu = 1/2$ and $\nu = 5/2$ state has been observed [1, 9] . The fractionized charge is believed to be $e/4$ in the latter case [19, 17] . This requires $n_b = 4$ allowing only (C, C) and (F, C) options. $n_i \geq 3$ holds true if coverings and factor spaces are correlates for Jones inclusions and this gives additional constraint. The minimal values of (ν_0, n_a, n_b) are $(2, 1, 4)$ for $\nu = 1/2$ and $(10, 1, 4)$ for $\nu = 5/2$) for both $C-C$ and $F-C$ option. Filling fraction $1/2$ corresponds in the composite fermion model and also experimentally to the limit of zero magnetic field [13] . $n_b = 2$ would be inconsistent with the observed fractionization of electric charge for $\nu = 5/2$ and with the vision inspired by Jones inclusions implying $n_i \geq 3$.

5. A possible problematic aspect of the TGD based model is the experimental absence of even values of m except $m = 2$ (Laughlin's model predicts only odd values of m). A possible explanation is that by some symmetry condition possibly related to fermionic statistics (as in Laughlin model) both n_a and n_b must be odd. This would require that $m = 2$ case differs in some manner from the remaining cases.

6. Large values of m in $\nu = n/m$ emerge as B increases. This can be understood from flux quantization. One has $e \int BdS = n\hbar$. By using actual fractional charge $e_F = e/n_b$ in the flux factor would give for (C, C) option $e_F \int BdS = nn_a\hbar_0$. The interpretation is that each of the n_b sheets contributes one unit to the flux for e. Note that the value of magnetic field at given sheet is not affected so that the build-up of multiple covering seems to keep magnetic field strength below critical value.

7. The understanding of the thermal stability is not trivial. The original FQHE was observed in 80 mK temperature corresponding roughly to a thermal energy of $T \sim 10^{-5}$ eV. For graphene the effect is observed at room temperature. Cyclotron energy for electron is (from $f_e = 6 \times 10^5$ Hz at $B = .2$ Gauss) of order thermal energy at room temperature in a magnetic field varying in the range 1-10 Tesla. This raises the question why the original FQHE requires such a low temperature. A possible explanation is that since FQHE involves several values of Planck constant, it is quantum critical phenomenon and is characterized by a critical temperature. The differences of single particle energies associated with the phase with ordinary Planck constant and phases with different Planck constant would characterize the transition temperature.

2.2.2 Could the dynamics of Kähler action predict the hierarchy of Planck constants?

The original justification for the hierarchy of Planck constants came from the indications that Planck constant could have large values in both astrophysical systems involving dark matter and also in biology. The realization of the hierarchy in terms of the singular coverings and possibly also factor spaces of CD and CP_2 emerged from consistency conditions. The formula for the Planck constant involves heuristic guess work and physical plausibility arguments. There are good arguments in favor of the hypothesis that only coverings are possible. Only a finite number of pages of the Big Book correspond to a given value of Planck constant, biological evolution corresponds to a gradual dispersion to the pages of the Big Book with larger Planck constant, and a connection with the hierarchy of infinite primes and p-adicization program based on the mathematical realization of finite measurement resolution emerges.

One can however ask whether this hierarchy could emerge directly from the basic quantum TGD rather than as a separate hypothesis. The following arguments suggest that this might be possible. One finds also a precise geometric interpretation of preferred extremal property interpreted as criticality in zero energy ontology.

1-1 correspondence between canonical momentum densities and time derivatives fails for Kähler action

The basic motivation for the geometrization program was the observation that canonical quantization for TGD fails. To see what is involved let us try to perform a canonical quantization in zero energy ontology at the 3-D surfaces located at the light-like boundaries of $CD \times CP_2$.

1. In canonical quantization canonical momentum densities $\pi_k^0 \equiv \pi_k = \partial L_K/\partial(\partial_0 h^k)$, where $\partial_0 h^k$ denotes the time derivative of imbedding space coordinate, are the physically natural quantities in terms of which to fix the initial values: once their value distribution is fixed also conserved charges are fixed. Also the weak form of electric-magnetic duality given by $J^{03}\sqrt{g_4} = 4\pi\alpha_K J_{12}$ and a mild generalization of this condition to be discussed below can be interpreted as a manner to fix the values of conserved gauge charges (not Noether charges) to their quantized values since Kähler magnetic flux equals to the integer giving the homology class of the (wormhole) throat. This condition alone need not characterize criticality, which requires an infinite number of deformations of X^4 for which the second variation of the Kähler action vanishes and implies infinite number conserved charges. This in fact gives hopes of replacing π_k with these conserved Noether charges.

2. Canonical quantization requires that $\partial_0 h^k$ in the energy is expressed in terms of π_k. The equation defining π_k in terms of $\partial_0 h^k$ is however highly non-linear although algebraic. By taking squares the equations reduces to equations for rational functions of $\partial_0 h^k$. $\partial_0 h^k$ appears in contravariant and covariant metric at most quadratically and in the induced Kähler electric field linearly and by multplying the equations by $det(g_4)^3$ one can transform the equations to a polynomial form so that in principle $\partial_0 h^k$ can obtained as a solution of polynomial equations.

3. One can always eliminate one half of the coordinates by choosing 4 imbedding space coordinates as the coordinates of the spacetime surface so that the initial value conditions reduce to those for the canonical momentum densities associated with the remaining four coordinates. For instance, for space-time surfaces representable as map $M^4 \to CP_2$ M^4 coordinates are natural and the time derivatives $\partial_0 s^k$ of CP_2 coordinates are multivalued. One would obtain four polynomial equations with $\partial_0 s^k$ as unknowns. In regions where CP_2 projection is 4-dimensional -in particular for the deformations of CP_2 vacuum extremals the natural coordinates are CP_2 coordinates and one can regard $\partial_0 m^k$ as unknows. For the deformations of cosmic strings, which are of form $X^4 = X^2 \times Y^2 \subset M^4 \times CP_2$, one can use coordinates of $M^2 \times S^2$, where S^2 is geodesic sphere as natural coordinates and regard as unknowns E^2 coordinates and remaining CP_2 coordinates.

4. One can imagine solving one of the four polynomials equations for time derivaties in terms of other obtaining N roots. Then one would substitute these roots to the remaining 3 conditions to obtain algebraic equations from which one solves then second variable. Obviously situation is very complex without additional symmetries. The criticality of the preferred extremals might however give additional conditions allowing simplifications. The reasons for giving up the canonical quantization program was following. For the vacuum extremals of Kähler action π_k are however identically vanishing and this means that there is an infinite number of value distributions for $\partial_0 h^k$. For small deformations of vacuum extremals one might however hope a finite number of solutions to the conditions and thus finite number of space-time surfaces carrying same conserved charges.

If one assumes that physics is characterized by the values of the conserved charges one must treat the the many-valuedness of $\partial_0 h^k$. The most obvious guess is that one should replace the space of space-like 4-surfaces corresponding to different roots $\partial_0 h^k = F^k(\pi_l)$ with four-surfaces in the covering space of $CD \times CP_2$ corresponding to different branches of the many-valued function $\partial_0 h^k = F(\pi_l)$ co-inciding at the ends of CD.

Do the coverings forces by the many-valuedness of $\partial_0 h^k$ correspond to the coverings associated with the hierarchy of Planck constants?

The obvious question is whether this covering space actually corresponds to the covering spaces associated with the hierarchy of Planck constants. This would conform with quantum classical correspondence. The hierarchy of Planck constants and hierarchy of covering spaces was introduced to cure

the failure of the perturbation theory at quantum level. At classical level the multivaluedness of $\partial_0 h^k$ means a failure of perturbative canonical quantization and forces the introduction of the covering spaces. The interpretation would be that when the density of matter becomes critical the space-time surface splits to several branches so that the density at each branches is sub-critical. It is of course not at all obvious whether the proposed structure of the Big Book is really consistent with this hypothesis and one also consider modifications of this structure if necessary. The manner to proceed is by making questions.

1. The proposed picture would give only single integer characterizing the covering. Two integers assignable to CD and CP_2 degrees of freedom are however needed. How these two coverings could emerge?

   (a) One should fix also the values of $\pi_k^n = \partial L_K/\partial h_n^k$, where n refers to space-like normal coordinate at the wormhole throats. If one requires that charges do not flow between regions with different signatures of the metric the natural condition is $\pi_k^n = 0$ and allows also multi-valued solution. Since wormhole throats carry magnetic charge and since weak form of electric-magnetic duality is assumed, one can assume that CP_2 projection is four-dimensional so that one can use CP_2 coordinates and regard $\partial_0 m^k$ as un-knows. The basic idea about topological condensation in turn suggests that M^4 projection can be assumed to be 4-D inside space-like 3-surfaces so that here $\partial_0 s^k$ are the unknowns. At partonic 2-surfaces one would have conditions for both π_k^0 and π_k^n. One might hope that the numbers of solutions are finite for preferred extremals because of their symmetries and given by n_a for $\partial_0 m^k$ and by n_b for $\partial_0 s^k$. The optimistic guess is that n_a and n_b corresponds to the numbers of sheets for singular coverings of CD and CP_2. The covering could be visualized as replacement of space-time surfaces with space-time surfaces which have $n_a n_b$ branches. n_b branches would degenerate to single branch at the ends of diagrams of the generaled Feynman graph and n_a branches would degenerate to single one at wormhole throats.

   (b) This picture is not quite correct yet. The fixing of π_k^0 and π_k^n should relate closely to the effective 2-dimensionality as an additional condition perhaps crucial for criticality. One could argue that both π_k^0 and π_k^n must be fixed at X^3 and X_l^3 in order to effectively bring in dynamics in two directions so that X^3 could be interpreted as a an orbit of partonic 2-surface in space-like direction and X_l^3 as its orbit in light-like direction. The additional conditions could be seen as gauge conditions made possible by symplectic and Kac-Moody type conformal symmetries. The conditions for π_0^k would give n_b branches in CP_2 degrees of freedom and the conditions for π_k^n would split each of these branches to n_a branches.

   (c) The existence of these two kinds of conserved charges (possibly vanishing for π_k^n) could relate also very closely to the slicing of the space-time sheets by string world sheets and partonic 2-surfaces.

2. Should one then treat these branches as separate space-time surfaces or as a single space-time surface? The treatment as a single surface seems to be the correct thing to do. Classically the conserved changes would be $n_a n_b$ times larger than for single branch. Kähler action need not (but could!) be same for different branches but the total action is $n_a n_b$ times the average action and this effectively corresponds to the replacement of the $\hbar_0/g_K^2$ factor of the action with $\hbar/g_K^2$, $r \equiv \hbar/\hbar_0 = n_a n_b$. Since the conserved quantum charges are proportional to $\hbar$ one could argue that $r = n_a n_b$ tells only that the charge conserved charge is $n_a n_b$ times larger than without multi-valuedness. $\hbar$ would be only effectively $n_a n_b$ fold. This is of course poor man's argument but might catch something essential about the situation.

3. How could one interpret the condition $J^{03}\sqrt{g_4} = 4\pi\alpha_K J_{12}$ and its generalization to be discussed below in this framework? The first observation is that the total Kähler electric charge is by $\alpha_K \propto 1/(n_a n_b)$ same always. The interpretation would be in terms of charge fractionization meaning that each branch would carry Kähler electric charge $Q_K = n g_K/n_a n_b$. I have indeed suggested explanation of charge fractionization and quantum Hall effect based on this picture.

4. The vision about the hierarchy of Planck constants involves also assumptions about imbedding space metric. The assumption that the M^4 covariant metric is proportional to $\hbar^2$ follows from the physical idea about $\hbar$ scaling of quantum lengths as what Compton length is. One can

always introduce scaled M^4 coordinates bringing M^4 metric into the standard form by scaling up the M^4 size of CD. It is not clear whether the scaling up of CD size follows automatically from the proposed scenario. The basic question is why the M^4 size scale of the critical extremals must scale like $n_a n_b$? This should somehow relate to the weak self-duality conditions implying that Kähler field at each branch is reduced by a factor $1/r$ at each branch. Field equations should posses a dynamical symmetry involving the scaling of CD by integer k and $J^{0\beta}\sqrt{g_4}$ and $J^{n\beta}\sqrt{g_4}$ by $1/k$. The scaling of CD should be due to the scaling up of the M^4 time interval during which the branched light-like 3-surface returns back to a non-branched one.

5. The proposed view about hierarchy of Planck constants is that the singular coverings reduce to single-sheeted coverings at $M^2 \subset M^4$ for CD and to $S^2 \subset CP_2$ for CP_2. Here S^2 is any homologically trivial geodesic sphere of CP_2 and has vanishing Kähler form. Weak self-duality condition is indeed consistent with any value of $\hbar$ and impies that the vacuum property for the partonic 2-surface implies vacuum property for the entire space-time sheet as holography indeed requires. This condition however generalizes. In weak self-duality conditions the value of $\hbar$ is free for any 2-D Lagrangian sub-manifold of CP_2.

   The branching along M^2 would mean that the branches of preferred extremals always collapse to single branch when their M^4 projection belongs to M^2. Magnetically charged light-light-like throats cannot have M^4 projection in M^2 so that self-duality conditions for different values of $\hbar$ do not lead to inconsistencies. For spacelike 3-surfaces at the boundaries of CD the condition would mean that the M^4 projection becomes light-like geodesic. Straight cosmic strings would have M^2 as M^4 projection. Also CP_2 type vacuum extremals for which the random light-like projection in M^4 belongs to M^2 would represent this of situation. One can ask whether the degeneration of branches actually takes place along any string like object $X^2 \times Y^2$, where X^2 defines a minimal surface in M^4. For these the weak self-duality condition would imply $\hbar = \infty$ at the ends of the string. It is very plausible that string like objects feed their magnetic fluxes to larger space-times sheets through wormhole contacts so that these conditions are not encountered.

Connection with the criticality of preferred extremals

Also a connection with quantum criticality and the criticality of the preferred extremals suggests itself. Criticality for the preferred extremals must be a property of space-like 3-surfaces and light-like 3-surfaces with degenerate 4-metric and the degeneration of the $n_a n_b$ branches of the space-time surface at the its ends and at wormhole throats is exactly what happens at criticality. For instance, in catastrophe theory roots of the polynomial equation giving extrema of a potential as function of control parameters co-incide at criticality. If this picture is correct the hierarchy of Planck constants would be an outcome of criticality and of preferred extremal property and preferred extremals would be just those multi-branched space-time surfaces for which branches co-incide at the the boundaries of $CD \times CP_2$ and at the throats.

2.2.3 Dark atoms and dark cyclotron states

The development of the notion of dark atom involves many side tracks which make me blush. The first naive guess was that dark atom would be obtained by simply replacing Planck constant with its scaled counterpart in the basic formulas and interpreting the results geometrically. After some obligatory twists and turns it became clear that this assumption is indeed the most plausible one. The main source of confusion has been the lack of precise view about what the hierarchy of Planck constants means at the level of imbedding space at space-time.

The rules are very simple when one takes the singular coverings assigned to the many-valuedness of the time-derivatives of imbedding space coordinates as functions of canonical momentum densities as a starting point.

1. The mass and charge of electron are fractionized as is also the reduced mass in Schrödinger equation. This implies the replacements $e \to e/r$, $m \to m/r$, and $\hbar \to r\hbar_0$, $r = n_a n_b$, in the general formula for the binding energy assigned with single sheet of the covering. If maximal number $n_a n_b$ are present corresponding to a full "Fermi sphere", the total binding energy is r times the binding energy associated with single sheet.

2. In the case of hydrogen atom the proportionality $E \propto m/\hbar^2$ implies that the binding energy for single sheet of the covering scales as $E \to E/(n_a n_b)^3$ and maximal binding energy scales as $E \to E/(n_a n_b)^2$. This conforms with the naive guess. For high values of the nuclear charge Z it can happen that the binding energy is larger than the rest mass and fractionization might take place when binding energy is above critical fraction of the rest mass.

3. In the case of cyclotron energies one must must decide what happens to the magnetic flux. Magnetic flux quantization states that the flux is proportional to $\hbar$ for each sheet separately. Hence one has $\Phi \to r\Phi$ for each sheet and the total flux scales as r^2. Since the dimensions of the flux quantum are scaled up by r the natural scaling of the size of flux quantum is by r^2. Therefore the quantization of the magnetic flux requires the scaling $B \to B/r$. The cyclotron energy for single sheet satisfies $E \propto \hbar qB/m$ and since both mass m and charge q become fractional , the energy E for single sheet remains invariant whereas total cyclotron energy is scaled up by r in accordance with the original guess and the assumption used in applications.

4. Dark cyclotron states are expected to be stable up to temperatures which are r times higher than for ordinary cyclotron states. The states of dark hydrogen atoms and its generalizations are expected to be stable at temperatures scaled down by $1/r^2$ in the first approximation.

5. Similar arguments allow to deduce the values of binding energies in the general case once the formula of the binding energy given by standard quantum theory is known.

The most general option option allows fractional atoms with proton and electron numbers varying from $1/r$ to 1. One can imagine also the possibility of fractional molecules. The analogs of chemical bonds between fractional hydrogen atoms with $N - k$ and k fractional electrons and protons can be considered and would give rise to a full shell of fractional electrons possessing an exceptional stability. These states would have proton and electron numbers equal to one.

Catalytic sites are one possible candidate for fractal electrons and catalyst activity might be perhaps understood as a strong tendency of fractal electron and its conjugate to fuse to form an ordinary electron.

2.2.4 Dark matter and mind: general ideas

Dark matter is identified as a macroscopic quantum phase with large $\hbar$ for which particles have complex conformal weights.

The sum of the imaginary parts of conformal weights assumed for number theoretical reasons to be expressible as sums of imaginary parts for the zeros of Riemann Zeta would define a new conserved quantum number, "scaling momentum" [17] . The conjugation of the complex conformal weight would distinguish between quantum states and their phase conjugates. This point is important since phase conjugate photons represent negative energy signals propagating into geometric past, assumed to be distinguishable from positive energy signals propagating into geometric future, play a key role in TGD based biology: this distinction cannot be made in QFT context.

Living matter could be matter with a large value of $\hbar$ and hence dark, and form conformally confined blobs behaving like single units with extremely quantal properties, including free will and intentional action in time scales familiar to us. Dark matter would be responsible for the mysterious vital force.

Any system for which some interaction becomes so strong that perturbation theory does not work, could give rise to this kind of system in a phase transition in which $\hbar$ increases to not lose perturbativity gives rise to this kind of "super-quantal" matter. In this sense emergence would corresponds to strong coupling. The interpretation would be that strong fluctuations at strong coupling give rise to a large number of orbifold points so that the S-matrix elements to a phase with larger Planck constant become large. Dark matter made possible by dynamical $\hbar$ is necessary for macroscopic and macro-temporal quantum coherence and is thus prerequisite for emergence.

Physically large $\hbar$ means a larger unit for quantum numbers and this requires that single particle states form larger particle like units. This kind of collective states with weak mutual interactions are of course very natural in strongly interacting systems. The N sheets of $M^4_\pm$, where N is the order of group G_b involved with the Jones inclusion in question. Each partonic 2-surface appears as N geometrically identical copies which can however carry different fermionic quantum numbers. Hence

the N-fold space-time sheet carry up to N G_b invariant partons with identical quantum numbers so that an effective breaking of Fermi statistics becomes possible.

One implication would be the notion of N-atom, which at the level of quantum jumps quantum jumps integrate effectively to single quantum jump and longer moments of consciousness result. Entire hierarchy of size scales for matter blobs is predicted corresponding to values of $\hbar$. The larger the value of $\hbar$ the longer the characteristic time scale of consciousness and of a typical life cycle.

In RHIC color glass condensate resembles incompressible liquid. Liquids might be liquids because they contain some dark matter at magnetic/Z^0 magnetic flux tubes (darkness follows from the large value of $\hbar$). Incompressibility of liquid could correspond to maximal density of flux tubes and to the fact that magnetic fields have no sources. In accordance with the previous ideas already water could be living and conscious system in some primitive sense.

The notion of field body in turn means that dark matter at the magnetic flux tubes would serve as an intentional agent using biological body as a motor instrument and sensory receptor. Dark matter would be the miraculous substance that living systems are fighting for, and perhaps the most important substance in metabolic cycle.

Hierarchy of dark matters and hierarchy of minds

The notion of dark matter is only relative concept in the sense that dark matter is invisible from the point of view of the ordinary matter. One can imagine an entire hierarchy of dark matter structures corresponding to the hierarchy of space-time sheets for which p-adic length scales differ by a factors $r = 2^{k_d}$ allowed by Mersenne hypothesis. The BE condensates of N_{cr} ordinary matter particles would serve as dynamical units for "doubly dark matter" invisible to the dark matter. The above discussed criticality criterion can be applied at all levels of the hierarchy to determine the value of the dynamical interaction strength for which BE condensates of BE condensates are formed.

The most interesting new physics would emerge from the interaction between length scales with different Planck constant but same scaled up variant of the p-adic length scale made possible by the decay of BE condensates of dark photons to ordinary photons having wavelength shorter by a factor $1/r$. This interaction could provide the royal road to the quantitative understanding how living matter manages to build up extremely complex coherent interactions between different length and time scales.

In the time domain dark matter hierarchy could allow to understand how moments of consciousness organize to a hierarchy with respect to the time scales of moment of consciousness coming as 2^{k_d} multiples of CP_2 time scale. Even human life span could be seen as single moment of consciousness at $k_d = 154$ level of the dark matter hierarchy.

Realization of intentional action and hierarchy of dark matters

How long length scales are able to control the dynamics in short length scales so that the extremely complex process extending down to atomic length scales realizing my intention to write this word is possible. This question has remained without a convincing answer in the recent day biology and there strong objections against the idea that this process is planned and initiated at neuronal level.

I have proposed a concrete mechanism for the realization of intentional action in terms of time mirror mechanism involving the emission of negative energy photons and proceeding as a cascade in a reversed direction of geometric time from long to short length scales [79] . This cascade would induce as a reaction analogous processes proceeding in the normal direction of geometric time as a response and would correspond to the neural correlates of intentional action in very general sense of the word.

The counterparts for the negative energy signals propagating to the geometric past would be phase conjugate (negative energy) laser beams identifiable as Bose-Einstein condensates of dark photons. In the time reflection these beams would transform to positive energy dark matter photons eventually decaying to ordinary photons. The space-time correlate would be MEs decaying into MEs and eventually to CP_2 type extremals representing ordinary photons.

The realization of intentional action as desires of boss expressed to lower level boss would naturally represented the decay of the phase conjugate dark laser beam to lower level laser beams decaying to lower level laser beams decaying to... . This would represent the desire for action whereas the time reflection at some level would represent the realization desire as stepwise decay to lower level laser beams and eventually to ordinary photons. The strong quantitative prediction would be that these

levels correspond to a length and time scale hierarchies consistent with Mersenne hypothesis or more general ruler and compass hypothesis.

Wave-length hierarchy, coherent metabolism, and proton-electron mass ratio

The fact that a given wavelength length corresponds to energies related to each other by a scaling with powers of v_0 provides a mechanism allowing to transfer energy from long to short long scales by a de-coherence occurring either in the standard or reversed direction of geometric time. De-coherence in the reversed direction of time would be associated with mysterious looking processes like self-assembly allowing thus an interpretation as a normal decay process in reversed time direction.

It is perhaps not an accident that the value of $v_0 \simeq 4.6 \times 10^{-4}$ is not too far from the ratio of $m_e/m_p \simeq 5.3 \times 10^{-4}$ giving the ratio of zero point kinetic energies of proton and electron for a given space-time sheet. Proton mass ratio $m_p/m_e = 1836.15267261$ corresponds in good approximation to $n = 2^2 \times 3^3 \times 17 = 1836$. This integer is of form $n = 9 \times n_F$. This co-incidence could in principle make possible a metabolic mechanism in which dark protons and ordinary electrons co-operate in the sense that dark protons generate dark photon BE condensates with wave length λ transforming to ordinary photons with wavelength $v_0\lambda$ absorbed by ordinary electrons.

Some examples are in order to illustrate these ideas.

1. As already found, in the case of dark atoms the scaling of binding energies as $1/\hbar^2$ allows the coupling of ~ 9 cm scale of brain hemisphere with the length scale ~ 50 μm of large neuron. $N_{cr} \leq 137$ ordinary IR photons would be emitted in single burst and interacting with neuron.

2. For a non-relativistic particle in a box of size L the energy scale is given by $E_1 = \hbar^2\pi^2/2mL^2$ so that the visible photons emitted would have energy scaled up by a factor $(\hbar_s/\hbar)^2 \simeq 4 \times 10^6$. The collective dropping of N_{cr} dark protons to larger space-time sheet would liberate a laser beam of dark photons with energy equal to the liberated zero point kinetic energy. For instance, for the p-adic length scale $L(k = 159 = 3 \times 53) \simeq .63$ μm this process would generate laser beam of IR dark photons with energy $\sim .5$ eV also generated by the dropping of ordinary protons from $k = 137$ atomic space-time sheet. There would thus be an interaction between dark protons in cell length scale and ordinary protons in atomic length scale. For instance, the dropping of dark protons in cell length scale could induce driving of protons back to the atomic space-time sheet essential for the metabolism [37] . Similar argument applies to electrons with the scale of the zero point kinetic energy about 1 keV.

3. If the energy spectrum associated with the conformational degrees of freedom of proteins, which corresponds roughly to a frequency scale of 10 GHz remains also invariant in the phase transition to dark protein state, coherent emissions of dark photons with microwave wave lengths would generate ordinary infrared photons. For instance, metabolic energy quanta of $\sim .5$ eV could result from macroscopic Bose-Einstein condensates of 58 GHz dark photons resulting from the oscillations in the conformational degrees of freedom of dark proteins. A second option is that the conformal energies are scaled by $\hbar_s/\hbar$ (ω would remain invariant). In this case these coherent excitations would generate ordinary photons with energy of about 1 keV able to drive electrons back to the atomic $k = 137$ space-time sheet.

4. Since magnetic flux tubes have a profound role in TGD inspired theory of consciousness, it is interesting to look also for the behavior of effective magnetic transition energies in the phase transition to the dark matter phase. This transition increases the scale of the magnetic interaction energy so that anomalously large magnetic spin splitting $\hbar_s eB/m$ in the external magnetic field could serve as a signature of dark atoms. The dark transition energies relate by a factor $\hbar_s/\hbar$ to the ordinary magnetic transition energies.

For instance, in the magnetic field $B_{end} = 2B_E/5 = .2$ Gauss, where $B_E = .5$ Gauss is the nominal value of the Earth's magnetic field, explaining the effects of ELF em fields on vertebrate brain, dark electron cyclotron frequency is 6×10^5 Hz and corresponds to ordinary microwave photon with frequency ~ 1.2 GHz and wavelength $\lambda \simeq 25$ cm. For proton the cyclotron frequency of 300 Hz would correspond to energy of ordinary photon with frequency of 6×10^5 Hz and could induce electronic cyclotron transitions and spin flips in turn generating for instance magneto-static waves.

It is easy to imagine a few step dark matter hierarchy connecting EEG frequencies of dark matter with frequencies of visible light for ordinary photons. This kind of hierarchy would give considerable concreteness for the notion of magnetic body having size scale of Earth.

A connection with bio-photons

The biologically active radiation at UV energies was first discovered by Russian researcher Gurwitz using a very elegant experimental arrangement [163] . Gurwitz christened this radiation mitogenetic radiation since it was especially intense during the division of cell.

A direct proof for the biological activity of mitogenetic radiation consisted of a simple experiment in which either quartz or glass plate was put between two samples. The first sample contained already growing onion roots whereas the second sample contained roots which did not yet grow. In the case of quartz plate no stimulation of growth occurred unlike for glass plate. Since quartz is not transparent to UV light whereas the ordinary glass is, the conclusion was that the stimulation of growth is due to UV light.

The phenomenon was condemned by skeptics as a pseudo science and only the modern detection technologies demonstrated its existence [132] , and mitogenetic radiation became also known as bio-photons (the TGD based model for bio-photons is discussed in [37]). Bio-photons form a relatively featureless continuum at visible wavelengths continuing also to UV energies, and are believed to be generated by DNA or at least to couple with DNA. The emission of bio-photons is most intense from biologically active organisms and the irradiation by UV light induces an emission of mitogenetic radiation by a some kind of amplification mechanism. It has been suggested that bio-photons represent some kind of leakage of a coherent light emitted by living matter.

According to Russian researcher V. M. Injushin [170] , mitochondrios emit red light at wavelengths 620 nm and 680 nm corresponding to energies 2 eV and 1.82 eV. According to the same source, the nucleus of cell sends UV light at wavelengths 190, 280 and 330 nm corresponding to the energies 6.5, 4.4 and 3.8 eV. The interpretation as a kind of leakage of coherent light would conform with the identification in terms of BE condensates of dark photons with $\hbar_s/\hbar \simeq 2^{k_d}$ decaying to photons with energies visible and UV range. The model for the cell membrane as almost vacuum extremal [23] leads to a successful prediction of the frequencies of peak sensitivity for four kinds of photoreceptors and allows to identify biophotons as decay products of dark Josephson photons. Also EEG photons can be understood as decay products of Josephson photons. Also a fractal generalization of EEG emerges.

The analysis of Kirlian photographs has shown that the pattern of visible light emitted by various body parts, for instance ear, code information about other body parts [162] . These bio-holograms for which a general model is discussed in [9] could be realized as dark photon laser beams.

In phantom DNA effect [148] a chamber containing DNA is irradiated with a visible laser light and the DNA generates as a response coherent visible radiation at same wavelength. Strangely enough, the chamber continues to emit weak laser light even after the removal of DNA. This effect could be due to the decay of a dark photon BE condensate remaining in the chamber. Also the findings of Peter Gariaev [149] about the effects of visible laser light on DNA, in particular the stimulated emission of radio waves in kHz-MHz frequency range might also relate to dark photons somehow.

A connection with the scaling law of homeopathy

The value of the parameter $1/v_0 \simeq 2083$ is essentially the ratio of CP_2 radius and Planck length scale (as also the ratio of Compton lengths of electron and proton) and rather near to $2^{11} = 2048$. This inspired the idea that powers of 2^{11} might define a hierarchy of preferred value of Planck constant. It however seems that this hypothesis is quite too restrictive. Interestingly, much larger number $2\times 10^{11} \simeq 3 \times 2^{36}$ appears in the simplest form for what I have christened the scaling law of homeopathy [34] . This rule has been proposed on basis of experimental findings [204] but has no convincing theoretical justification. The scaling law of homeopathy states that high frequency em radiation transforms to a low frequency radiation and vice versa preferably with the frequency ratio $f_{high}/f_{low} \simeq 2 \times 10^{11}$.

The proposed hierarchy of dark matter and ensuing hierarchy of dark laser beams decaying into lower level beams might provide a deeper explanation for the scaling law of homeopathy. The factor 2×10^{11} is with 3 per cent accuracy equal to the integer $n_F = 3 \times 2^{36} \simeq 2.06 \times 10^{11}$ characterizing ruler and compass quantum phase. Hence the interpretation in terms of a phase transition leading from a phase with a large value of Planck constant $\hbar = n_F\hbar_0$ to ordinary phase is possible.

In [34] I have discussed some mechanisms for the transformation of high energy photons to low energy photons consistent with the rule and proposed a generalization of the rule based on p-adic length scale hypothesis. For instance, high energy visible photons of frequency f could induce an excitation of the receiving system having same frequency, propagating with velocity $\beta = v/c \simeq 10^{-11}/2$, and having wave length equal $\lambda_0 = f/v = \lambda/\beta$. This excitation would in turn couple to photons of wavelength λ_0 and frequency $f_0 = \beta f$.

2.2.5 Dark matter hierarchy, sensory representations, and motor action

Dark matter hierarchy allows to develop a detailed model for how magnetic bodies use biological bodies as sensory receptors and motor instruments [23] leading among other things to a generalization of the notion of genome.

For ordinary quantum mechanics photons at EEG frequencies correspond to ridiculously small energies. Dark matter hierarchy is accompanied by a hierarchy of EEGs and its generalizations with the scalings of frequencies predicted by Mersenne hypothesis to come as powers 2^{-k_d} [23] . For $k_d = 44$ the energies of EEG photons are above thermal threshold at room temperature for $f \geq 1$ Hz,.

The fact that arbitrarily small frequencies can correspond to energies above thermal threshold at higher levels of dark matter hierarchy implies that photons with arbitrarily low frequencies can have sizable physical effects on matter. This conforms with the findings about the effects of ELF em fields on living matter [23] , and these effects allow to develop a rather detailed model for EEG and identify the parts of EEG correlating with communications of sensory data to the magnetic body and with quantum control performed by the magnetic body [23] .

Bose-Einstein condensates at magnetic flux quanta in astrophysical length scales

The new model for the topological condensation at magnetic flux quanta of Earth's magnetic field is based on the dark matter hierarchy with levels characterized by the value of $\hbar = 2^{k_d}\hbar_0$, where k_d is given by Mersenne hypothesis.

1. There are several levels of dynamics. In topological condensation the internal dynamics of ions is unaffected and $\hbar$ has the ordinary value. The formation of Cooper pairs involves dynamics at relatively lo level of dark matter hierarchy. Also the dynamics of ionic Cooper pairs remains unaffected in the topological condensation to magnetic flux quanta with larger value of Planck constant.

2. Cyclotron energies scale as as $\hbar$ so that for a sufficiently high value of k thermal stability of cyclotron states at room temperature is achieved for given value of field strength.

3. If the flux quanta of Earth's magnetic field correspond to $k = 44$ level of dark matter hierarchy, cyclotron energies $E = (\hbar/2\pi) \times ZeB/Am_p$ are scaled up by a factor 2^{44} from their ordinary values and are above thermal energy at room temperature for $A \leq 233Z$, where Z is the charge of the ion. Even for $Z = 1$ this includes all stable nuclei. Bose-Einstein condensates of bosonic ions are thus possible at room temperatures at Earth's surface.

Fractal hierarchy of magnetic flux sheets

The notion of magnetic body is central in the TGD inspired theory of living matter. Every system possesses magnetic body and there are strong reasons to believe that the magnetic body associated with human body is of order Earth size and that there could be hierarchy of these bodies with even much larger sizes. Therefore the question arises what distinguishes between the magnetic bodies of Earth and human body. The quantization of magnetic flux suggests an answer to this question.

1. If Josephson photons are transformed to a bunch of ordinary small $\hbar$ photons magnetic flux tubes can correspond to the ordinary value of Planck constant. If one assumes the quantization of the magnetic flux in the form

$$\int BdA = n\hbar$$

used in super-conductivity, the radius of the flux tube must increase as $\sqrt{\hbar}$ and if the Josephson frequency is reduced to the sound frequency, the value of $\hbar$ codes for the sound frequency. This leads to problems since the transversal thickness of flux tubes becomes too large. This does not however mean that the condition might not make sense: for instance, in the case of flux sheets going through DNA strands the condition might apply.

2. The quantization of magnetic flux could be replaced by a more general condition

$$\oint (p - ZeA)dl = n\hbar \ , \tag{2.2.5}$$

where p represents momentum of particle of super-conducting phase at the boundary of flux tube. In this case also $n = 0$ is possible and poses no conditions on the thickness of the flux tube as a function of $\hbar$. This option looks reasonable in length scales assignable to biological body (say flux tubes assignable to axonal membranes and DNA strands since the charged particles at the boundary of flux tube would act as sources of the magnetic field. At the level of magnetic body of Earth the currents might vanishing and flux quantization would pose a condition of the size of the flux quantum.

As an example consider flux sheets, which have thickness $L(151) = 2.5$ nm carrying magnetic field having strength of Earth's magnetic field. At $k_d = 44$ level of dark matter hierarchy necessary in order that the energies associated with cyclotron frequencies are above thermal threshold these flux sheets would have minimum thickness of DNA double strand and total transversal length $L(169 + 5 \times 22) = L(257) = 1.6 \times 10^8$ km from flux quantization without supra currents.Fux quantization without supra currents is not satisfied at the level of single nucleus or even organism. The simplest possibility is that the flux sheets of cells fuse to larger flux sheets representing organs and organisms and that even the flux sheets assignable to separate organisms fuse in turn to larger flux sheets for which quantization condition for magnetic flux can be satisfied without assuming $n = 0$ and supra currents flowing at the boundaries of flux sheets.

Suppose that the magnetic flux flows in head to tail direction so that the magnetic flux arrives to the human body through a layer of cortical neurons. Assume that the flux sheets traverse through the uppermost layer of neurons and also lower layers and that DNA of each neuronal nuclei define a transversal sections organized along flux sheet like text lines of a book page. The total length of DNA in single human cell is about one meter. It seem that single brain cannot provide the needed total length of DNA if DNA dominates the contribution: this if of course not at all necessarily.

This leads to the notion of super- and hyper genes. Super genes consist of genes in different cell nuclei arranged to threads along magnetic flux sheets like text lines on the page of book whereas hyper genes traverse through genomes of different organisms. Super and hyper genes provide an enormous representative capacity and together with the dark matter hierarchy allow to resolve the paradox created by the observation that human genome does not differ appreciably in size from that of wheat.

Charge entanglement as a tool of generalized motor action

The charge entanglement by W MEs is an essentially new element in the model for generalized motor actions by magnetic body. Also the telepathic sharing of mental images could rely on charge entanglement. The notion was originally applied in the model of nerve pulse generation [57] . Neutral MEs would in turn be related to communications and memory. The reduction of charge entanglement can induce a quantum jump to a state in which local Bose-Einstein condensates become exotically ionized with certain probability depending on the intensity of W field. Bose-Einstein condensates define pixels of generalized motor maps.

Exotic ionization induces dark plasma oscillations in turn generating various physiological responses such as Ca^{++}, Mg^{++} waves, and nerve pulse patterns giving rise to the motor action as an asymptotic self-organization pattern. Plasma oscillation patterns utilize typically dark microwave photons as metabolic energy. Field code is the correspondence between the spatio-temporal pattern of plasma oscillations and generalized motor action and the number theoretical model for genetic code [19] generalizes to this context.

Overview about quantum control and coordination

The following general overview about quantum communication and control emerges in this framework.

1. Cyclotron frequencies relate to the control of the biological body by the magnetic body and could be assigned with the magnetic flux sheets going through DNA since it is genome where protein synthesis is initiated and is thus the optimal intermediate step in the cellular control.

2. One of the basic functions of cell membranes is to perceive the chemical environment using various kinds of receptors as sensors. Neurons have specialized to receive symbolic representations of the sensory data of primary sensory organs about the situation in the external world. Receptor proteins would communicate cell level sensory input to the magnetic body via MEs parallel to magnetic flux tubes connecting them to the magnetic body. We ourselves would be in an abstract sense fractally scaled up counterparts of receptor proteins and associated with dark matter iono-lito Josephson junction connecting the parts of magnetosphere below litosphere and above magnetosphere.

3. This picture would explain why the temperature of brain must be in the narrow range 36-37 K to guarantee optimal functionality of the organism. If interior superconductivity is lost, magnetic body receives sensory data but is paralyzed since its desires cannot be realized. If boundary superconductivity is lost, magnetic body can move but is blind.

4. In the length scales below the weak length scale L_w also charged weak bosons behave as massless particles and the exchange of virtual W bosons makes possible a nonlocal charge transfer. Dark quark-antiquark pairs associated with the color bonds of the atomic nuclei can become charged via the emission of dark W boson and thus produce and exotic ion. The same can happen at the higher levels of dark matter hierarchy. This provides a nonlocal quantal mechanism inducing or changing electromagnetic polarization in turn inducing ordinary charge flows and thus making possible quantum control.

5. Massless extremals (MEs, topological light rays) serve as correlates for dark bosons. Besides neutral massless extremals (em and Z^0 MEs) TGD predicts also charged massless extremals obtained from their neutral counterparts by a mere color rotation (color and weak quantum numbers are not totally independent in TGD framework). The interpretation of the charged MEs has remained open hitherto. Charged W MEs (hierarchy of WEGs!) could induce long length scale charge entanglement of Bose-Einstein condensates by inducing exotic ionization of ionic nuclei. State function reduction could lead to a state containing a Bose-Einstein condensate in exotically ionized state.

   In this manner the dark charge inside neuron and thus by Faraday's law also membrane potential could be affected by magnetic body. The generation of nerve pulse could rely on the reduction of the resting potential below the critical value by this kind of mechanism inducing charge transfer between cell interior and exterior. The mechanism might apply even in the scale of magnetic body and make possible the control of central nervous system. Also remote mental interactions, in particular telekinesis, might rely on this mechanism.

Summarizing, charged massless extremals could be seen as correlates for nonlocal quantum control by affecting charge equilibria whereas neutral MEs would serve as correlates for coordination and communication. Color charged MEs could also induce color charge polarization and flows of color charges and thus generate visual color qualia by the capacitor mechanism discussed in [31] .

2.3 MEs and mes

The development of the model for the detailed identification of the sensory qualia and brain led to a general vision about the evolution of consciousness and information processing in brain. In this section various properties of MEs are summarized.

2.3.1 Massless extremals

Massless extremals (MEs) are an extremely general solution set of field equations associated with Kähler action [35] and representing various gauge – and gravitational fields [50] . Being scale invariant, MEs come in all size scales. The geometry has axial symmetry in the sense that CP_2 coordinates are arbitrary functions of two variables constructed from Minkowski coordinates: light-like coordinate $t - z$ and arbitrary function of the coordinates of the plane orthogonal to the z-axis defining the direction of propagation. The polarization of the electromagnetic field depends on the point of the plane but is temporally constant. MEs represent waves propagating with velocity of light in single direction so that there is no dispersion: preservation of the pulse shape makes MEs ideal for classical communications.

Electric and magnetic parts of various gauge fields are orthogonal to each other and to the direction of propagation. Classical gauge field is sum of a free part plus part having as its source light-like vacuum current. The time dependence of the vacuum current is arbitrary, this is only possible by its light-likeness. This makes it possible to code all kinds of physical information to the time dependence of the vacuum current. MEs can have finite spatial size and in this case they are classical counterparts of virtual photons exchanged between charged particles and represent classical communication between material space-time sheets. MEs carry gravitational waves and also classical Z^0 fields propagating with light velocity.

MEs can also carry constant electric field. In this case either vacuum charges or actual charges near the boundaries of ME contain define the sources of this field. This situation can be also achieved if MEs form double-sheeted structures and wormhole contacts serve as effectively sources of the field. TGD allows the possibility that the two sheets have opposite time orientations and therefore also opposite classical energies. More generally, the exchange of two or more MEs between material space-time sheets can be such that no net momentum exchange occurs so that the absolute minimum of Kähler action only in a finite region of space-time and gives rise to new degenerate absolute minimum of Kähler action since ME has vanishing action. This kind of structures are obvious candidates for cognitive structures since classical nondeterminism is localized in a finite space-time volume. The Universe should be full of MEs with all possible sizes since they have vanishing action: addition of ME with finite time duration yields new absolute minimum of Kähler action since Kähler action does not change in this operation. This suggests that MEs should be of crucial importance in TGD Universe.

MEs serve as receiving and sending quantum antennae [50] . Light-like vacuum current generates coherent light. Also coherent gravitons are generated. MEs serve also as templates for BE condensation of photons and gravitons with momenta parallel to the light-like vacuum current. Linear structures, say DNA and micro-tubules, are natural but not the only candidates for structures accompanied by MEs. Since MEs are massless, they carry maximal possible momentum. This makes exchange of ME ideal mechanism for locomotion. The possibility of negative energy MEs is especially fascinating since it suggests 'buy now, pay later' mechanism of energy production: perhaps living matter uses MEs to generate coherent motions [52, 53] .

Massless extremals as general solutions of field equations

Let $k = (k^0, k^3, 0, 0)$ be a light like vector of M^4 and $u = u(m^1, m^2)$ arbitrary function of the Minkowski coordinates m^1 and m^2 in the plane orthogonal to the direction of the 3-vector $(k^3, 0, 0)$ associated with k. The surfaces defined by the map

$$s^k = f^k(k \cdot m, u) \ , \tag{2.3.1}$$

where f^k and u are arbitrary functions define massless extremals. They describe the propagation of massless fields in the direction of k: the fields are periodic with a period $\lambda = 2\pi/k$ so that only k and its integer multiples are possible wave vectors. The polarization associated with various induced gauge fields depends on the position in (m^1, m^2)-plane and is in the direction of the gradient of u. Field equations involve tensor contractions of the energy momentum tensor and gauge current but these are proportional to kk and k respectively and vanish by the light-likeness of k. Linear superposition holds true only in a restricted sense since both the propagation direction and the polarization direction in each $(m^1, m^2) = const$ plane is fixed.

What is remarkable that these solutions are not solutions of the ordinary Maxwell equations in vacuum: Kähler current density J_K is in general non-vanishing(!) and proportional to the light like four-momentum k. As a consequence, also a light-like electromagnetic current is in general (but not necessarily) present. The interpretation of the em current J as charged elementary particle current is impossible and the correct interpretation as a vacuum current associated with the induced gauge fields. The finite length of the micro-tubule plus the requirement that the total vacuum charge vanishes, implies that the Fourier decompositions of the massless fields contain only integer multiples of the basic four-momentum k. The direct detection of the light-like vacuum current inside a micro-tubule would provide strong support for TGD.

The physical importance of these extremals is suggested by the fact they are in certain sense elementary particle like objects: in fact, the original interpretation was as a model for the exterior space-time of a topologically condensed massless particle. The solution set is also very general involving several arbitrary functions. Although the minimization of the Kähler action favors the formation of Kähler electric fields, massless extremals might well appear as space-time sheets of the effective space-time. These space-time sheets should not contain ordinary charges since their presence implies a transition to the Maxwell phase described in an excellent approximation by the ordinary Maxwell electrodynamics. The fact that vacuum em current and vacuum Einstein tensor do not in general vanish, could mean that massless extremals serve as sources of coherent photons and gravitons.

Massless extremals can also reduce to vacuum extremals of the Kähler action in the case that the CP_2 projection is, in general two-dimensional, Legendre manifold of CP_2. These extremals are however not gravitational vacua.

Generalization of the solution ansatz defining MEs

The solution ansatz for MEs has developed gradually to an increasingly general form and the following formulation is the most general one achieved hitherto. Rather remarkably, it rather closely resembles the solution ansatz for the CP_2 type extremals and has direct interpretation in terms of geometric optics. Equally remarkable is that the latest generalization based on the introduction of the local light-cone coordinates was inspired by quantum holography principle.

The solution ansatz for MEs has developed gradually to an increasingly general form and the following formulation is the most general one achieved hitherto. Rather remarkably, it rather closely resembles the solution ansatz for the CP_2 type extremals and has direct interpretation in terms of geometric optics. Equally remarkable is that the latest generalization based on the introduction of the local light-cone coordinates was inspired by quantum holography principle.

1. Local light-cone coordinates

The solution involves a decomposition of M^4_+ tangent space localizing the decomposition of Minkowski space to an orthogonal direct sum $M^2 \oplus E^2$ defined by light-like wave vector and polarization vector orthogonal to it. This decomposition defines what might be called local light-cone coordinates.

1. Denote by m^i the linear Minkowski coordinates of M^4. Let (S_+, S_-, E_1, E_2) denote local coordinates of M^4_+ defining a *local* decomposition of the tangent space M^4 of M^4_+ into a direct *orthogonal* sum $M^4 = M^2 \oplus E_2$ of spaces M^2 and E^2. This decomposition has interpretation in terms of the longitudinal and transversal degrees of freedom defined by local light-like four-velocities $v_\pm = \nabla S_\pm$ and polarization vectors $\epsilon_i = \nabla E_i$ assignable to light ray.

2. In accordance with this physical picture, S_+ and S_- define light-like curves and thus satisfy the equation:

$$(\nabla S_\pm)^2 = 0 \quad .$$

   The gradients of $S_\pm$ are obviously analogous to local light like velocities $v = (1, \overline{v})$ and $\tilde{v} = (1, -\overline{v})$. These equations are also obtained in geometric optics from Hamilton Jacobi equation by replacing photon's four-velocity with the gradient ∇S: this is consistent with the interpretation of MEs as Bohr orbits of em field.

3. With these assumptions the coordinates $(S_\pm, E_i)$ define local light-cone coordinates with the metric element having the form

$$ds^2 = g_{S_+S_-}dS_+dS_- + g_{11}dE_1^2 + g_{22}dE_2^2 \ .$$

Conformal transformations of M_+^4 leave the general form of this decomposition invariant. The task is to find all possible local light-cone coordinates defining one-parameter families 2-surfaces defined by the condition $S_i = constant$, $i = +\ or\ = -$, dual to each other and expanding with light velocity.

2. A conformally invariant family of local light-cone coordinates

The simplest solutions to the equations defining local light-cone coordinates are of form $S_\pm = k \cdot m$ giving as a special case $S_\pm = m^0 \pm m^3$. For more general solutions of from

$$S_\pm = m^0 \pm f(m^1, m^2, m^3) \ , \ (\nabla_3 f)^2 = 1 \ ,$$

where f is an otherwise arbitrary function, this relationship reads as

$$S_+ + S_- = 2m^0 \ .$$

This condition defines a natural rest frame. One can integrate f from its initial data at some two-dimensional $f = constant$ surface and solution describes curvilinear light rays emanating from this surface and orthogonal to it. The flow velocity field $\overline{v} = \nabla f$ is irrotational so that closed flow lines are not possible in a connected region of space and the condition $\overline{v}^2 = 1$ excludes also closed flow line configuration with singularity at origin such as $v = 1/\rho$ rotational flow around axis.

One can identify E^2 as a local tangent space spanned by polarization vectors and orthogonal to the flow lines of the velocity field $\overline{v} = \nabla f(m^1, m^2, m^3)$. Since the metric tensor of any 3-dimensional space allows always diagonalization in suitable coordinates, one can always find coordinates (E_1, E_2) such that (f, E_1, E_2) form orthogonal coordinates for $m^0 = constant$ hyperplane. Obviously one can select the coordinates E_1 and E_2 in infinitely many manners.

3. Closer inspection of the conditions defining local light-cone coordinates

Whether the conformal transforms of the local light-cone coordinates $\{S_\pm = m^0 \pm f(m^1, m^2, m^3), E_i\}$ define the only possible compositions $M^2 \oplus E^2$ with the required properties, remains an open question. The best that one might hope is that any function S_+ defining a family of light-like curves defines a local decomposition $M^4 = M^2 \oplus E^2$ with required properties.

1. Suppose that S_+ and S_- define light-like vector fields which are not orthogonal (proportional to each other). Suppose that the polarization vector fields $\epsilon_i = \nabla E_i$ tangential to local E^2 satisfy the conditions $\epsilon_i \cdot \nabla S_+ = 0$. One can formally integrate the functions E_i from these condition sonce the initial values of E_i are given at $m^0 = constant$ slice.

2. The solution to the condition $\nabla S_+ \cdot \epsilon_i = 0$ is determined only modulo the replacement

   $$\epsilon_i \to \hat{\epsilon}_i = \epsilon_i + k\nabla S_+ \ ,$$

   where k is any function. With the choice

   $$k = -\frac{\nabla E_i \cdot \nabla S_-}{\nabla S_+ \cdot \nabla S_-}$$

   one can satisfy also the condition $\hat{\epsilon}_i \cdot \nabla S_- = 0$.

3. The requirement that also $\hat{\epsilon}_i$ is gradient is satisfied if the integrability condition

   $$k = k(S_+)$$

   is satisfiedin this case $\hat{\epsilon}_i$ is obtained by a gauge transformation from ϵ_i. The integrability condition can be regarded as an additional, and obviously very strong, condition for S_- once S_+ and E_i are known.

4. The problem boils down to that of finding local momentum and polarization directions defined by the functions S_+, S_- and E_1 and E_2 satisfying the orthogonality and integrability conditions

$$(\nabla S_+)^2 = (\nabla S_-)^2 = 0 \ , \quad \nabla S_+ \cdot \nabla S_- \neq 0 \ ,$$

$$\nabla S_+ \cdot \nabla E_i = 0 \ , \qquad \frac{\nabla E_i \cdot \nabla S_-}{\nabla S_+ \cdot \nabla S_-} = k_i(S_+) \ .$$

   The number of intebrability conditions is 3+3 (all derivatives of k_i except the one with respect to S_+ vanish): thus it seems that there are not much hopes of finding a solution unless some discrete symmetry relating S_+ and S_- eliminates the integrability conditions altogether.

A generalization of the spatial reflection $f \to -f$ working for the separable Hamilton Jacobi function $S_\pm = m^0 \pm f$ ansatz could relate S_+ and S_- to each other and trivialize the integrability conditions. The symmetry transformation of M^4_+ must perform the permutation $S_+ \leftrightarrow S_-$, preserve the light-likeness property, map E^2 to E^2, and multiply the inner products between M^2 and E^2 vectors by a mere conformal factor. This encourages the conjecture that all solutions are obtained by conformal transformations from the solutions $S_\pm = m^0 \pm f$.

4. General solution ansatz for MEs for given choice of local light-cone coordinates

Consider now the general solution ansatz assuming that a local wave-vector-polarization decomposition of M^4_+ tangent space has been found.

1. Let $E(S_+, E_1, E_2)$ be an arbitrary function of its arguments: the gradient ∇E defines at each point of E^2 an S_+-dependent (and thus time dependent) polarization direction orthogonal to the direction of local wave vector defined by ∇S_+. Polarization vector depends on E^2 position only.

2. The most general MEs correspond to the solution family of the field equations having the general form

$$s^k = f^k(S_+, E) \ ,$$

   where s^k denotes CP_2 coordinates and f^k is an arbitrary function of S_+ and E. The solution represents a wave propagating with light velocity and having definite S_+ dependent polarization in the direction of ∇E. By replacing S_+ with S_- one obtains a dual solution. Field equations are satisfied because energy momentum tensor and Kähler current are light-like so that all tensor contractions involved with the field equations vanish: the orthogonality of M^2 and E^2 is essential for the light-likeness of energy momentum tensor and Kähler current.

3. The simplest solutions of the form $S_\pm = m^0 \pm m^3$, $(E_1, E_2) = (m^1, m^2)$ and correspond to a cylindrical MEs representing waves propagating in the direction of the cylinder axis with light velocity and having polarization which depends on point (E^1, E^2) and S_+ (and thus time). For these solutions four-momentum is light-like: for more general solutions this cannot be the case. Polarization is in general case time dependent so that both linearly and circularly polarized waves are possible. If m^3 varies in a finite range of length L, then 'free' solution represents geometrically a cylinder of length L moving with a light velocity. Of course, ends could be also anchored to the emitting or absorbing space-time surfaces.

4. For the general solution the cylinder is replaced by a three-dimensional family of light like curves and in this case the rectilinear motion of the ends of the cylinder is replaced with a curvilinear motion with light velocity unless the ends are anchored to emitting/absorbing space-time surfaces. The non-rotational character of the velocity flow suggests that the freely moving particle like 3-surface defined by ME cannot remain in a infinite spatial volume. The most general ansatz for MEs should be useful in the intermediate and nearby regions of a radiating object whereas in the far away region radiation solution is excepted to decompose to cylindrical ray like MEs for which the function $f(m^1, m^2, m^2)$ is a linear linear function of m^i.

2.3.2 About the electro-weak and color fields associated with massless extremals

Space-time sheets carrying em fields carry usually also Z^0 and W fields and it is not possible to speak about em or Z^0 type MEs. It is however possible to speak about neutral and W MEs. The CP_2 projection of ME is 2-dimensional and in a special case it reduces to a geodesic sphere. There are two kinds of geodesic spheres in CP_2.

1. For space-time sheets for which CP_2 projection is $r = \infty$ homologically non-trivial geodesic sphere of CP_2 one has

$$\gamma = (\frac{3}{4} - \frac{sin^2(\theta_W)}{2})Z^0 \simeq \frac{5Z^0}{8} \quad .$$

   The induced W fields vanish in this case and they vanish also for all geodesic sphere obtained by $SU(3)$ rotation.

2. For homologically trivial geodesic sphere a standard representative is obtained by using for the phase angles of standard complex CP_2 coordinates constant values. In this case induced em, Z^0, and Kähler fields vanish but induced W fields are non-vanishing. This holds also for surfaces obtained by color rotation. Hence one can say that for non-vacuum extremals with 2-D CP_2 projection color rotations and weak symmetries commute.

The MEs corresponding to these two geodesic spheres could be called neutral and W MEs and they carry color fields for which the color group $SU(3)$ reduces to some of its $U(1)$ subgroups. Quite generally, the holonomy algebra of color group is Abelian since the induced color field is of the form $g^A_{\alpha\beta} \propto H^A J_{\alpha\beta}$, where H^A denotes color Hamiltonian. Neutral MEs are excellent candidates for mediating EEG type communications from the biological body to the magnetic body whereas charge entanglement induced by W MEs would be ideal for the realization of motor actions of the magnetic body.

MEs are excellent candidates for the space-time correlates of laser beams. Dark matter hierarchy implies that also MEs can be classified by the level of the dark matter hierarchy involved. Mersenne hypothesis [23] is an explicit conjecture about the hierarchy of weak physics and their dark counterparts and allow to make explicit quantitative predictions about the role of weak interactions in living matter since as many as four Gaussian Mersennes are in the p-adic length scale range 10 nm-528 nm.

2.3.3 MEs as absorbing and emitting quantum antennae

How massless extremals generate coherent states of photons?

ME:s can be in 'dormant' or active state according to whether the em current associated with the ME is vanishing or not. In active state ME:s generate Bose Einstein condensate type state for ordinary photons. This means in TGD context the emission of (topological) vapour phase photons (CP_2 type extremals), which can condense on other condensate levels. ME:s generate gravitonic BE condensate and the possible biological role of this condensate will be discussed later.

Assuming that the coupling of quantized photon field to the massless extremal is given by regarding the massless extremal as a classical background field one obtains QED with a light like source J^α:

$$\begin{aligned} D_\beta F^{\alpha\beta} &= eJ^\alpha \ , \\ J^\alpha &= Jk^\alpha \ . \end{aligned} \tag{2.3.2}$$

The system is equivalent with an infinite number of harmonic oscillators each driven by a harmonic external force and a basic exercise in the quantum mechanics shows that the solutions of the field equations give the new oscillator operators as sums of free oscillator operators plus c-number term, which is essentially the Fourier component of the light like current in the direction of the polarization.

In the limit that ME has infinite duration and is a cylindrical structure of finite length L (that is micro-tubule) one has for $J \propto sin(k_z(t-z))$

$$
\begin{aligned}
a^\dagger(p) &\rightarrow a^\dagger(p) + g(p) \ , \\
g(p) &= \sum_n \delta(p^0, k_n^0) K(p, k_n) J(k_n^z, p_T) \ , \\
K(p,k) &= \epsilon(p) \cdot k \frac{1}{i(p_z - k_z)} (exp(ip_z L) - 1) \ , \\
k_n &= nk_0 = \frac{n2\pi}{L}(1,1,0,0) \ .
\end{aligned} \tag{2.3.3}
$$

Here p denotes the momentum of the photon and k the 4-momentum associated with the Fourier component of a light-like current. $\epsilon(p)$ denotes the polarization of the photon. $J(k_n^z, p_T)$ is essentially the 3-dimensional Fourier transform of the scalar function J. The infrared behavior of $J(k_z, p_T)$ as a function of the transversal momentum p_T can be deduced from the fact that the transverse dimension of the micro-tubule is small (about 25 nm) as compared to $1/p_T$ so that the Fourier component is in good approximation independent of p_T.

For the frequencies present in the Fourier decomposition of the massless extremal, the ordinary oscillator vacuum is transformed to a coherent state in the corresponding Fourier mode of the quantized photon field. The essential point is that the wave vectors of the radiation field and massless extremal are nonorthogonal. The radiation pattern resembles the ordinary antenna pattern associated with an oscillating current $J(t) = exp(i\omega t)$ in that the intensity of radiation vanishes at angles $\theta = \pi/2$ and $\theta = 0$. For $J \propto sin(k_z(z-t))$ $|K|^2$ has maxima for $\theta = 48.6$ degrees and 131.4 degrees. For an ordinary dipole with $J = sin(\omega t)$, $\omega = 2\pi/L$ the radiation pattern is concentrated at angles $\theta \geq 40$ degrees with maximum and 69.3 degrees and 110.7 degrees.

A more complicated situation corresponds to a group of several massless extremals (say micro-tubules). If massless extremals are parallel and have same length the previous expression generalizes with superposition of terms

$$
g(p) \rightarrow \sum_n exp(i\phi_n) exp(ip_z z_n) exp(ip_T \cdot x_T) g_n(p) \ . \tag{2.3.4}
$$

The phase ϕ_n is the phase difference between n:th light like current with respect to some reference current. If the positions of micro-tubules and/or phases of the individual light like currents are suitably chosen then various terms interfere constructively and macroscopic quantum coherence is obtained at resonant frequencies. Suffice it so say that the needed timing is extremely accurate: less than 10^{-12} seconds! Since p_z is small rather larger transversal distances are allowed by the requirement of constructive interference. In a more general situation also the orientations of micro-tubules can vary in certain limits. Note that light-like energy momentum generates also gravitonic BE condensates at preferred frequencies.

Massless extremal is accompanied by a Bose-Einstein condensate of parallel photons

The interaction Lagrangian describing the interaction of photon field with the light-like vacuum current does not couple to the photons collinear with the vacuum current (light-like wave vector has vanishing length squared). Therefore the ground states of the system are degenerate since one can add to any coherent state generated by the vacuum current any number of photons collinear with the vacuum current and topologically condensed inside the massless extremal. This means Bose-Einstein condensation in collinear degrees of freedom.

Collinear Bose-Einstein condensates of photons are crucial for the model of the quantum correlates of the sensory qualia. Sensory quale is characterized partially by the BE condensate of photons associated with the massless extremal parallel to the axon. The existence of the BE condensate makes possible induced emission. For instance, Josephson currents generate photons with frequencies which are multiples of the Josephson frequency. If the potential difference in Josephson junction equals to a multiple of the cyclotron frequency of some super conducting ion, the current flows resonantly in the sense that Josephson current serves as a harmonic perturbation generating quantum jumps and gives rise to a large dissipative current and also quantum jumps in either super conductor. Since the

emission rate for photons by the current is proportional to N^2, where N is the number of photons already in the state, the presence of the BE condensate of photons with this frequency amplifies the emission rate. This kind of resonance mechanism is assumed in the model of sensory experience since it elegantly explains why given neuron corresponds to single quale. Since the potential difference over the Josephson junction can correspond to only single cyclotron frequency, the dominance of single quale is unavoidable even when all macroscopic quantum phases are present.

The existing BE condensate increases the probability of topological condensation of coherent photons generated by other massless extremals to the massless extremal. This mechanism could provide inter-neuronal communication mechanism and realize the metaphor about brain as a society of neutrons, the notion of neuronal window idea and also give a more precise content to the music metaphor. In particular, neurons far away from each other could communicate using wavelengths in a narrow wave length range by this mechanism.

The wave vectors of the photons are multiples of $k = \pi/L$. This means that the length of the massless extremal correlates with the maximal allowed wavelength. For ELF photons associated with EEG frequencies of order 10 Hz the length of massless extremal is of order Earth's circumference. This suggests that more general massless extremals with a topology of torus instead of linear topology could characterize the topological field quanta of ELF fields. It is however impossible to say, whether the field equations allow more general solutions resembling massless extremals.

2.3.4 Quantum holography and quantum information theory

Sokolov and collaborators [10] have proposed a model of quantum holographic teleportation in which the *classical* photocurrents from the sender to receiver take the role of a dynamical hologram. The connection with MEs is obvious.

1. MEs are carriers of classical light-like vacuum currents (one of the basic differences between TGD and Maxwell theory). This suggests that MEs could be interpreted also as *classical* holograms, which are *dynamical* as in quantum information theory. Light-like current would be like a dynamical (four-dimensional) diffraction grating. Light-like vacuum currents and vacuum Einstein tensor generate also coherent states of photons and gravitons and MEs serve as templates for the topological condensation of photons and gravitons to the Bose-Einstein condensate of photons collinear with ME. The Bose-Einstein condensation of collinear photons and their generalizations to colored configuration space photons should affect the vacuum current by adding to the reference current what might be called evoked response. This condensation process could generate conscious experience and higher level qualia. Thus it would seem that MEs have a triple role as receiving and sending quantum antennae as well as classical holograms.

2. The proposal of [10] generalizes to the case of MEs provided one can device a method of coding quantum states of photon field to the vacuum currents. The high efficiency photodetector matrix is in which each pixel gives rise to a photocurrent [10] , is replaced with ME or set of parallel MEs. The neural window hypothesis [58] states that neuronal axons are accompanied by parallel MEs carrying information between sensory organs and brain and various parts of brain. This is only a less standard manner to say that ME represents classical dynamical hologram. The possibility of local light-cone coordinates allows also MEs which define curved deformations of the simplest cylindrical MEs.

   The concrete realization of holographic teleportation proposed in [10] brings strongly in mind the architecture of the visual pathways. Thus one can wonder whether brain is perfoming internal teleportation of photonic quantum states with spike patterns being directly coded to the pattern of the vacuum currents flowing along MEs. If spike patterns code the dynamical hologram, a surprisingly close relationship with Pribram's views about hologrammic brain results. Nerve pulse patterns could be seen as specifying the necessary classical aspects of the quantum teleportation (in TGD classical physics is essential part of quantum physics, rather than some effective theory).

3. Vacuum current at a 3-dimensional time-like section of ME as a function function of time defines a dynamical 3-dimensional hologram. This is consistent with the fact that our visual experience is two-dimensional: the information is always about outer boundaries of the objects of the perceptive field. The values of the vacuum current at a given point are non-deterministic which

means that vacuum current is ideal for coding information. Classical data also propagate without dispersion with light velocity obeying the laws of geometric optics and MEs imply channelling so that MEs are taylor-made for classical information transfer.

4. Space-time sheets can have both positive and negative time orientations and the sign of energy depends on time orientation in TGD framework. This means that classical communication can occur both in the direction of the geometric future and past: this is essential for the classical model of the long term memories as a question communicated to the geometric past followed by answer. The dynamical nature of the holograms means that there is no need to combine 2- or 3-dimensional holograms associated with several moments of geometric time to single hologram. To remember is to perceive an object located in the geometric past. Of course, fractality might make possible temporally scaled down versions of the geometric past but the principle would remain the same.

5. Quantum hologram view suggests that the super-symplectic representations at the light-like boundaries of MEs characterized by gigantic almost-degeneracies are the real carriers of biological information. According to the general theory of qualia [31] this information would become conscious since elementary qualia would correspond to quantum jumps for which increments of the quantum numbers correspond to the quantum numbers labelling super-symplectic generators in the complement of Cartan algebra. In this view super-conducting magnetic flux tubes could perhaps be seen as intermediate level in the control circuitry controlled by MEs and controlling atomic level.

6. This picture leaves open whether there is a level controlling the thicknesses of the magnetic flux tubes and thus also magnetic transition frequency scales, and what this level might be. The entrainment of the endogenous frequencies to exogenous frequencies [34] explains water memory and the effects of homeopathic remedies [204] and could make possible also endogenous NMR spectroscopy and chemical senses. The key to the puzzle might be a purely mathematical problem: how the boundary conditions at the boundaries of the magnetic flux tubes can be satisfied? It might be that the induced metric must become degenerate at the boundaries ($\sqrt{g} = 0$) implying a degeneracy of the induced metric at the boundary of the magnetic space-time sheet. This need not however mean that the M^4_+ projection of the boundary is a light-like surface: the projection could well be completely static. This supports the view that the boundaries do not carry super-symplectic representations, which are associated with the imbedding space projection of the boundary rather than the boundary itself. One can imagine that ME with the same transversal section as magnetic flux tube is glued to the magnetic flux tube along this section: this kind of gluing results in a singular 4-surface analogous to the vertex region of Feynmann diagram and somekind of smoothing-out procedure is needed. The smoothed-out vertex region would make possible for ME to control magnetic flux tube thickness by varying its own transversal thickness.

MEs as quantum holograms in the sense of quantum gravitation

Quantum holography principle naturally generalizes to an approximate principle expected to hold true also in non-cosmological length and time scales.

1. The most general ansatz for MEs (inspired by the quantum holographic thinking) relies on the introduction of the notion of local light-cone coordinates S_+, S_-, E_1, E_2. The gradients ∇S_+ and ∇S_- define two light-like directions just like Hamilton Jacobi functions define the direction of propagation of wave in geometric optics. The two polarization vectori fields ∇E_1 and ∇E_2 are orthogonal to the direction of propagation defined by either S_+ or S_-. Since also E_1 and E_2 can be chosen to be orthogonal, the metric of M^4_+ can be written locally as $ds^2 = g_{+-}dS_+dS_- + g_{11}dE_1^2 + g_{22}dE_2^2$. In the earlier ansatz S_+ and S_- where restricted to the variables $k\cdot m$ and $\tilde{k}\cdot m$, where k and $\tilde{k}$ correspond to light-like momentum and its mirror image and m denotes linear M^4 coordinates: these MEs describe cylindrical structures with constant direction of wave propagation expected to be most important in regions faraway from the source of radiation.

2. Boundary conditions are satisfied if the 3-dimensional boundaries of MEs have one light-like direction (S_+ or S_- is constant). This means that the boundary of ME has metric dimension $d = 2$ and is characterized by an infinite-dimensional super-symplectic and super-conformal symmetries just like the boundary of the imbedding space $M^4_+ \times CP_2$: The boundaries are like moments for mini big bangs (in TGD based fractal cosmology big bang is actually replaced with what might be called a silent whisper amplified to not necessarily so big bang). Quantum holography would mean that effectively 2-dimensional conformal field theory at the boundary of M^4_+ region determined by ME determines what happens in the interior at QFT limit when space-time surface is not regarded as a dynamical object.

3. These observations inspire the conjecture that boundary conditions for M^4 like space-time sheets fixed by the absolute minimization of Kähler action quite generally require that space-time boundaries correspond to light-like 3-surfaces with metric dimension equal to $d = 2$. Quantum holography principle would state that the dynamics related to the metric of the configuration space, that is genuine quantum gravitation, would reduce to the boundaries of space-time sheets. The dynamics in zero modes and quaternion conformal degrees of freedom crucial for elementary particle physics would not however allow this kind of reduction. This would be consistent with the fractality which is expected to be a basic characteristic of the quantum critical Universe predicted by TGD. The approximate super-symplectic and conformal symmetries would be associated with the light-like boundaries of the space-time sheets. super-symplectic invariance would be broken only by quantum gravitational effects at the level of the configuration space by the fact that the boundaries of space-time surfaces are actually dynamical rather than fixed. The cosmological light-cone boundary would be however non-dynamical and this would guarantee the exactness of the cosmological super-symplectic invariance.

More concrete view about MEs as holograms

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MEs and super-symplectic and super-conformal symmetries

TGD predicts two kinds of super-conformal symmetries [73] . Quaternion conformal symmetries correspond to the gauge symmetries of fundamental interactions. Cosmological super-symplectic symmetries act on the boundary of light-cone and are cosmological symmetries.

The non-determinism of Kähler action however implies that the light-like M^4_+projections of light-like boundaries of MEs take the role of the boundary of future light-cone as quantum holograms and super-symplectic symmetry becomes ordinary macroscopic symmetry. Thus there is a fractal hierarchy of quantum holograms inside quantum holograms. One can identify the light-like boundaries of MEs as geometric correlates for selves. Also space-like selves are very probably needed and magnetic

flux tube structures could represent them. Indeed, the non-determinism of CP_2 type extremals representing elementary particles (their M^4_+ projections are random light-like curves) makes it impossible to characterize the quantum state completely by the data on the light-like boundaries of MEs.

MEs are natural carriers of super-symplectic representations obtained by multiplying ordinary physical states by configuration space Hamiltonians (functions of CP_2 coordinates and coordinates E_1, E_2 and S_+ or S_- which can obviously be arranged into irreducible representations of the color group $SU(3)$) and define an excellent candidate for a hierarchy of higher level life forms. The intuitive belief that quantum gravitation is crucial for higher level consciousness can be indeed justified in this framework: the 'worlds about worlds' aspect of higher level consciousness is what requires genuine quantum gravitational states.

The boundary of ME having one light-like direction gives rise to conformal quantum hologram representing quantum correlation functions for quantum field theory defined in the interior of ME. This 3-dimensional dynamical quantum hologram should code for conscious information about external world. This information could be determined by coherent light and gravitons scattered from the outer boundaries of other space-time sheets and could provide a quantum representation for the geometry of the boundaries of the other space-time sheets.

super-symplectic degrees of freedom makes MEs ideal candidates for the correlates of higher level consciousness.

1. The states of super-symplectic representations have gigantic almost-degeneracies broken only by non-commutativity of super-symplectic and Poincare symmetries which means huge information storage capacities. super-symplectic representations can be realized in real context using Bose Einstein condensates of massless elementary particles on MEs. super-symplectic representations correspond to genuine quantum gravitational effects since wave functionals in the space of three-surfaces are involvedspace-time ceases to be a passive arena of quantum dynamics. In fact, symplectic transformations of CP_2 are approximate symmetries of the theory broken only by classical gravitation. The notion of 'configuration space photon' having nontrivial dependence on configuration space degrees of freedom characterized by Hamiltonian suggests strongly itself and seems to be crucial for understanding of the visual colors.

2. super-symplectic representations have universal transition frequency spectrum given as multiples of the fundamental frequency determined by the length of ME. If one assumes that MEs have lengths given by p-adic length scale hypothesis, fundamental frequencies turn out to correspond to important resonance frequencies in EEG.

For these reasons super-symplectic representations are ideal candidates for an infinite hierarchy of life forms associated with MEs. The great vision is that MEs and magnetic super-conductors associated with the magnetic flux tube structures form a fractal hierarchy interacting with the ordinary bio-matter via the classical gauge fields associated with MEs [31, 23, 59] .

The standard manner to see the evolution of organism is as an initial value problem with data given at time=constant space-like section of Minkowski space. This view is definitely wrong in TGD framework, where the classical non-determinism of Kähler action is absolutely essential for the understanding of bio-systems and consciousness. Rather, one should see the problem as a boundary value problem with data given at light-like surfaces bounding MEs analogous to light-cone boundary identifiable as the moment of big bang. This view conforms nicely with the active intentional aspects of the biological evolution: system can decide what it will be and life is more like a narrative with definite goals than random Brownian zigzag curve. The life cycle of the organism is specified by posing some requirements which it must satisfy in the form of boundary conditions and organism does it best to satisfy them.

Mechanism for generation of configuration space photons

The super-symplectic representations should have some interaction mechanism with ordinary matter, if they are to be important for life. In particular, a mechanism making MEs to emit and absorb configuration space photons coupling to em charge, should exist. There are good reasons to expect that direct couplings between exotic super-symplectic states and ordinary elementary particles are very weak. The quantum number $L_0 = n$ defined by the Virasoro generator $L_0 = zd/dz$ (complex scaling) acting effectively as Hamiltonian in string diagrams is conserved in vertices. For matter

representations massless ground states correspond have scaling quantum number $n = n_0$, where n_0 defines the negative value of the vacuum weight. It must be emphasized that for super-symplectic representations L_0 does not seem to allow the interpretation as mass squared operator as in the case of quaternion conformal representations. The vertices in which $L_0 = O(p^k)$ state emits ordinary particle correspond to $np^k \leftrightarrow (np^k - m_0) + (m_0)$. The intermediate state is with $L_0 = np^k - m_0$ is has ultralarge scaling quantum number so that the amplitude is suppressed by a huge propagator factor. The processes involving only $L_0 = O(p^k)$ states are however not suppressed.

The interaction of the exotic super-symplectic states with the classical gauge fields associated with MEs provides a unique mechanism of 'matter-mind interaction'. The vanishing of the vacuum weight of Super Virasoro is very much analogous to the vanishing of the Higgs vacuum expectation value in ordinary gauge theories. Indeed, the exotic super-symplectic representations have unbroken gauge symmetries, which means that electro-weak and color interactions occur like in symmetry-nonbroken unconfined gauge theory. The presence of long range classical color and electro-weak gauge fields implying unbroken symmetries at classical level is important part of the story.

MEs have already at the space-time level symmetries supporting the view that super-symplectic algebra acts as isometry algebra of the configuration space.

First, symplectic transformations of $E^2 \times CP_2$, where E^2 is plane orthogonal to the light-like wave vector k associated with ME, are symmetries of MEs. Also symplectic transformations made local with respect to the light-like coordinate u and coordinate variable v orthogonal to u are also symmetries.

Secondly, arbitrary dependence on the variable u is equivalent with the invariance with respect to hypercomplex analytic transformations

$$x + ey \to f(x + ey) \quad ,$$

$$e^2 = 1 \quad .$$

where f is arbitrary function. These transformations obey Lie-algebra which is essentially identical with the Virasoro algebra spanned by the infinitesimal holomorphic transformations.

The general interaction Hamiltonian for this interaction can be guessed by recognizing the following facts.

1. Interaction Hamiltonian should have the general current-vector potential form

$$H_{int} = \sum_D \int G^A_\mu(D) J^{A\mu}(x|D) \sqrt{g_4} d^4x \quad ,$$

   where sum is over the representations D of color group defined by color Hamiltonians and where $G^A(D)$ represents analog of the classical gluon field associated with a particular color representation. In the case of color octet representation $G^A_\mu(\text{"8"})$ represents classical gluon field and is simply the projection of the Killing vector field of the color isometry to the space-time surface. The obvious generalization is that also in general case the vector field defined by the color transformation defines the classical gluon field. $J^{A\mu}(x|D)$ is the local current defined as the superposition of symplectic generators continued to a function of space-time coordinates.

2. The construction of a local current defined on entire space-time surface having super-symplectic generator as conserved charge is highly nontrivial task. It should be based on the observation that for ME there is a unique decomposition of M^4 tangent space to $M^4 = M^2 \times E^2$ such that E^2 is space-like plane orthogonal to the light-like wave vector k associated with ME. Let u denote the coordinate

$$u = k \cdot m \quad .$$

   The task is to continue the symplectic generator localized with respect to the radial coordinate of the light-cone boundary to a function in entire M^4_+. A possible manner to do this is to multiply the generator by a plane wave

$$exp(i2\pi f(u - u_0)) \quad ,$$

where u denotes the restriction of the coordinate u to the light-cone boundary

$$u_0 = u_{|\delta M^4_+} \quad .$$

The task is to fix the physical identification of the ME frequency. It turns out that interpretation as energy is the most plausible identification.

It might well be that only classical color fields define interaction vertices leading to the generation of configuration space photons. If this is the case the octet representation for configuration space photons would have a unique role. This would explain why visual colors, which can be identified as counterparts of the charged Hamiltonians associated with configuration space photons, are in a special role. Furthermore, MEs have always 2-dimensional CP_2 projection and carry classical color fields and currents restricted to $U(1)$ sub-algebra of color algebra, which need not be however color neutral. This implies that only particular configuration space photon and its conjugate are emitted and that only single color is created by the BE condensation of configuration space photons generated by a particular ME on other MEs.

2.3.5 MEs and quantum control

MEs and classical de-coherence

TGD approach inspires the idea that classical de-coherence corresponds to the decomposition of a space-time sheet carrying superposition of em fields to separate space-time sheets carrying the em fields appearing in the superposition. Since em fields live at different space-time sheets, interference effects are indeed absent which means de-coherence. A more precise and rather far reaching form of this hypothesis is that classical em field is unstable against decomposition to MEs. This mechanism allows to understand what might happen when amplitude modulated em field acts with living matter in the experiments of Blackman [17].

The extreme nonlinearity of the dynamics of absolute miminization of Kähler action implies that ELF modulated radio frequency field induces also em field component with modulating ELF frequency. If classical de-coherence generates MEs then classical amplitude modulated em fields leads to the generation of a large number of MEs at various frequencies and directions of wave vector. For instance, modulation frequency and carrier frequency could correspond to different MEs glued to each other by 'wormhole contacts'. Classical de-coherence and geometrically realized Fourier analysis would be the geometric and classical counterparts for field quantization reflecting the fact that absolute minimization of Kähler action implies that space-time surfaces are analogous to Bohr orbits.

MEs and conscious holograms

The notion of conscious hologram is much more practical than the concept of quantum gravitational hologram and generalizes the notion of ordinary hologram by fusing it with the notion of self [9] . Universe is an extremely complex fractal Feynmann diagram with lines replaced by 4-dimensional space-time sheets and MEs are particular kinds of lines analogous to photon lines. These lines are like laser beams, which interfere in the vertices of the Feynmann diagram: vertices correspond to material space-time sheets, atoms, molecules, ..., cells, ... The 3-D hologram vision corresponds at the level of conscious hologram stereo consciousness resulting when the mental images associated with different points of the hologram fuse to single mental image by quantum entanglement involving also the sharing of mental images.

An important piece of the picture is fact that MEs appear as pairs of high frequency and low frequency MEs. The low frequency MEs serve as correlates for remote quantum entanglement, now between different parts of brain. High frequency MEs travel like massless particles along the bridges defined by the low frequency MEs and serve as bridges between different space-time sheets at the receiving end. This induces a leakage of ions between different space-time sheets, breaking of super-conductivity and dissipative self-organization: this process which is analogous to the formation of hologram, is responsible for homeostasis and metabolism and gives rise to many-sheeted ionic flow equilibrium. Also many-sheeted lasers acting in a very wide range of frequencies become possible. The frequencies correspond to differences for the energies of ions at the space-time sheets involved.

MEs parallel to axons can also act as Josephson junctions connecting space-time sheets which can correspond to different p-adic primes.

Phase conjugate laser beams have as their counterpart negative energy MEs and negative energy photons resulting in time reversal. The time reversal for the dissipation induced by super current leakage seems also to be a key mechanism of bio-control. This leads to the working hypothesis that negative energy MEs are responsible for motor control whereas positive energy MEs are involved with perception and cognition: motor action is time reversed sensory perception in appropriate p-adic time scale. Among other things negative energy MEs make possible emission of negative energies making possible buy now-pay later (or let others pay) mechanism and thus extreme flexibility of energy economy.

Many-sheeted ionic flow equilibrium controlled by MEs

A crucial empirical ingredient supporting the view about a hierarchy of magnetic super-conductors are the puzzling observations of cell biology (for a summary see the first chapter of [196]) challenging the association of ionic channels and pumps to cell membrane. The paradoxes disappear if cell and its exterior are assumed to be in a many-sheeted ionic flow equilibrium with ionic currents flowing from super-conducting space-time sheets to atomic space-time sheets and back, so that the densities of ions at atomic space-time sheets are controlled by the the very small densities and quantized currents of dark ions at super-conducting magnetic flux tube space-time sheets and coding the information about homeostasis of bio-matter [13] . Also a reason why for liquid crystal and electret properties of bio-matter emerges and one can understand the function of electric circuitry associated with body [15] .

In this picture ionic channels and pumps would play the role of sensors detecting the concentrations of various ions and membrane voltages. The dominant part of the ionic currents would flow between cell interior and exterior as (possibly dark) supra currents and would dissipate very little. The dominant part of the metabolic energy would be used to build-up of dark EEG with photon energies above thermal threshold. Also negative dark W MEs responsible for motor actions would suck metabolic energy.

W MEs connecting magnetic body and biological body can induce charge entanglement by superposition of pairs of exotically ionized states with opposite exotic charges. State function reduction then selects either of the resulting states. Exotic ionization generates dark plasma oscillations which induce by Faraday law electric fields at the space-time sheets of the ordinary matter. The resulting ohmic currents in turn realize the control action on the ordinary matter (nerve pulse patterns, Ca^{2+} waves, etc...).

Neutral MEs can induce supra currents in super-conducting magnetic circuits by magnetic induction mechanism, serve as Josephson junctions between magnetic flux tubes, and induce magnetic quantum phase transitions. MEs can generate reference waves or their phase conjugates (time reversals) acting on lower level MEs serving as dynamical holograms. The induced coherent light pattern and its phase conjugate could act as a control command and its time reversed version. Conjugate reference waves provide an extremely simple mechanism of healing by time reversal allowing the living matter to fight against second law.

MEs could "read" DNA strand to the light-like vacuum current by moving along it and thus code DNA strand/conjugate strand to a hologram or its phase conjugate in turn acting as a control command or its time reversal. ELF MEs could do the same at the level of axons: instead of DNA sequences nerve pulse patterns would be read now. Thus living matter could be regarded as a symbiosis in which MEs control super-conducting magnetic flux tubes controlling ordinary matter at atomic space-time sheets via many-sheeted ionic flow equilibrium. DNA would represent the ROM of this system.

What makes this so interesting is that MEs are at the highest level of quantum control in the TGD based view about bio-system as a symbiosis in which MEs control super-conducting magnetic flux tubes controlling ordinary matter at atomic space-time sheets via many-sheeted ionic flow equilibrium. The coherent light pattern emitted by ME resulting from the interaction of ME with the reference wave (its phase conjugate) could act as a control command (time reversed control command) inducing process (time reversed process). Conjugate reference waves would thus provide an incredibly simple and general mechanism of healing by time reversal allowing the living matter to fight against second law. This would be like a general initiating a war by just nodding or shaking his head.

The formation of the phase conjugates could occur completely routinely and explain also why DNA appears in double strands. ME could read DNA strand to the pulse pattern of the light-like vacuum current by moving along the strand and thus code DNA strand (conjugate strand) to a hologram (its phase conjugate) in turn acting as a control command (its time reversal). ELF MEs could do the same at the level of axons: instead of DNA sequences nerve pulse patterns would be read now. DNA would clearly represent the ROM of this system. The coding of proteins would thus not be the only function related to DNA: DNA would be for the cell society what the first written laws were for human society, and the presence of the conjugate strand would make possible a systematic self repair at the cellular level by time reversal. More detailed considerations along these lines, in particular some empirical evidence for the hologrammic realization of the genetic code in terms of light-like vacuum currents, are represented in [48] .

MEs as Josephson junctions?

MEs can induce Josephson junctions between bio-structures. Since the electric field of ME is orthogonal to the direction of the propagation of vacuum current, the Josephson junction with potential difference is formed most naturally when super conductors are joined by join along boundaries bonds to ME in the direction of the electric field associated with ME. MEs can in principle be arbitrary thin so that the thickness of Josephson junction can be much smaller than the dominating wavelength of ME.

ME electric field can contain also constant component. In this case is however ME is necessary double sheeted since constant electric field is created by wormhole throats on boundaries of ME serving as effective charges. These MEs could give rise to the Josephson junctions with constant potential difference. An attractive hypothesis is that these ME pairs have opposite time orientations so that total energy of ME pair can vanish and can be created from vacuum without any energy cost. Clearly, these structures are cognitive in the strong sense of the word.

This coding of the transversal potential difference associated with ME pair to Josephson frequency is expected to be fundamental information coding mechanism in living matter. ME pair can contain also oscillating electric field over Josephson junction at magnetic or some other transition frequency so that MEs are ideal for control purposes.

MEs and the interaction of the classical em fields with bio-matter

MEs acting as Josephson junctions and containing oscillating em field at ELF frequency give rise to a harmonic perturbation inducing quantum jumps of the magnetic states of ions and explains the effect of ELF em fields on bio-matter. Also the presence of the mysterious intensity windows [18, 19] can be understood. Josephson current paradigm allows to understand this effect if RF or MW MEs associated with the external field act as Josephson junctions.

1. The external electric field oscillating with frequency ω (now radio frequency) defines slowly varying potential difference over Josephson junction of length d acting as Josephson junction provided that the condition

$$\omega \ll \omega_J(max) = ZeV = ZeEd$$

holds true. This gives

$$d \gg \frac{\omega}{ZeE} \ .$$

For $E \sim .1$ V/m and $\omega \sim GHz$ which are typical values used in experiments [17], this condition gives $d \gg 10^{-6}$ meters which is satisfied if Josephson junctions have size not smaller than cell length scale.

2. For fixed length of Josephson junction amplitude window results if the maximal Josephson frequency $\omega_J(max)$ is slightly above some transition frequency since in this case the stationary maxima and minima of amplitude lead to long lasting resonant excitation of quantum transitions. Denoting the relative width of the resonance by $\Delta\omega/\omega = P$, the ratio of the time spent in resonance at $\Omega_J(max)$ to the time spent off resonance at Ω_J is of order

$$\frac{t(max)}{t} \sim \sqrt{1 - \frac{\Omega_J^2}{\Omega_J^2(max)}} \times \frac{1}{\sqrt{P}} \ .$$

For a narrow resonance width this ratio can be very large so that amplitude window results for fixed value of d.

3. Amplitude window results if there is a correlation between the thickness of ME and transversal electric field so that $\omega_J(max) = ZeEd(E)$ satisfies resonance condition for some values of E only, if any. In absence of this correlation Josephson junctions must have discrete spectrum of effective lengths for amplitude window to result.

4. For electric fields in the range .1 V/m the frequencies ω_J are above GHz for d larger than 3×10^{-5} meters and correspond to the frequencies for the conformational dynamics of proteins. There are obviously a large number of frequencies of this kind and several intensity windows. EM fields with these strengths should have special effects on living matter: it could be even that some kind of feature recognition process involving self-organization occurs at these field strengths. Note that the minimal size of Josephson junctions corresponds to the p-adic length scale $L(173) \simeq 1.6 \times 10^{-5}$ meters characterizing structures next to cells in the p-adic length scale hierarchy.

The interaction of MEs with super-conducting magnetic flux tubes

The interaction of brain with MEs could mean that the super-conducting magnetic fluxtube circuitry associated with brain effectively acts as magnetometer somewhat in the same way as SQUID magnetometer measures the magnetic fields generated by brain. The resulting conceptual framework makes it easier to develop a quantum level model for the generation of nerve pulse and for the interaction of MEs and bio-super-conductors in terms of Josephson currents and super currents and relying on the notion of stochastic resonance.

Brain could measure the magnetic fields of MEs by using a mechanism which is very much like the mechanism of SQUID based magnetometers [25] used to measure the magnetic fields induced by brain.

1. A large collecting circuit in which the magnetic field of ME generates a compensating current by the quantization of the magnetic flux might be involved.

2. The amplification of this field could be achieved if the circuit contains a part which is spiral like and contains large number of loops in a small area.

3. In the core region the current flowing in the loop gives rise to an amplified magnetic field which in turn can penetrate into a super-conductor in form of flux tubes and in multiples of flux quantum. By counting the number of flux quanta one obtains rough measure for the magnetic field. In the case of brain the quantized magnetic flux would directly affect the state of neurons and the model for the generation of nerve pulse specifies this interaction. This effect on neurons would be long lasting as compared with the short-lasting action induced by the nerve pulse patterns.

4. The deviation of the flux of the amplified magnetic field from an integer number of flux quanta could be measured by a neuronal counterpart of SQUID, which basically consists of a closed loop decomposing to two parts which are joined together by insulator so that current rapidly dissipates to a minimum value forced by the flux quantization. The current in SQUID serves as a measure for very weak magnetic fields of MEs. The non-linear dynamics of SQUID allows also stochastic resonance allowing to amplify very weak periodic signals. This measurement mechanism might be interpreted as a mechanism of interaction between super-conducting magnetic flux tubes and neuronal circuits inducing also an interaction between MEs and neuronal circuits. One might guess that nerve pulse generation might involve this kind of mechanism: stochastic resonance seems to be indeed involved but not in this manner.

The collecting circuits for the neuronal SQUIDs could be of order body size or even larger. In [31] I have proposed the notion of magnetic circulation analogous to blood circulation to be a basic control

system in bio-systems. This circulation could be seen also as a collecting circuitry for magnetic flux amplified in brain, where amplifying and SQUID type components of the circuitry are located. Amplifying and SQUID type parts of the circuitry might be also located in other organs like heart: perhaps even muscles contain amplifying circuits and neuronal SQUIDs. One cannot exclude the possibility of much larger collecting circuits making possible the control of the organism by the higher levels of self hierarchy.

The spiral loops used in SQUIDs to amplify the magnetic field bring in mind the spiral structures associated with the self-organizing excitable media [37] . I have proposed in [52, 53] that spiral structures might in TGD framework correspond to magnetic or Z^0 magnetic flux tubes which enter along the first space-time sheet to the vertex of the spiral structure, flow to the second space-time sheet, and return along the spiral loop. These spiral loops could be also ionic em or Z^0 super-conductors. This kind of spiral loop might perhaps serve as an amplifier of the magnetic flux generated by the super current flowing along the loop.

Very general empirical inputs [196] in dramatic conflict with the standard vision about what homeostasis between cell interior and exterior means, lead naturally to a model in which the interaction of MEs with neuron occurs via magnetic induction mechanism leading also to the generation of nerve pulses. The notion of flow equilibrium in the many-sheeted space-time is essentially involved. The mechanism can also involve stochastic resonance as a means of transforming the oscillatory motion of the gravitational pendulum serving as an analog system to a rotational motion. The necessary noise could correspond to the noisy part of the super current perhaps induced by the incoming nerve pulses.

Genetic code and color?

It is gradually becoming clear that the possibility of classical color gauge fields, the center of mass color degrees of freedom of space-time sheets analogous to rigid body degrees of freedom, and configuration space color might have deep implications for the understanding of living matter and consciousness. Colored MEs, or what what might be called configuration space photons, are one possible candidate for colored particles involved with the realization of color vision. They might be also an essential element of bio-control using the analogs of laser beams and there phase conjugates to represent control commands and their time reversals. This raises the question whether color might relate somehow with the realization of genetic code. The following speculations are just first speculations but might help to open gates of imagination.

1. Minimal translation of the genetic code to holograms

Configuration space photons represent genuinely quantum gravitational states, state functionals in the 'world of worlds', and thus they should correspond to highest level of self hierarchy and perform quantum control. Since color and polarization represented as angular momentum component in direction of ME characterize configuration space dependence, they could play a fundamental role in the control mechanism and control commands represented by quantum holograms should be characterized by a collection of these quantum numbers. In particular, genetic code might be expressible in terms of these basic quantum numbers.

There is a thought provoking connection with the TGD based model of genetic code predicting entire hierarchy of genetic codes.

1. At the first interesting level one has 4 nucleotides corresponding to $2^2 = 4$ mutually consistent statements in the set of $7 = 2^3 - 1$ statements coded by 3 bits and one statement thrown away.

2. DNA triplets correspond to the subset of $2^6 = 64$ mutually consistent statements of $2^7 - 1 = 127$ statements coded by 7 bits with one statement thrown away. At the next level one has $2^{127} - 1$ statements and the number of the mutually consistent statements is $2^{126} = 2^{6\times 21}$. It is not an accident that 126 decomposes into the product of numbers 6 and 21, where 21 is the number of different aminoacids with stopping sign counted formally as an aminoacid.

What makes the bell ringing is the appearance of the number $6 = 3 + 3$ primary colors and their conjugates. Could the number of nucleotides in the DNA triplet and its conjugate somehow correspond to the 3 primary colors and their complementary colors somehow? Note that also the 2-dimensional configuration spin is involved, and has two symmetry-related values J and $-J$ (configuration space spin should be responsible for polarization sense). How could this correspondence be consistent with

the idea about MEs generating coherent states of configuration space photons having configuration space color and spin and acting as control commands?

Consider first a minimal model in which, somewhat disappointingly, color is not necessarily needed.

1. The proposal of Gariaev and collaborators that DNA can be effectively regarded as a static sequence of laser mirrors [148] suggests a concrete guess for the coding of genes to sequences of MEs. In TGD framework laser mirrors could correspond to transversal MEs associated with DNA nucleotides. The requirement that two orthogonal polarizations are possible, implies that there must be a pair of mutually orthogonal MEs associated with each nucleotide and orthogonal to the DNA strand.

2. Configuration space spin of ME, which is 2-dimensional spin, is either J or $-J$ so that $2 \times 2 = 4$ spin combinations $(\pm J, \pm J)$ are possible for the pair of MEs. The four nucleotides A,C,T,G naturally code for these spin configurations and the reversal of spin orientations corresponds naturally to the conjugations $A \leftrightarrow T$, $C \leftrightarrow G$ conjugations. Clearly, this model does not require color.

2. How color could emerge in the translation of the genetic code to holograms?

Color does not code for anything in the minimal model of the genetic code, and one could realize the genetic code using non-colored configuration space photons having only polarization degree of freedom or even ordinary polarized coherent light. There are some motivations for color however.

Each hologrammic command should have time reversed version giving rise to the phase conjugate command. Color and spin conjugation is a very natural manner to represent this operation. The conjugate hologram is naturally associated with the conjugate DNA strand. This observation allows to considerably generalize the model by only requiring that MEs correspond to any of the six basic colors and that complementary nucleotides correspond to conjugate colors. This option raises the possibility that DNA code words, genes or some other sub-units of DNA strands could define color singlets. This would obviously provide a very elegant manner to decompose genetic text to subunits. A more general, and perhaps more plausible, manner to decompose genetic text to subunits is as tensor products of unentangled and irreducible color representations.

This option however allows the possibility that genetic codewords are self conjugate. What if one excludes this possibility? It is possible to exclude the possibility of self conjugate commands by using 3+3 decomposition of color algebra corresponding to colors and complementary colors. The pairs of MEs associated with the subsequent nucleotides could be assumed to correspond to, say, (red, blue, white) in this order so that the conjugate strand corresponds to (green, yellow, black). In fact, the ordering of the colors is not essential since spin states of MEs code for the information. At quantum level the requirement that three colors are different would boil down to the requirement that there is complete asymmetry with respect to the permutations of the colors of three parallel MEs. Note that in this case the color quantum numbers of the DNA strand or its complementary strand cannot sum up to zero.

Note that the three different colors for the subsequent nucleotides might make possible that the corresponding control commands act on different MEs, which could be MEs associated with DNA itself.

3. Color confinement and bio-control

If color is really there, it must have some crucially important function besides making it possible to define time reversals of the control commands and decomposition of DNA to unentangle linguistic subunits. A good guess is that color confinement is involved with this function very intimately. Color confinement in the length scale of DNA MEs requires color neutrality in this length scale. DNA strand and its conjugate, even triplet and its conjugate, can give rise to a color singlet state but this is not possible if only the MEs associated with DNA strand are activated. In this case color confinement requires that somewhere else another colored state is activated so that the resulting overall state is color singlet. Thus long range correlations in the length scale of MEs perhaps crucial for biological self organization are unavoidable.

The work of Gariaev and collaborators is based on effects associated with visible laser light interacting with DNA. This encourages to think that the lengths of DNA MEs should be of order $E-7-E-6$ meters. This conforms with the idea that genes should directly control the functioning of the cell or

at least the cell nucleus. Note that genes might be regarded as longitudinally color entangled portions of DNA acting. Configuration space color entanglement in length scale of chromosome and nucleus could obviously be possible. If this picture is correct, color confinement would be much more, that an eternal nuisance of elementary particle theorist.

4. Also memetic codewords could be coded to holograms

One can imagine also the translation of the memetic code to a sequence of orthogonal ME pairs. The $6 \times 21 = 126$ bits for the maximal number of mutually consistent statements of the memetic code decompose into a sequence of 21 6-bit sequences interpreted as statements consisting of 21 words. Each 6-bit sequence consisting of three 2-bit units in turn is in one-one correspondence with a DNA triplet. Each 2-bit unit would code for the configuration space spins $\pm J$ for a a pair of orthogonal MEs possibly forming an antisymmetrized triplet of the basic colors. The duration of the memetic codeword corresponds to the secondary p-adic time scale $T_2(M_{127}) = .1$ seconds so that by Uncertainty Principle memetic code could imply long range color correlations in the length scale of Earth. ELF MEs propagating in phase with the nerve pulse sequence (this is essential and explains why ELF MEs must scan the cortex!) could translate the memetic codewords represented by the sequences of the cognitive neutrino pairs to quantum holograms.

2.3.6 Experimental evidence for MEs

There is indeed evidence for the presence of MEs in bio-system. In CASYS'2000 conference Peter Marcer reviewed the work done by him in collaboration with Russian group [148] led by Peter Gariaev providing experimental evidence for the hypothesis that DNA acts as a receiving and sending quantum antenna. What was observed that irradiation of DNA with visible laser light induced emission of coherent light with both visible and radio frequencies. The emitted radiation was also modulated in time scale of about .01 seconds. The modulation could be due to propagation of soliton sequences propagating along Josephson junction formed by the strands of DNA or due to nonpropagating spatially constant Josephson current: both cases are mathematically equivalent with gravitational pendulum. Phantom DNA effect [197] has explanation in terms of mind like space-time sheets identifiable as MEs. The experiments of Russian group replicated the observations of Poponin.

With inspiration coming from the experimental results, Gariaev has also suggested that DNA is accompanied by a sequence of some kind of laser mirrors. TGD suggests their interpretation as MEs [148] . The assumption that each nucleotide is accompanied by an orthogonal pair of MEs (two orthogonal polarizations) allows a holographic realization of the genetic code. Four nucleotides are mapped to four pairs of values of the configuration spin $\pm J$ in the simplest realization [31] . Color degrees of freedom would bring in the long term correlations forced by color confinement in the length scale of DNA ME, which should be of order of wavelength of visible light, and thus forcing structures of this size to behave like coherent units.

The bio-photons of Popp [132] could correspond to coherent photons generated by MEs. Homeopathy could also have explanation in terms of MEs coding relevant frequency information to MEs about medicine, whose effect is also based on MEs [84] . MEs would simply mimic the medicine. There are well documented effects related to the ability of water to absorb and transmit frequencies [35] . The ability of water to absorb and transmit frequencies could rely on the generation of mind like space-time sheets, most naturally MEs, oscillating with the same frequency as stimulus. Water would form cognitive representation for the stimulus, mimic it, in terms of light-like vacuum current giving rise to classical em or Z^0 field providing nonlike hologram like representation for the stimulus.

MEs are predicted to form a scale invariant family and quite recent cosmological data provides support for MEs in cosmological(!) length scales [9] . An intense beam of photons with energies of roughly 100 proton masses from a blazar at distance of about 10^8 light years have been observed. Blazar is so called gamma ray burster producing extremely intense energy fluxes in form of two jets. How these jets are produced is mystery of its own in standard physics. In TGD these jets correspond to the ends of cosmic string decaying like a cosmic firecracker into ordinary matter giving rise to galaxies. What makes observation 'impossible' is that photons with these energies should never reach Earth but lose their energy via scattering with cosmic microwaves background. Somehow these photons are however able to defy laws of standard physics. One TGD based model for phenomenon is very simple: photons are Bose-Einstein condensed on and travel, not along material space-time sheet were energy would be rapidly lost, but along 'massless extremal' (ME) of cosmic size scale. Cosmic laser beam is

in question. One can also consider the possibility that the light-like vacuum current associated with cosmic ME generates the observed photons.

The general model for quantum control and coordination relies crucially on the existence of a hierarchy of superconductors associated with the self hierarchy (self defined as a quantum system able to avoid bound state entanglement with environment) controlling the ionic densities at atomic space-time sheets via many-sheeted ionic flow equilibrium and being quantum controlled with the mediation of the fractal hierarchy of MEs.

2.4 Bio-systems as superconductors

TGD Universe provides also the hardware for the realization of bio-system, in particular brain, as a macroscopic quantum system involving various kinds of super conductors. The essential elements are quantum criticality, spin glass analogy and generalization of the space-time concept and TGD based gauge field concept.

2.4.1 General mechanisms for superconductivity

The many-sheeted space-time concept provides a very general mechanism of superconductivity based on the 'dropping' of charged particles from atomic space-time sheets to larger space-time sheets. The first guess was that larger space-time sheets are very dry, cool and silent so that the necessary conditions for the formation of high T_c macroscopic quantum phases are met.

The possibility of large $\hbar$ quantum coherent phases makes however the assumption about thermal isolation between space-time sheets un-necessary. At larger space-time sheet the interactions of the charged particles with classical em fields generated by various wormhole contacts feeding gauge fluxes to and from the space-time sheet in question give rise to the necessary gap energy. The simplest model for Cooper pair is space-time sheet containing charged particles having attractive Coulombic interaction with the quarks and antiquarks associated with the throats of the wormhole contacts.

A crucial element is quantum criticality predicting that superconductivity appears at the fluctuating boundaries of competing ordinary and large $\hbar$ phases for nuclei. This assumption predicts several anomalous phenomena such as cold fusion and nuclear transmutations. Also high T_c superfluidity of bosonic atoms dropped to space-time sheets of electronic Cooper pairs becomes possible besides ionic super conductivity. Even dark neutrino superconductivity can be considered below the weak length scale of scaled down weak bosons.

Magnetic and Z^0 magnetic flux tubes and walls are especially interesting candidates for supra current carries. In this case the Cooper pairs must have spin one and this is indeed possible for wormholy Cooper pairs. The fact that the critical magnetic (Z^0 magnetic) fields can be very weak or large values of $\hbar$ is in accordance with the idea that various almost topological quantum numbers characterizing induced magnetic fields provide a storage mechanism of bio-information.

This mechanism is extremely general and works for electrons, protons, ions and even charged molecules so that an entire zoo of high T_c bio-superconductors and super-fluids is predicted. All atoms and ions can be regarded as completely ionized Z^0 ions and also Z^0 superconductors (or super fluids) are predicted.

1. The experimental data about the effects of ELF em fields at cyclotron frequencies of various ions in Earth's magnetic field on bio-systems [46] provide support for this scenario. Most remarkably, the cyclotron frequencies of biologically important ions correspond to the important frequencies of EEG and the time scale of nerve pulse corresponds to $n = 3$ multiple of proton cyclotron frequency so that a direct quantitative contact with brain consciousness results.

2. Electronic super conductors are of type II with defect regions being typically cylindrical: DNA sequences, proteins, microtubules,... could provide examples of the defect regions. One ends up also with a model of high T_c super conductors in which the interaction of the electrons with wormhole BE condensate gives rise to Cooper pairs. The model explains elegantly the basic peculiar features of the high T_c superconductors.

3. Long ranged Z^0 force due to anomalous weak isospin of nuclei [69, 24] and Z^0 charged wormholes make possible also Z^0 ionic superconductivity and even dark neutrino super conductivity. For

instance, Z^0 ionic superconductivity is crucial in the model for the quantum correlate of hearing: audible frequencies are mapped to Z^0 cyclotron frequencies. Dark neutrino super conductors are of type I in the interesting length scale range and defect regions are stripe like. Besides cell and endoplasma membranes, epithelial sheets consisting of two cell layers and some larger structures in cortex could correspond to regions of this kind and the interpretation as a physical realization of cognitive hierarchy suggests itself.

2.4.2 Superconductivity at magnetic flux quanta in astrophysical length scales

Magnetic flux tubes of endogenous magnetic field $B_{end} = 2B_E/5 = .2$ Gauss, where $B_E = .5$ Gauss is the nominal value of the Earth's magnetic field, are crucial for the TGD based model of superconductivity. Since the models of auroras assume that the magnetic flux lines act effectively as conducting wires, the natural hypothesis is that superconductivity is an astrophysical phenomenon. This leads to a model of auroras explaining the latest findings and providing further insights to the superconductivity and the manner how it breaks down. Critical temperature can be identified as the temperature at which the join along boundaries bonds making possible the leakage of the supra currents to the non-superconducting space-time sheets become possible and can be gigantic as compared to the temperature at the superconducting space-time sheets if space-time sheets are thermally isolated. On the other hand, the possibility of large $\hbar$ phases in principle makes possible arbitrarily high critical temperatures in a given length scale.

p-Adic length scale hierarchy and the hierarchy of dark matters labelled by values of $\hbar$ suggest the existence of an entire hierarchy of super conducting space-time sheets giving rise to a hierarchy of cognitive representations (abstractions about abstractions about...). The possibility of complex conformal weights expressible in terms of zeros of Riemann Zeta such that the net conformal weight is real, and the hierarchy of algebraic extensions of p-adic number fields suggest the existence of additional hierarchies.

2.4.3 Fractal hierarchy of EEGs and ZEGs

There are three contributions to EEG besides neural noise: Schumann frequencies, cyclotron frequencies, and the frequencies associated with Josephson junctions determined by the sum of the constant voltage and voltage perturbation determined by the superposition of cyclotron frequencies. Cyclotron contribution can be interpreted as a control signal from a magnetic body in question labelled by k_d and affects both the ions at the flux sheets traversing DNA and the Josephson junction. The coherent state of photons generated by Josephson current corresponds to a reaction to this signal received by the magnetic body as a feedback. Schumann frequencies can be assigned to the control by magnetic body of Earth and correlate with the collective aspects of consciousness.

The analysis of the Josephson current [23] leads to the conclusion that the frequencies in the coherent state of photons are in general sums and differences of Josephson frequency and harmonics of cyclotron frequencies. For small amplitudes this implies that alpha band to which the cyclotron frequencies most biologically important bosonic ions corresponds has as satellites theta and beta bands. Higher harmonics correspond to gamma and higher bands having also satellites. For large amplitudes EEG becomes chaotic which is indeed the property of beta band during say intense concentration or anxiety. The findings of Nunez [38] about narrow 1-2 Hz wide bands at 3,5,7 Hz and 13,15,17 Hz confirm with the prediction of satellite bands and fix the Josephson frequency to 5 Hz. This picture explains the general characteristics of EEG in wake-up state qualitatively and quantitatively.

In order to understand the characteristics during various stages of deep sleep one must assume that the cyclotron frequency scale of ions is scaled down by a factor of 1/2. One explanation is that right *resp.* left brain hemisphere corresponds to $Z = 2$ *resp.* $Z = 1$ quantization condition $Z \int BdS = n\hbar$ for the magnetic flux. $Z = 2$ case allows only doubly charged bosonic ions at magnetic flux sheets. $Z = 1$ case also also singly charged ions be their bosons or fermions and for this option magnetic field is scaled down by a factor of 1/2. The alternative explanation is that during sleep only Bose-Einstein condensates of singly charged exotic ions resulting when color bond inside nucleus becomes charged are present. This reduces the scale of cyclotron frequencies by a factor 1/2 and leaves only theta and delta bands. During stage 4 sleep only only DNA cyclotron frequencies in delta band are around 1 Hz and just above the thermal threshold are predicted to be present. For $k_d = 3$ and magnetic field

scaled up by λ and flux tube area scaled down by λ^{-2} DNA frequencies are scaled up to kHz for $Z = 2$ flux quantization and might define neuronal synchronization frequencies.

The generalization of the model for EEG hierarchy to the case of ZEG is straightforward and cyclotron frequency spectrum is essentially the same [23] . Z^0 ions are obtained when nuclear color bonds become charged and the combination of ordinary and exotic ionization can produce also em neutral Z^0 ions. Any atom, almost always boson, has an exotically charged counterpart with same statistics so that very rich spectrum of Bose-Einstein condensates results.

2.4.4 TGD assigns 10 Hz biorhythm to electron as an intrinsic frequency scale

p-Adic coupling constant evolution and origins of p-adic length scale hypothesis have remained for a long time poorly understood. The progress made in the understanding of the S-matrix of the theory (or rather, its generalization M-matrix) [16] has however changed the situation. The unexpected prediction is that zero energy ontology assigns to elementary particles macroscopic times scales. In particular, the time scale assignable to electron correspond to the fundamental biorhythm of 10 Hz.

M-matrix and coupling constant evolution

The final breakthrough in the understanding of p-adic coupling constant evolution came through the understanding of S-matrix, or actually M-matrix defining entanglement coefficients between positive and negative energy parts of zero energy states in zero energy ontology [16] . M-matrix has interpretation as a "complex square root" of density matrix and thus provides a unification of thermodynamics and quantum theory. S-matrix is analogous to the phase of Schrödinger amplitude multiplying positive and real square root of density matrix analogous to modulus of Schrödinger amplitude.

The notion of finite measurement resolution realized in terms of inclusions of von Neumann algebras allows to demonstrate that the irreducible components of M-matrix are unique and possesses huge symmetries in the sense that the hermitian elements of included factor $\mathcal{N} \subset \mathcal{M}$ defining the measurement resolution act as symmetries of M-matrix, which suggests a connection with integrable quantum field theories.

It is also possible to understand coupling constant evolution as a discretized evolution associated with time scales T_n, which come as octaves of a fundamental time scale: $T_n = 2^n T_0$. Number theoretic universality requires that renormalized coupling constants are rational or at most algebraic numbers and this is achieved by this discretization since the logarithms of discretized mass scale appearing in the expressions of renormalized coupling constants reduce to the form $log(2^n) = nlog(2)$ and with a proper choice of the coefficient of logarithm log(2) dependence disappears so that rational number results.

p-Adic coupling constant evolution

Could the time scale hierarchy $T_n = 2^n T_0$ defining hierarchy of measurement resolutions in time variable induce p-adic coupling constant evolution and explain why p-adic length scales correspond to $L_p \propto \sqrt{p}R$, $p \simeq 2^k$, R CP_2 length scale? This looks attractive but there is a problem. p-Adic length scales come as powers of $\sqrt{2}$ rather than 2 and the strongly favored values of k are primes and thus odd so that $n = k/2$ would be half odd integer. This problem can be solved.

1. The observation that the distance traveled by a Brownian particle during time t satisfies $r^2 = Dt$ suggests a solution to the problem. p-Adic thermodynamics applies because the partonic 3-surfaces X^2 are as 2-D dynamical systems random apart from light-likeness of their orbit. For CP_2 type vacuum extremals the situation reduces to that for a one-dimensional random light-like curve in M^4. The orbits of Brownian particle would now correspond to light-like geodesics γ_3 at X^3. The projection of γ_3 to a time=constant section $X^2 \subset X^3$ would define the 2-D path γ_2 of the Brownian particle. The M^4 distance r between the end points of γ_2 would be given $r^2 = Dt$. The favored values of t would correspond to $T_n = 2^n T_0$ (the full light-like geodesic). p-Adic length scales would result as $L^2(k) = DT(k) = D2^k T_0$ for $D = R^2/T_0$. Since only CP_2 scale is available as a fundamental scale, one would have $T_0 = R$ and $D = R$ and $L^2(k) = T(k)R$.

2. p-Adic primes near powers of 2 would be in preferred position. p-Adic time scale would not relate to the p-adic length scale via $T_p = L_p/c$ as assumed implicitly earlier but via $T_p = L_p^2/R_0 = \sqrt{p}L_p$, which corresponds to secondary p-adic length scale. For instance, in the case of electron with $p = M_{127}$ one would have $T_{127} = .1$ second which defines a fundamental biological rhythm. Neutrinos with mass around .1 eV would correspond to $L(169) \simeq 5$ μm (size of a small cell) and $T(169) \simeq 1. \times 10^4$ years. A deep connection between elementary particle physics and biology becomes highly suggestive.

3. In the proposed picture the p-adic prime $p \simeq 2^k$ would characterize the thermodynamics of the random motion of light-like geodesics of X^3 so that p-adic prime p would indeed be an inherent property of X^3.

4. The fundamental role of 2-adicity suggests that the fundamental coupling constant evolution and p-adic mass calculations could be formulated also in terms of 2-adic thermodynamics. With a suitable definition of the canonical identification used to map 2-adic mass squared values to real numbers this is possible, and the differences between 2-adic and p-adic thermodynamics are extremely small for large values of for $p \simeq 2^k$. 2-adic temperature must be chosen to be $T_2 = 1/k$ whereas p-adic temperature is $T_p = 1$ for fermions. If the canonical identification is defined as

$$\sum_{n\geq 0} b_n 2^n \to \sum_{m\geq 1} 2^{-m+1} \sum_{(k-1)m\leq n<km} b_n 2^n \quad .$$

It maps all 2-adic integers $n < 2^k$ to themselves and the predictions are essentially same as for p-adic thermodynamics. For large values of $p \simeq 2^k$ 2-adic real thermodynamics with $T_R = 1/k$ gives essentially the same results as the 2-adic one in the lowest order so that the interpretation in terms of effective 2-adic/p-adic topology is possible.

p-Adic length scale hypothesis and biology

The basic implication of zero energy ontology is the formula $T(k) \simeq 2^{k/2}L(k)/c = L(2,k)/c$. This would be the analog of $E = hf$ in quantum mechanics and together hierarchy of Planck constants would imply direct connection between elementary particle physics and macroscopic physics. Especially important this connection would be in macroscopic quantum systems, say for Bose Einstein condensates of Cooper pairs, whose signature the rhythms with $T(k)$ as period would be. The presence of this kind of rhythms might even allow to deduce the existence of Bose-Einstein condensates of hitherto unknown particles.

1. For electron one has $T(k) = .1$ seconds which defines the fundamental $f_e = 10$ Hz bio-rhythm appearing as a peak frequency in alpha band. This could be seen as a direct evidence for a Bose-Einstein condensate of Cooper pairs of high T_c super-conductivity. That transition to "creative" states of mind involving transition to resonance in alpha band might be seen as evidence for formation of large BE condensates of electron Cooper pairs.

2. TGD based model for atomic nucleus [1] , [1] predicts that nucleons are connected by flux tubes having at their ends light quarks and anti-quarks with masses not too far from electron mass. The corresponding p-adic frequencies $f_q = 2^k f_e$ could serve as a biological signature of exotic quarks connecting nucleons to nuclear strings . $k_q = 118$ suggested by nuclear string model would give $f_q = 2^{18} f_e = 26.2$ Hz. Schumann resonances are around 7.8, 14.3, 20.8, 27.3 and 33.8 Hz and f_q is not too far from 27.3 Hz Schumann resonance and the cyclotron frequency $f_c(^{11}B^+) = 27.3$ Hz for $B = .2$ Gauss explaining the effects of ELF em fields on vertebrate brain.

3. For a given $T(k)$ the harmonics of the fundamental frequency $f = 1/T(k)$ are predicted as special time scales. Also resonance like phenomena might present. In the case of cyclotron frequencies they would favor values of magnetic field for which the resonance condition is achieved. The magnetic field which in case of electron gives cyclotron frequency equal to 10 Hz is $B_e \simeq 3.03$ nT. For ion with charge Z and mass number A the magnetic field would be $B_I = \frac{A}{Z}(m_p/m_e)B_e$. The $B = .2$ Gauss magnetic field explaining the findings about effects of ELF em fields on vertebrate

brain is near to B_I for ions with f_c alpha band. Hence the value of B could be understood in terms of resonance with electronic B-E condensate.

4. The hierarchy of Planck constants predicts additional time scales $T(k)$. The prediction depends on the strength of the additional assumptions made. One could have scales of form $nT(k)/m$ with m labeling the levels of hierarchy. $m = 1$ would give integers multiples of $T(k)$. Integers n could correspond to ruler and compass integers expressible as products of first powers of Fermat primes and power of 2. There are only four known Fermat primes so that one has $n = 2^n \prod_i F_i$, $F_i \in \{3, 5, 17, 257, 2^{16} + 1\}$. In the first approximation only 3- and 5- and 17-multiples of 2-adic length scales would result besides 2-adic length scales. In more general case products $m_1 m_2$ and ratios m_1/m_2 of ruler and compass integers and their inverses $1/m_1 m_2$ and $m_2 m_1$ are possible.

5. Mersenne primes are expected to define the most important fundamental p-adic time scales. The list of real and Gaussian (complex) Mersennes M_n possibly relevant for biology is given by n=89, 107, 113*, 127, 151*,157*, 163*, 167* ('*' tells that Gaussian Mersenne is in question).

n	89	107	113	127
f/Hz	2.7×10^{12}	1.0×10^7	1.6×10^5	10
n	151	157	163	167
T	19.4 d	3.40 y	218.0 y	3.49×10^3 y

(2.4.1)

2.5 Many-sheeted space-time, universal metabolic quanta, and plasmoids as primitive life forms

In the following the evidence for many-sheeted space-time will be discussed.

2.5.1 Evidence for many-sheeted space-time

The dropping of particle to a larger space-time sheet liberates energy which is the difference of the energies of the particle at two space-time sheets. If the interaction energy of the particle with the matter at space-time sheet can be neglected the energy is just the difference of zero point kinetic energies. This energy depends on the details of the geometry of the space-time sheet. Assuming p-adic length scale hypothesis the general formula for the zero point kinetic energy can be written as

$$E(k) = x \times E_0(k) \quad , \quad E_0(k) = \frac{3}{2} \frac{\pi^2}{mL^2(k)} \quad .$$

Here x is a numerical factor taking into account the geometry of the space-time sheet and equals to $x = 1$ for cubic geometry.

The liberated zero point kinetic energy in the case that the particle drops to a space-time sheet labelled by $k_f = k + \Delta k$ with same value of x is

$$\Delta E(k, \Delta k) = x \times E_0(k) \times (1 - 2^{-\Delta k}) \quad .$$

The transitions are seen as discrete lines for some resolution $\Delta k \leq \Delta k_{max}$. At the limit $k \to \infty$ transitions give rise to a quasicontinuous band. The photon energy for $k \to \infty$ transition is same as the energy from $k - 1 \to k$ transition, which brings in additional option to the model building.

For a proton dropping from the atomic space-time sheet $k = 137$ to very large space-time sheet ($\Delta k \to \infty$) one has $\Delta E(k) = E(k) \sim x \times .5$ eV. Since the ratio of electron and proton masses is $m_p/m_e \simeq .94 \times 2^{11}$, the dropping of electron from space-time sheet $k_e = k_p + 11$ liberates zero point kinetic energy which is by is by a factor .9196 smaller. For $k_p = 137$ one would have $k_e = 148$. This energy corresponds to the metabolic energy currency of living systems and the idea is that the differences of zero point kinetic energies define universal metabolic energy currencies present already in the metabolism of pre-biotic systems. In the following fit electron's zero point kinetic energy will be taken to be $E_0(148) = .5$ eV so that for proton the zero point kinetic energy would be $E_0(137) = .544$ eV.

The hypothesis predicts the existence of anomalous lines in the spectrum of infrared photons. Also fractally scaled up and scaled down variants of these lines obtained by scaling by powers of 2 are predicted. The wavelength corresponding to .5 eV photon would be $\lambda = 2.48$ μm. These lines should be detectable both in laboratory and astrophysical systems and might even serve as a signature for a primitive metabolism. One can also consider dropping of Cooper pairs in which case zero point kinetic energy is scaled down by a factor of 1/2.

Interestingly, the spectrum of diffuse interstellar medium exhibits three poorly understood structures [48] : Unidentified Infrared Bands (UIBs), Diffuse Interstellar Bands (DIBs) [27] , and Extended Red Emission (ERE) [206] allowing an interpretation in terms of dropping of protons or electrons (or their Cooper pairs) to larger space-time sheets. The model also suggests the interpretation of bio-photons in terms of generalizes EREs.

Unidentified Infrared Bands

Unidentified infrared bands (UIBs) contain strong bands at $\lambda = 3.3, 6.2, 11.3$ microns [48] . The best fit for the values of k and Δk assuming dropping of either electron or proton are given by the following table. The last row of the table gives the ratio of predicted photon energy to the energy characterizing the band and assuming $x = 1$ and $E_0(148, e) = .5$ eV. Discrepancies are below 8 per cent. Also the dropping of protonic Cooper pair from $k = 137$ space-time sheet could reproduce the line $\Delta E = .2$ eV. The fit is quite satisfactory although there is of course the uncertainty related to the geometric parameter x.

λ/nm	$E/.5eV$	k	Δk	$\Delta E(k, \Delta k)/E$	p/e
3300	.7515	137	$\sim \infty$	1.002	e
6200	.4000	138	3	1.067	e
11300	.2195	139	3	0.878	p
11300	.2195	139+11=150	3	1.076	e

Table 1. Table gives the best fit for UIBs assuming that they result from dropping of proton or electron to a larger space-time sheet and one has $E_0(148, e) = .5$ eV. The fourth column the table gives the ratio of predicted photon energy to the energy characterizing the band and assuming $x = 1$. e/p tells whether electron or proton is in question.

According to [48] , UIBs are detected along a large number of interstellar sight-lines covering a wide range of excitation conditions. Recent laboratory IR spectra of neutral and positively charged poly-cyclic aromatic hydrocarbons (PAHs) has been successfully used by Allamandola [177] to model the observed UIBs. It is believed that PAHs are produced in reactions involving photosynthesis and are regarded as predecessors of biotic life [36] . This would conform with the presence of metabolic energy quanta.

DNA sugar backbone, some aminoacids, and various hallucinogens involve 5- and 6-cycles and the proposal is that these cycles involve free electron pairs, which possess Planck constant $\hbar = n\hbar_0$, $n = 5, 6$. These free electron pairs would explain the anomalous conductivity of DNA and would be an essential characteristic of living matter. The emergence of $n = 5, 6$ levels could be seen as the first step in the pre-biotic evolution.

Diffuse Interstellar Bands

There are diffuse interstellar bands (DIBs) at wavelengths 578.0 and 579.7 nanometers and also at 628.4, 661.4 and 443.0 nm. The 443.0 nm DIB is particularly broad at about 1.2 nm across - typical intrinsic stellar absorption features are 0.1 nm [48] . The following table proposes a possible identification of these lines in terms of differences of zero point kinetic energies. Also now the best fit has errors below 7 per cent.

λ/nm	$E/.5eV$	k	Δk	$\Delta E(k,\Delta k)/E$	p/e
628.4	3.947	$135 = 3^3 \times 5$	$\sim \infty$	0.987	p
661.4	3.750	$135 + 11 = 2 \times 73$	3	0.985	e
443.0	5.598	$134 = 2 \times 67$	2	0.933	p
578.0	4.291	$135 + 11 = 2 \times 73$	$\sim \infty$	0.986	e
579.7	4.278	$135 + 11 = 2 \times 73$	$\sim \infty$	0.984	e

Table 2. Table gives the best fit for DIBs assuming that they result from dropping of proton or electron to a larger space-time sheet. Notations are same as in the previous table.

The peak wavelengths in chlorophyll and photosynthesis are around 650 nm and 450 nm and would correspond to second and third row of the table.

The Extended Red Emission

The Extended Red Emission (ERE) [48, 206] is a broad unstructured emission band with width about 80 nm and located between 540 and 900 nm. The large variety of peak wavelength of the band is its characteristic feature. In majority of cases the peak is observed in the range 650-750 nm but also the range 610-750 nm appears. ERE has been observed in a wide variety of dusty astronomical environments. The necessary conditions for its appearance is illumination by UV photons with energies $E \geq 7.25$ eV from source with $T \geq 10^4$ K. The position of the peak depends on the distance from the source [206] .

According to [48] the current interpretation attributes ERE to a luminescence originating from some dust component of the ISM, powered by UV/visible photons. Various carbonaceous compounds seem to provide a good fit to the observational constraints. However, the real nature of ERE is still unknown since most candidates seem to be unable to simultaneously match the spectral distribution of ERE and the required photon conversion efficiency.

1. Consider first the band 650-750 nm appearing in the majority of cases. The most natural interpretation is that the lower end of the band corresponds to the zero point kinetic energy of electron at $k = 135+11 = 146 = 2\times 73$ space-time sheet. This would mean that the lines would accumulate near 650 nm and obey the period doubling formula

$$\frac{\lambda(k) - \lambda(\infty)}{\lambda(\infty)} = \frac{2^{-k}}{1-2^{-k}} \ .$$

   By the estimate of Table 2 the lower end should correspond to $\lambda = 628.4$ nm with a correction factor $x < 1$ reducing the zero point kinetic energy. The reduction would be smaller than 4 per cent. $\Delta k = 3$ transition would correspond to 744 nm quite near to the upper end of the band. For $\Delta k = 2$ transition one has $\lambda = 867$ nm not to far from the upper end 900 nm. $\Delta k = 1$ corresponds to 1.3 μm.

2. For proton with $k = 135 = 146$ the energy band would shift by the factor $2^{11}m_e/m_p \simeq 1.0874$ giving the range (598,690) nm.

3. The variation for the position of the peak can be understood if the charged particles at the smaller space-time sheet can have excess energy liberated in the dropping to the larger space-time sheet. This excess energy would determine the position of the lower end of the band in the range $(540, 650)$ nm.

4. One should also understand the role of UV photons with energy larger than 7.25 eV. For proton the energy would be 8.76 eV. For proton the energy would be 8.76 eV. UV photon with energy $E \geq 8$ eV could kick electrons from large space-time sheets to $k = 144 = 146-4$ space-time sheet where they have zero point kinetic energy of 8 eV plus possible additional energy (for proton the energy would be 8.76 eV). One possibility is that these electrons drop first to $k = 145$ by the emission of ~ 4 eV UV photon and then to $k = 144$ by the emission ~ 2 eV photon corresponding to 650 nm line. The further dropping to larger space-time sheets would produce besides this line also the lines with longer wavelengths in the band.

The energy of UV photons brings in mind the bond energy 7.36 eV of N_2 molecule and the possibility of metabolic mechanism using UV light as metabolic energy and based on the dissociation of N_2 followed by re-association liberating metabolic energy kicking protons or electrons to a smaller space-time sheet. For the $k \to k+3$ transition of electron the energy would be 7 eV which suggests that this transition defines important metabolic energy quantum for living interstellar dust using dissociation and its reversal as basic metabolic mechanism.

2.5.2 Laboratory evidence for plasmoids as life forms

From dust to dust

The article *From Plasma crystals and helical structures towards inorganic living matter* of Tsytovich *et al* in August issue of New Journal of Physics provides new empirical support for plasmoids as living life forms. The results of article suggest that interstellar dust could behave like living matter in some respects: it could even have variant of genetic code. This is a really shattering finding and with single blow destroys the standard dogma about life as something purely chemical. It should also give also some headaches for those influental colleagues who have decided that it is necessary to accept the anthropic principle. Here is little popularization of the result.

SCIENTISTS have discovered that inorganic material can take on the characteristics of living organisms in space, a development that could transform views of alien life.

An international panel from the Russian Academy of Sciences, the Max Planck institute in Germany and the University of Sydney found that galactic dust could form spontaneously into helixes and double helixes and that the inorganic creations had memory and the power to reproduce themselves.

A similar rethinking of prospective alien life is being undertaken by the National Research Council, an advisory body to the US government. It says Nasa should start a search for what it describes as weird life - organisms that lack DNA or other molecules found in life on Earth.

The new research, to be published this week in the New Journal of Physics, found nonorganic dust, when held in the form of plasma in zero gravity, formed the helical structures found in DNA. The particles are held together by electromagnetic forces that the scientists say could contain a code comparable to the genetic information held in organic matter. It appeared that this code could be transferred to the next generation.

Professor Greg Morfill, of the Max Planck institute of extra-terrestrial physics, saidGoing by our current narrow definitions of what life is, it qualifies.

The question now is to see if it can evolve to become intelligent. Its a little bit like science fiction at the moment. The potential level of complexity we are looking at is of an amoeba or a plant.

I do not believe that the systems we are talking about are life as we know it. We need to define the criteria for what we think of as life much more clearly.

It may be that science is starting to study territory already explored by science fiction. The television series The X-Files, for example, has featured life in the form of a silicon-based parasitic spore.

The Max Planck experiments were conducted in zero gravity conditions in Germany and on the International Space Station 200 miles above earth.

The findings have provoked speculation that the helix could be a common structure that underpins all life, organic and nonorganic.

To sum up the essentials, plasma phase is involved and the dust life is able to construct analogs of DNA double helices and this has been achieved also in laboratory. "From dust to dust" seems to have a very deep side meaning!

Here is a more quantitative summary of the results reported in [130] .

1. The scale of the dust balls seems to be few micrometers. It is essential that the system is open in the sense that there is both metabolic energy feed and continual feed of plasma to negatively charged dust particles to preserve their charges. Authors speak about effective "gravitational" instability as a mechanism leading to the formation of the helices and identify effective gravitational coupling (the formula contains a trivial typo) as a function of charge and mass of the particle plus dimensionless parameter characterizing the modification of Debye model implied by the fact that dust particles are not electrically closed systems. Authors give a long list of life-like properties possessed by the helical structures.

2. Helical structures are generated spontaneously and possess negative charges. The repulsion of the helical structures transforms to attraction at some critical distance interval due to the fact that the large electrostatic self energy depends on the distance between helices and this makes possible double helices (authors speak about over-screening in the formal model). Similar mechanism might work also in the case of ordinary DNA double helices whose stability is poorly understood since also in this case the large negative charge could be preserved by continual feed of charge.

3. The twist angle of the helix makes bifurcations as a function of radius of helix and the values of twist angle could define the letters of genetic code. Also a mechanism for how the twist angle is communicated to neighboring helix is proposed. Also dust vortices are observed and might be those which one can occasionally observe during hot summer days.

4. Authors do not mention magnetic fields but my guess is that the helical structures reflect directly the geometry of the helical magnetic flux tubes, and that dark electron pairs with large Planck constant at these tubes might be the quantal aspect of the system. These currents might relate closely to the plasma current, which charges the dust particles. Also DNA, which is insulator, is known to be able to act as conductor, and here the free electron pairs associated with aromatic rings having $\hbar = n \times hbar_0$, $n = 5$ or 6, could make conduction possible since their Compton size would be n-fold.

Elephant trunks in astrophysics

TGD Universe is fractal and this means that the visible structures are formed around magnetic flux quanta containing dark matter with large hbar appear in all length scales and have geometric patterns reflecting the exact discrete symmetries of dark matter acting as rotational symmetries of the field body and at the level of visible matter giving rise to broken symmetries typical for molecular structures. The helical structures found from the rings of some planets could be one example of fractal life.

For some time ago I learned about "elephant trunks" found by Hubble (I am grateful for Miika Väisälä telling about the trunks and for giving references to the papers about the finding). They appear in very wide range of length scales: at least from 1000 au to 1 pc. They are found in close connection with molecular clouds and HII regions excite by one or more young hot stars (a "metabolic connection" with the above mentioned unidentified bands and lines and PAHs present only if there is also UV source present does not look like a bad guess). In general the trunks are

Another important finding supporting TGD view about Universe which might be seen as a fractally scaled variant of above helices. pointing like fingers to the hot stars. Here is abstract of the paper by P. Carlquist, G. F. Gahm, and H. Kristen [191] .

Using the 2.6 m Nordic Optical Telescope we have observed a large number of elephant trunks in several regions. Here, we present a small selection of this material consisting of a few large, well-developed trunks, and some smaller ones. We find that: (i) the well-developed trunks are made up of dark filaments and knots which show evidence of twisted structures, (ii) the trunks are connected with essentially two filamentary legs running in V-shape, and (iii) all trunks have the maximum extinction in their heads. We advance a theory of twisted elephant trunks which is based on the presence of magnetic flux ropes in molecular clouds where hot OB stars are formed. If the rope contains a local condensation it may adopt a V-shape as the region around the hot stars expands. If, in addition, the magnetic field in the rope is sufficiently twisted, the rope may form a double helix at the apex of the V. The double helix is identified with the twisted elephant trunks. In order to illustrate the mechanisms behind the double helix we have constructed a mechanical analogy model of the magnetic flux rope in which the rope has been replaced by a bundle of elastic strings loaded by a weight. Experiments with the model clearly show that part of the bundle will transform into a double helix when the twist of the bundle is sufficiently large. We have also worked out a simple theoretical model of a mass-loaded magnetic flux rope. Numerical calculations show that a double helix will indeed form when the twist of the rope exceeds a certain critical limit. Numerical model calculations are applied to both the analogy model experiments and one of the well-developed elephant trunks. On the basis of our model we also suggest a new interpretation of the so called EGGs.

The double helix mechanism is quite general, and should be active also in other suitable environments. One such environment may be the shell of supernova remnants. Another example is the expanding bubble outlined by the North Celestial Pole Loop.

For fractally thinking physicist consisting mostly of dark matter with large Planck constant this does not leave many options: life and even intelligent life is everywhere and in all length scales. This provides also a new view about Fermi paradox: see the article [2] , which summarizes also the essentials of TGD, TGD based ontology, and TGD based quantum biology.

2.5.3 Universal metabolic quanta

Universal energy quanta might have rather interesting implications. For instance, irradiation of cells could provide a direct metabolic mechanism when the normal metabolic machinery fails. The universal metabolic quanta should have also played a key role during pre-biotic evolution when chemical storage mechanism were absent or primitive so that energy metabolism relied on direct absorption of photons.

Direct support for universal metabolic energy quanta

There is direct support for the notion of universal energy quanta. The first support comes from the effect of low-power laser light on living matter. More than 30 years ago a method known with various names such as low-power laser therapy, biostimulation, or photobiomodulation emerged [173] and has now a wide range of applications. The treatment can apply both non-coherent (light emitting diodes) or coherent (laser light). In the case of of non-coherent light the method applies thin structures with thickness smaller than coherence length of light so that there is no difference between non-coherent and laser light. Laser light applies to situation when both the thickness of the surface layer and structure itself in range 1 mm- 1 cm and shorter than coherence length. Often the irradiation is applied to wounds and sites of injuries, acupuncture points, and muscle trigger points. The method involves several parameters such as wavelength in the range 400-900 nm (IR and near IR light), output power (10 100 mW), continuous wave and pulsed operation modes, and pulse parameters.

1. What is known?

The article of Karu [173] gives a good summary about what is known.

1. The action spectrum characterizes the maxima of the biological response as a function of wavelength. Action spectrum is essentially universal. For near IR and IR light the maxima of spectra are at 620, 680, 760, 820-830 nm. The spectrum continues also to visible light [173] but I do not have access these data.

2. The action can induce both physiological and morphological changes in non-pigmental cells via absorption in mitochondria. HeNe laser ($\lambda = 632.8$ nm) can alter the firing pattern of nerves and can mimic the effect of peripheral stimulation of a behavioral reflex.

2. Biochemical approach

In [173] the biochemical approach to the situation is discussed.

1. In standard biochemistry based approach the natural hypothesis is that the maxima correspond to some molecular absorption lines and the task is to identify the photo acceptor. The primary acceptor in IR-to red spectral region is believed to be the terminal enzyme of the respiratory chain cytochrome c oxidase located in mitochondrion but this is just an assumption.In the violet-to-blue spectral region flavoproteins (e.g. NADHdehydrogenace in the beginning of respiratory chain) are among the photo acceptors as terminal oxidases. It is known that also non-mitochondrial enhancement of cellular metabolism exist, which does not fit well with the vision about mitochondria as power plants of cell. It is believed that electronic excitation occurs and somehow leads to the biological effect.

2. The natural assumption in biochemistry framework is that the stimulation increases the effectiveness of cellular metabolism by making the utilization of oxygen more effective. The effect of the light would occur at the control level and induce secondary reactions (cellular signaling cascades or photo signal transduction and amplification) affecting eventually the gene expression.

3. Three different regulation pathways have been suggested [173] . Since small changes in ATP level can alter cellular metabolism significantly, the obvious idea is that photoacceptor controls

the level of intracellular ATP. In starving cells this looks especially attractive hypothesis. In many cases however the role of redox homeostasis is however believed to be more important than that of ATP. The second and third pathways would indeed affect cellular redox potential shifting it to more oxidized direction. The mechanism of regulation is however not understood. Hence one can say that there is no experimental proof or disproof for the standard approach.

3. TGD inspired approach

In TGD framework the first guess is that irradiation pumps directly metabolic energy to the system by kicking particles to smaller space-time sheets. This kind of direct energy feed would be natural when the cell is starving or injured so that its control mechanisms responsible for the utilization of oxygen are not working properly. For Bose-Einstein condensate of photons this effect would be especially strong being proportional to N^2 rather than N, where N is photon number. The effect would also appear coherently in a region whose size is dictated by coherence length when the target is thick enough.

There is a simple killer test for the proposal. The predicted energies are universal in the approximation that the interactions of protons (or electrons) kicked to the smaller space-time sheets with other particles can be neglected. The precise scale of metabolic energy quanta can be fixed by using the nominal value of metabolic energy quantum .5 eV in case of proton. This predicts the following spectrum of universal energy quanta for proton and electron

$$\begin{aligned}
&\Delta E_{k,n}(p) = E_0(k,p) \times (1-2^{-n}) \ , \\
&E_0(k,p) = E_0(137,p)2^{137-k} \simeq 2^{137-k} \times .5 \ \ eV \ \ .
\end{aligned}$$

$$\begin{aligned}
&\Delta E_{k,n}(e) = E_0(k,e) \times (1-2^{-n}) \ , \\
&E_0(k,e) = \tfrac{m_p}{2^{11}m_e} E_0(137,p)2^{148-k} \simeq 2^{148-k} \times .4 \ \ eV \ \ .
\end{aligned}$$

k characterizes the p-adic length scale and the transition corresponds to the kicking of charged particle from space-time sheet having $k_1 = k+n$ to $k = n$.

The shortest wavelength 630 nm is rather close to the wavelength of HeNe laser and corresponds to red light with $E_0 = 2.00$ eV. Thus one would have $k = 135$ in the case of proton which corresponds to roughly one of atomic radius for ordinary value of $\hbar$. For electron one would have $k = 150$ which corresponds to $L(151)/\sqrt{2}$: $L(151) = 10$ nm corresponds to cell membrane thickness. The following table gives the energies of photons for action spectrum and predicted values in the case of proton, which provides a better fit to the data.

n	2	3	4	5
λ/nm	825	760	680	620
E_{exp}/eV	1.50	1.63	1.82	2.00
E_{pred}/eV	1.50	1.75	1.88	1.94
E_{pred}/E_{exp}	1.00	1.07	1.02	0.97

(2.5.1)

The largest error is 7 per cent and occurs for $n = 3$ transition. Other errors are below 3 per cent. Note that also in experiments of Gariaev [148, 149] laser light consisting of 2 eV photons was used: in this case the induced radio wave photons - possibly dark photons with energy 2 eV - had positive effect on growth of potatoes.

Possible explanation for the effect of IR light on brain

The exposure of brain to IR light at wavelength of 1072 nm is known to improve learning performance and give kick start to cognitive function [66] . The simplest explanation is that this light reloads the metabolic energy batteries of neurons by kicking electrons or protons or their Cooper pairs to larger space-time sheets. The wavelength in question is roughly one half of the wavelength associated with metabolic energy quantum with average energy .5 eV (2480 μm) assignable to the dropping of proton to a very large space-time sheet from k=137 space-time sheet or of electron from k=137+11= 148 space-time sheet. This if the electron and proton are approximated to be free particles. Energy band is in question since both the particles can have additional interaction energy.

For the kicking of electron from very large space-time sheet to $k = 147$ space-time sheet the wave length would be below 1240 nm which is more than 10 per cent longer than 1072 nm. This would suggest that the final state electron is in excited state. The surplus energy is consistent with the width about 100 nm for the UIBs. This identification - if correct - would support the view that metabolic energy quanta are universal and have preceded the evolution of the biochemical machinery associated with metabolism and that the loading of metabolic energy batteries at the fundamental level correspond to the kicking of charged particles to smaller space-time sheets.

Connection between laser induced healing, acupuncture, and association of DC currents with the healing of wounds

The findings of Robert Becker (the book "Electromagnetism and Life" by Becker and Marino can be found from web [15]) meant a breakthrough in the development of bioelectromagnetics. One aspect of bioelectromagnetic phenomena was the discovery of Becker that DC currents and voltages play a pivotal role in various regeneration processes. Why this is the case is still poorly understood and Becker's book is a treasure trove for anyone ready to challenge existing dogmas. The general vision guiding Becker can be summarized by a citation from the introduction of the book.

Growth effects include the alteration of bone growth by electromagnetic energy, the restoration of partial limb regeneration in mammals by small direct currents, the inhibition of growth of implanted tumors by currents and fields, the effect upon cephalocaudal axis development in the regenerating flatworm in a polarity-dependent fashion by applied direct currents, and the production of morphological alterations in embryonic development by manipulation of the electrochemical species present in the environment. This partial list illustrates the great variety of known bioelectromagnetic phenomena.

The reported biological effects involve basic functions of living material that are under remarkably precise control by mechanisms which have, to date, escaped description in terms of solution biochemistry. This suggests that bioelectromagnetic phenomena are fundamental attributes of living things ones that must have been present in the first living things. The traditional approach to biogenesis postulates that life began in an aqueous environment, with the development of complex molecules and their subsequent sequestration from the environment by membranous structures. The solid-state approach proposes an origin in complex crystalline structures that possess such properties as semiconductivity, photoconductivity, and piezoelectricity. All of the reported effects of electromagnetic forces seem to lend support to the latter hypothesis.

1. Observations relating to CNS

The following more quantitative findings, many of them due to Becker, are of special interest as one tries to understand the role of DC currents in TGD framework.

1. CNS and the rest of perineural tissue (tissue surrounding neurons including also glial cells) form a dipole like structure with neural system in positive potential and perineural tissue in negative potential. There is also an electric field along neuron in the direction of nerve pulse propagation (dendrites correspond to - and axon to +) (note that motor nerves and sensory nerves form a closed loop). Also microtubules within axon carry electric field and these fields are probably closely related by the many-sheeted variants of Gauss's and Faraday's laws implying that voltages along two different space-time sheets in contact at two points are same in a static situation.

2. A longitudinal potential along front to back in brain with frontal lobes in negative potential with respect to occipital lobes and with magnitude of few mV was discovered. The strength of the electric field correlates with the level of consciousness. As the potential becomes weaker and changes sign, consciousness is lost. Libet and Gerard observed traveling waves of potentials across the cortical layers (with speeds of about 6 m/s: TGD inspired model of nerve pulse predicts this kind of waves [57]). Propagating potentials were discovered also in glial cells. The interpretation was in terms of electrical currents.

3. It was found that brain injury generated positive polarization so that the neurons ceased to function in an area much larger than the area of injury. Negative shifts of neuronal potentials were associated with incoming sensory stimuli and motor activity whereas sleep was associated with a positive shift. Very small voltages and currents could modulate the firing of neurons without affecting the resting potential. The "generating" potentials in sensory receptors inducing

nerve pulse were found to be graded and non-propagating and the sign of the generating potential correlated with sensory input (say increase/reduction of pressure). Standard wisdom about cell membrane has difficulties in explaining these findings.

4. The natural hypothesis was that these electric fields are accompanied by DC currents. There are several experimental demonstrations for this. For instance, the deflection of assumed DC currents by external magnetic field (Hall effect) was shown to lead to a loss of consciousness.

2. Observations relating to regeneration

The second class of experiments used artificial electrical currents to enhance regeneration of body parts. These currents are nowadays used in clinical practice to induce healing or retard tumor growth. Note that tissue regeneration is a genuine regeneration of an entire part of organism rather than mere simple cell replication. Salamander limb generation is one of the most studied examples. Spontaneous regeneration becomes rare at higher evolutionary levels and for humans it occurs spontaneously only in the fractures of long bones.

1. An interesting series of experiments on Planaria, a species of simple flatworm with a primitive nervous system and simple head-to-tail axis of organization, was carried out. Electrical measurements indicated a simple head-tail dipole field. The animal had remarkable regenerative powers; it could be cut transversely into a number of segments, all of which would regenerate a new total organism. The original head-tail axis was preserved in each regenerate, with that portion nearest the original head end becoming the head of the new organism. The hypothesis was that the original head-tail electrical vector persisted in the cut segments and provided the morphological information for the regenerate. The prediction was that the reversal of the electrical gradient by exposing the cut surface to an external current source of proper orientation should produce some reversal of the head-tail gradient in the regenerate. While performing the experiment it was found found that as the current levels were increased the first response was to form a head at each end of the regenerating segment. With still further increases in the current the expected reversal of the head-tail gradient did occur, indicating that the electrical gradient which naturally existed in these animals was capable of transmitting morphological information.

2. Tissue regeneration occurs only if some minimum amount of neural tissue is present suggesting that CNS plays a role in the process although the usual neural activity is absent. The repeated needling of the stump had positive effect on regeneration and the DC current was found to be proportional to innervation. Hence needling seems to stimulate innervation or at least inducing formation of DC currents. Something like this might occur also in the case of acupuncture.

3. Regeneration involves de-differentiation of cells to form a blastema from which the regenerated tissue is formed. Quite early it was learned that carcinogens induce de-differentiation of cells because of their steric properties and by making electron transfer possible and that denervation induces tumor formation. From these findings Becker concluded that the formation of blastema could be a relatively simple process analogous to tumor growth whereas the regeneration proper is a complex self-organization process during which the control by signals from CNS are necessary and possibly realized in terms of potential waves.

4. Regeneration is possible in salamander but not in frog. This motivated Becker and collaborators to compare these situations. In an amputated leg of both salamander and frog the original negative potential of or order -1 mV went first positive value of order +10 mV. In frog it returned smoothly to its original value without regeneration. In salamander it returned during three days to the original base line and then went to a much higher negative value around -20 mV (resting potential is around -70 mV) followed by a return to the original value as regeneration had occurred. Thus the large negative potential is necessary for the regeneration and responsible for the formation of blastema. Furthermore, artificial electron current induced regeneration also in the case of frog and in even in the denervated situation. Thus the flow of electrons to the stump is necessary for the formation of blastema and the difference between salamander and frog is that frog is not able to provide the needed electronic current although positive potential is present.

5. It was also learned that a so called neural epidermic junction (NEJ) formed in the healing process of salamander stump was responsible for the regeneration in the presence of nervation. The conclusion was that the DC voltage and electronic current relevant for regeneration can be assigned the interface between CNS and tissue rather than with the entire nerve and regeneration seems to be a local process, perhaps a feed of metabolic energy driving self-organization. Furthermore, NEJ seems to make possible the flow of electrons from CNS to the stump.

6. The red blood cells of animals other than mammals are complete and possess thus nuclei. Becker and collaborators observed that also red blood cells dedifferentiated to form blastema. Being normally in a quiescent state, they are ideal for studying de-differentiation. It was found that electric current acted as a trigger at the level of cell membrane inducing de-differentiation reflected as an increased amount of mRNA serving as signal for gene expression. Also pulsed magnetic field was found to trigger the de-differentiation, perhaps via induced electric field. By the way, the role of the cell membrane fits nicely with the view about DNA-cell membrane system as topological quantum computer with magnetic flux tubes connecting DNA and cell membrane serving as braids.

7. The experiments of Becker and collaborators support the identification of the charge carriers of DC currents responsible for the formation of large negative potential of stump as electrons. The test was based on the different temperature dependence of electronic and protonic conductivities. Electronic conductivity increases with temperature and protonic conductivity decreases and an increase was observed. In TGD based model also super-conducting charge carriers are possible and this finding does not tell anything about them.

3. A TGD based model for the situation

On basis of these observations one can try to develop a unified view about the effects of laser light, acupuncture, and DC currents. It is perhaps appropriate to start with the following - somewhat leading - questions inspired by a strong background prejudice that the healing process - with control signals from CNS included - utilizes the loading of many-sheeted metabolic batteries by supra currents as a basic mechanism. In the case of control signals the energy would go to the "moving of the control knob".

1. Becker assigns to the system involved with DC currents an effective semiconductor property. Could the effective semiconductor property be due the fact that the transfer of charge carriers to a smaller space-time sheet by first accelerating them in electric field is analogous to the transfer of electrons between conduction bands in semiconductor junction? If so, semiconductor property would be a direct signature of the realization of the metabolic energy quanta as zero point kinetic energies.

2. Supra currents flowing along magnetic flux tubes would make possible dissipation free loading of metabolic energy batteries. This even when oscillating Josephson currents are in question since the transformation to ohmic currents in semiconductor junction makes possible energy transfer only during second half of oscillation period. Could this be a completely general mechanism applying in various states of regeneration process. This might be the case. In quantal situation the metabolic energy quanta have very precise values as indeed required. For ohmic currents at room temperature the thermal energies are considerably higher than those corresponding to the voltage involved so that they seem to be excluded. The temperature at magnetic flux tubes should be however lower than the physiological temperature by a factor of order 10^{-2} at least for the voltage of -1 mV. This would suggest high T_c super-conductivity is only effective at the magnetic flux tubes involved. The finding that nerve pulse involves a slight cooling of the axonal membrane proposed in the TGD based model of nerve pulse [57] to be caused by a convective cooling due the return flow of ionic Josephson currents would conform with this picture.

3. What meridians are and what kind of currents flow along them? Could these currents be supra currents making possible dissipation-free energy transfer in the healthy situation? Does the negative potential of order -1 mV make possible flow of protonic supra currents and loading of metabolic batteries by kicking protons to smaller space-time sheets? Could electronic supra currents in opposite direct induce similar loading of metabolic batteries? Could these tow miniature metabolisms realize control signals (protons) and feedback (electrons)?

The model answering these questions relies on following picture. Consider first meridians.

1. The direct feed of metabolic energy as universal metabolic currencies realized as a transfer of charge carriers to smaller space-time sheets is assumed to underly all the phenomena involving healing aspect. Meridian system would make possible a lossless metabolic energy feed - transfer of "Chi" - besides the transfer of chemically stored energy via blood flow. The metabolic energy currencies involved are very small as compared to .5 eV and might be responsible only for "turning control knobs". The correlation of the level of consciousness with the overall strength of DC electric fields would reduce to the level of remote metabolic energy transfer.

2. The model should explain why meridians have not been observed. Dark currents along magnetic flux tubes are ideal for the energy transfer. If the length of the superconducting "wire" is long in the scale defined by the appropriate quantum scale proportional to $\hbar$, classical picture makes sense and charge carriers can be said to accelerate and gain energy ZeV. For large values of $\hbar$ an oscillating Josephson current would be in question. The semiconductor like structure at the end of meridian -possibly realized in terms of pair of space-time sheets with different sizes- makes possible a net transfer of metabolic energy even in this case as pulses at each half period of oscillation. The transfer of energy with minimal dissipation would thus explain why semiconductor like property is needed and why acupuncture points have high value of conductivity. The identification of meridians as invisible magnetic flux tubes carrying dark matter would explain the failure to observe them: one further direct demonstration for the presence of dark matter in biological systems.

3. In the case of regeneration process NEJs would be accompanied by a scaled down version of meridian with magnetic flux tubes mediating the electronic Josephson current during blastema generation and protonic supra current during the regeneration proper. Space-time sheets of proton *resp.* electron correspond to k_p and $k_e = k_p + 11$. In a static situation many-sheeted Gauss law in static situation would guarantee that voltages over NJE are same.

4. One can of course worry about the smallness of electrostatic energies ZeV as compared to the thermal energy. Zero point kinetic energy could correspond also to the magnetic energy of the charged particle. For sufficiently large values of Planck constant magnetic energy scale is higher than the thermal energy and the function of voltage could be only to drive the charged particles along the flux tubes to the target: and perhaps act as a control knob with electrostatic energy compensating for the small lacking energy. Suppose for definiteness magnetic field strength of $B = .2$ Gauss explaining the effects of ELF em fields on brain and appearing in the model of EEG. Assume that charged particle is in minimum energy state with cyclotron quantum number $n = 1$ and spin direction giving negative interaction energy between spin and magnetic field so that the energy is $(g-2)\hbar eB/2m_p$. Assume that the favored values of hbar correspond to number theoretically simple ones expressible as a product of distinct Fermat primes and power of 2. In the case of proton with $g \simeq 2.7927$ the standard metabolic energy quantum $E_0 = .5$ eV would require roughly $\hbar/\hbar_0 = 17 \times 2^{34}$. For electron $g - 2 \simeq \alpha/\pi \simeq .002328$ gives $\hbar/\hbar_0 = 5 \times 17 \times 2^{30}$.

Consider next NEJs and semiconductor like behavior and charging of metabolic batteries.

1. Since NEJ seems resembles cell membrane in some respects, the wisdom gained from the model of cell membrane and DNA as tqc can be used. The model for nerve pulse and the model for DNA as topological quantum computer suggest that dark ionic currents flowing along magnetic flux tubes characterized by a large value of Planck constant are involved with both meridians and NJEs and might even dominate. Magnetic flux tubes act as Josephson junctions generating oscillatory supra currents of ions and electrons. For large values of $\hbar$ also meridians are short in the relevant dark length scale and act as Josephson junctions carrying oscillatory Josephson currents.

2. The findings of Becker suggest that acu points correspond to sensory receptors which are normally in a negative potential. The model for the effects of laser light favors (but only slightly) the assumption that in a healthy situation it is protons arriving along magnetic flux tubes which are kicked to the smaller space-time sheets and that negative charge density at acu point attracts protons to the acu point. Electrons could of course flow in reverse direction along their own

magnetic flux tubes and be kicked to the smaller space-time sheets at the positive end of the circuit. In the case of brain, protonic end would correspond to the frontal lobes and electronic end to the occipital lobes. This kind of structure could appear as fractally scaled variants. For instance, glial cells and neurons could form this kind of pair with neurons in negative potential and glial cells in positive potential as suggested by the fact that neuronal damage generates positive local potential.

3. Classically the charge carriers would gain energy $E = ZeV$ as they travel along the magnetic flux tube to NJE. If this energy is higher than the metabolic energy quantum involved, it allows the transfer of charge carrier to a smaller space-time sheet so that metabolic resources are regenerated. Several metabolic quanta could be involved and the value of $V(t)$ would determine, which quantum is activated. The reduction of the V below critical value would lead to a starvation of the cell or at least to the failure of control signals to "turn the control knob". This should relate to various symptoms like pain at acupuncture points. In a situation requiring acupuncture the voltage along flux tubes would be so small that the transfer of protons to the smaller space-time sheets becomes impossible. As a consequence, the positive charge carriers would accumulate to the acu point and cause a further reduction of the voltage. Acupuncture needle would create a "wound" stimulating large positive potential and the situation would be very much like in regeneration process and de-differentiation induced by acupuncture could be understood.

Many questions remain to be answered.

1. What causes the de-differentiation of the cells? The mere charging of metabolic energy batteries perhaps? If so then the amount of metabolic energy- "chi"- possessed by cell would serve as a measure for the biological age of cell and meridian system feeding "chi" identified as dark metabolic energy would serve as a rejuvenating agent also with respect to gene expression. Or does the electric field define an external energy feed to a self-organizing system and create an electromagnetic environment similar to that prevailing during morphogenesis inducing a transition of cells to a dedifferentiated state? Or could DNA as tqc allow to understand the modification of gene expression as being due to the necessity to use tqc programs appropriate for regeneration? Or should cells and wounded body part be seen as intentional agents doing their best to survive rather than as passive parts of biochemical system?

2. Acupuncture and DC current generation are known to induce generation of endorphins. Do endorphins contribute to welfare by reducing the pain or do they give a conscious expression for the fact that situation has improved as a result of recharging of the metabolic energy batteries?

3. Could the continual charging of metabolic energy batteries by DC currents occur also in the case of cell membrane? The metabolic energy quantum would be around .07 eV in this case and correspond to p-adic length scale $k = 140$ for proton (the quantum is roughly a fraction 1/8 of the fundamental metabolic energy quantum .5 eV corresponding to $k = 137$).

Gene activation by electrostatic fields?

The basic question concerns the method of activation. The discovery of chemists Guido Ebner and Guido Schuerch [28] , [6] raises the hope that these ideas might be more than over-active imagination and their work also provides a concrete proposal for the activation mechanism. These findings are briefly described in the article of Hardmuth Mueller [28] who proposes quite different explanation for the strange findings. Ebner and Schuerch studied the effect of electrostatic fields on the growth and morphogenesis of various organisms. Germ, seeds, or eggs were placed between conducting plates creating an electric field in the range .5-2 kV/m: note that the Earth's electric field is in the range $.1 - 4$ kV/m and of the same order of magnitude.

The outcome was rather surprising and in the year 1989 their employer Ciba Geigy (now Novaris) applied for a patent "Method of enhanced fish breeding" [6] for what is called Ciba Geigy effect. The researchers describe how fishes (trouts) develop and grow much better, if their eggs have been conditioned in an electrostatic field. The researchers report [6] that also the morphology of the fishes was altered to what seems to represent an ancient evolutionary form: this was not mentioned in the patent.

The chemists founded their own Institute of Pharmaceutical Research near Basel, where Guido Ebner applied for another very detailed patent, which was never granted (it is not difficult to guess the reasons why!). In the patent he describes the effect of electrostatic fields on several life forms (cress, wheat, corn, fern, micro-organisms, bacteria) in their early stage of development. A clear change in the morphogenesis was observed. For instance, in one example fern had all sort of leaves in single plant apparently providing a series of snapshots about the evolution of the plant. The evolutionary age of the first leaf appeared to be about 300 million years whereas the last grown-up leaf looked close to its recent form.

If one takes these finding seriously, one must consider the possibility that the exposure to an electrostatic field can activate passive genes and change the gene expression so that older morphologies are expressed. The activation of not yet existing morphologies is probably more difficult since strong consistency conditions must be satisfied (activation of program requires activation of a proper hardware). This would suggest that genome is a kind of archive containing also older genomes even potential genomes or that topological quantum computer programs [26] determine the morphology to certain extent and that external conditions such as electric field determine the self-organization patters characterizing these programs.

It is known that the developing embryo has an electric field along the head-tail axis and that this field plays an important role in the control of growth. These fields are much weaker than the fields used in the experiment. p-Adic length scale hierarchy however predicts an entire hierarchy of electric fields and living matter is indeed known to be full of electret structures. The strength of the electric field in some p-adic length scale related to DNA might somehow serve as the selector of the evolutionary age. The recapitulation of phylogeny during the ontogeny could mean a gradual shift of the activated part of the memone, perhaps assignable to tqc programs, and be controlled by the gradually evolving electric field strength.

The finding that led Ebner to his discovery was that it was possible to "wake up" ancient bacteria by an exposure to an electrostatic field. The interpretation would be in terms of loading of metabolic batteries. This would also suggest that in the case of primitive life forms like bacteria the electric field of Earth has served as metabolic energy source whereas in higher life forms endogenous electric fields have taken the role of Earth's electric field.

Could UV photons have some metabolic role?

The correlation between UV photons and ERE brings in mind the vision that high temperature plasmoids are primitive life-forms possibly having universal metabolic energy quanta in UV range. One can imagine that the development of chemical energy storage mechanisms has made it possible to use visible light from Sun as a source of metabolic energy and get rid of UV quanta having disastrous biological effects. Ozone layer shields out most of UV light and also air absorbs the UV light below wavelength 200 nm, which justifies the term vacuum UV (VUV) for this range.

Δk	1	2	≥ 3	∞
$\Delta E(144, \Delta k)/eV$	4	6	≥ 7	8
λ/nm	310(UVB)	207(UVB)	≤ 177 (VUV)	155 (VUV)

Table 3. The lines corresponding to the dropping of electron from $k = 144$ space time sheet defining a candidate for UV light inducing generation of ERE in the interstellar dust.

From Table 3 one finds that $\Delta k > 2$ electronic transitions cascading to 8 eV (155 nm) by period doubling) belong to vacuum UV (VUV) absorbed by air. The lines 310 nm and 207 nm corresponding to $\Delta k = 1$ and $\Delta k = 2$ could however define frequency windows since these lines need not correspond to any atomic or molecular electronic transitions.

In the solar photosphere the temperature is about 5800 K, roughly half of the minimum temperature 10^4 K needed to generate the UV radiation inducing ERE in interstellar dust. Solar corona however has temperature of about 10^6 K, which corresponds to a thermal energy of order 100 eV and the UV radiation from corona at above mentioned discrete frequencies resulting in dropping of electrons could serve as a metabolic energy source for pre-biotics in the interstellar space. This raises obvious questions. Should the stellar sources inducing ERE possess also corona? Could 4 eV and 6 eV

UV photons from the solar corona serve as a source of metabolic energy for some primitive organisms like blue algae?

A simple model for the metabolism of plasmoids

Extended Red Emissions (EREs) are associated with the interstellar dust in presence of UV light with energies above 7.25 eV and source with temperature not below 10^4 K (maximum of wave length distribution of black body radiation corresponds to the energy 4.97 eV at this temperature). This suggests that plasmoids using UV photons as metabolic energy are involved.

1. Since the bond energies of molecules vary in few eV range and their formation typically liberates photons in UV range, the natural hypothesis is that the metabolic cycle is based on the formation of some molecule liberating UV photon kicking electron/proton to a smaller space-time sheet. UV photons from energy source would in turn induce dissociation of the molecule and thus drive the process. The process as a whole would involve several p-adic length scales and several metabolic currencies.

2. This situation is of course encountered also in the ordinary biology but with highly developed sharing of labor. Biosphere would burn hydrocarbons in animal cells with carbon dioxide as the eventual outcome. Carbon dioxide would in turn be used by plants to regenerate the hydrocarbons. Note that in the recent day technology the loop is open: hydrocarbons are burned but there is no process regenerating them: perhaps photons with large Planck constant might some day used to regenerate the fuel and give rise to "living" and perhaps tidier technology.

3. It is believed that complex organic molecules like amino-acids can form in the interstellar dust and the spontaneous formation of aminoacids is known to be possible in the interstellar ice under UV radiation. Hence at least N_2 and perhaps also CO can be expected to be present. The table below gives dissociation energies of some simple molecules.

Molecule	H_2	O_2	N_2	CO	NO
E_D/eV	4.48	5.08	7.37	11.11	5.2

   (a) N_2 has bond energy 7.37 eV is slightly above the UV threshold 7.26 eV for ERE, which strongly suggests that N_2 is one of the molecules involved with the metabolism of interstellar plasmoids.

   (b) If ice is present then carbon monoxide CO would be an excellent candidate for a metabolic molecule since its bond energy is as high as 11.11 eV. The exceptionally large bond energy would naturally relate to the fact that carbon and oxygen are the key molecules of life.

Anomalous light phenomena as plasmoids

TGD suggests that anomalous light phenomena (ALPs, or light balls, or UFOs depending on one's tastes and assumptions) are identifiable as plasmoids behaving as primitive life forms. In the conference held in Röros Björn Gitle-Hauge told about the determination of the spectrum of visible light emitted by some light balls observed in Hessdalen [1] ("Hessdalen phenomenon" is the term used).

1. The spectrum is a band in the interval 500-600 nm whereas the typical ERE [206] is concentrated in the interval 650-750 nm. The peak is in the interval 540-900 nm, the width of the band is also now 100 nm, and there are no sharp peaks. Therefore the interpretation as ERE can be considered.

2. Because Hessdalen is an old mining district, authors propose that the light ball could consist of burning dust containing some metals. Author proposes that the burning of Titanium and Scandium (encountered only in Scandinavia) might provide the energy for the light ball. Sc reacts vigorously with acids and air (burning in oxygen gives Sc_2O_3 as end product). Ti burns in oxygen and is the only element that burns in nitrogen. Ti is used in fireworks since it produces spectacular fires.

Author notices that the emission lines of N^+, Al^{++}, *resp.* Sc^+ at 528.02 nm, 528.2 nm, *resp.* 528.576 nm might contribute to the band. This might be the case but the explanation of the band solely in terms of molecular transitions is not favored by its smoothness.

3. The bond energies of TiO and TiN are 6.9 eV and 5.23 eV so that the radiation resulting in their formation is in UV range and could provide part of the metabolic energy. I do not know about bond energy of Scandium oxide.

4. TiO_2 is known to catalyze photolysis in the presence of UV light [81, 82], which in turn is basic step in [83] [83] , the basic step of which in TGD Universe would be the kicking of electrons/protons to smaller space-time sheets. Therefore the UV photons liberated in the formation of molecules containing Ti could catalyze photosynthesis like process.

2.5.4 Life as a symbiosis of plasmoids and biological life

If evolution has discovered something it usually keeps it so that plasmoids and UV metabolism should be still there. This suggests that plasmoids are still in ionosphere. What could this mean? There also also other questions and I am grateful for Sampo Vesterinen for some of them. The key questions are perhaps the following ones. Do plasmoids and biological life forms live in symbiosis in some sense? If this is the case, what plasmoids can give to us and what we can give to plasmoids?

1. Magnetic bodies as quantum plasmoids and plasmoids in magnetosphere

One must make clear what one means with plasmoid. One can consider a plasma made of ordinary visible matter and also large $\hbar$ quantum plasma at magnetic bodies in a form of Bose-Einstein condensates of charged particles. The symbiosis of plasmoids and biomatter could correspond to the symbiosis of magnetic body and biological body.

One can imagine also the possibility that visible matter plasmoids and bio-matter are in symbiosis via the mediation of magnetic bodies. Note that DNA strands are negatively charged so that there is a resemblance with a plasma like state. One aspect of symbiosis would be that magnetic body would feed charged particles to DNA.

2. Some basic facts about magnetosphere

Magnetosphere would be a natural environment for plasmoid population. If one restricts plasmoids to to visible matter, then ionosphere, plasma sphere and plasma sheet are the most interesting objects of interest.

1. The temperature in the highest F layer of the ionosphere (extending from 150 km to 1500 km depending on source) is about 1200-1300 K: the photon energy is about .6-.65 eV at the maximum wavelength of thermal distribution. Hence F layer plasmoids might receive metabolic energy in the form of .5 eV metabolic energy quanta via thermal photons. Self-organization occurs in transition layers and especially interesting is the transition region 85-300 km from mesosphere to ionosphere at which temperature increases 300 K to about 1200 K.

2. Inner magnetosphere is a toruslike structure whose extension varies between $4R_E$ (day side) and $8R_E$ (night side) and shielded from solar wind. In the inner magnetosphere the typical density is about 1 ion per cubic centimeter. Inner magnetosphere is bounded by a transition layer of thickness of $\sim R$ (magneto-pause). In this region the density of the ions drops rapidly.

   Inner magnetosphere contains plasma sphere whose radius varies in the range $2R_E - 4R_E$ at day side and $2R_E - 6R_E$ at night side. Plasma has a ionospheric origin. The density of the cold plasma consisting mainly of protons sphere varies in the range $10 - 10^3$ ions/cm^3, whereas the temperature is $\sim 5 \times 10^3$ K, which corresponds to metabolic energy quantum of .5 eV. Note however that the energy of photon at maximum of thermal distribution is about 2.5 eV which suggests 2 eV metabolic quantum.

   The cold, dense plasma of plasma sphere is frozen around magnetic flux lines which co-rotate with Earth. In TGD framework this means that flux tubes co-rotate and thus change shape. In the equitorial plane the density of the plasma sphere drops sharply down to ~ 1 ion/cm^3 at $r = 4R$. This transition region is known as a plasma pause. During magnetic storms the outer radius decreases since the pressure of the solar wind compresses the plasma sphere. The

day-night variation of the shape of the plasma sphere is rather small. Within this region the magnetic field has in a reasonable approximation dipole shape with radiation belts forming an exception.

The surface temperature of Sun is 6×10^3 K. This temperature is roughly half of the minimum temperature 10^4 K needed for EREs from interstellar dust [206] . This corresponds to photon energy of 3 eV at the maximum of thermal distribution and cannot induce dissociation of N_2 and other simple diatomic molecules. There is also solar corona but its temperature is about 10^6 K (10^2 eV) so that the flux of thermal photons at UV energies is very low.

Taking seriously the finding that $T \geq 10^4$K for source is necessary for EREs, one might ask whether the plasmoids at the day side are able to receive enough metabolic energy from UV radiation of Sun. If course, there is is no need to assume that dissociation of N_2 molecules is key element in metabolic mechanism. The temperatures in both F layer and plasma sphere allow kicking of protons and electrons to smaller space-time sheets and this might save the situation. Hence metabolism is not a problem for the plasmoids except perhaps during night-time when the plasma cools down somewhat.

3. The plasma sheet [40] , [37] at the night side of Earth dark is the most prominent feature of the outer magnetosphere. It has a thickness about Earth radius R_E and extends beyond Moon's orbit (with radius $10^3 R_E$). The average densities of charged particles are very low and same order of magnitude as in plasma sphere: about .4-2 per cm^3 for both protons and electrons and correlates with solar wind density.

   The temperature is very high: the thermal energy of electrons is in keV range and ionic temperatures are even higher. The high temperature is due to the leakage of matter from solar wind. Note that up to the distance $d \sim 10^2 R_E$ equator region of outer magnetosphere at the night side of Earth experiences a continual solar eclipse so that this region does not receive radiation energy from Sun: the high temperature of plasma sheet solves this metabolic problem.

   The presence of keV photons would destroy molecules at plasma sheet and induce a high degree of ionization so that plasmoid life must be based on ions and electrons. The energy needed to kick an electron to an atomic space-time sheet is about keV from $m_e/m_p \sim 2^{-11}$: hence the dropping of electrons from atomic space-time sheets would be the natural metabolic mechanism for plasmoid life at plasma sheet.

   One of the original motivations for the plasmoid hypothesis was the strange finding that plasma sheet at the equator at the dark side of Earth is highly self-organized structure and the velocity distributions of electrons present patterns like "flowers", "eyes", "butterflies" [40] .

3. What plasmoids could give to us and what we could give to plasmoids?

An attractive general motivation for the symbiosis would be that magnetic bodies would give us ability to think and we would give them ability to sense.

1. The model of cognitive representations relies on the intersections of magnetic bodies with corresponding p-adic space-time sheets possessing literally infinite size in the real sense. The larger the magnetic body, the better the representations. Magnetic bodies could thus provide us with cognitive representations and an interesting question is whether and how this relates to the strange self-organization patterns at plasma sheet.

2. We could provide for magnetic bodies sensory input and serve as their motor instruments. These magnetic bodies might be also associated with plasma sheet and the plasmoids of ionosphere and plasma sphere and could also use plasmoids of visible matter as sensory receptors and perhaps even primitive motor instruments.

One can imagine also more concrete motivations for the symbiosis.

1. Plasmoids in the day-side ionosphere could shield biosphere from UV light by "eating" the incoming UV light. Magnetic bodies could also feed negative electronic charge from the plasmoids of magnetosphere to DNA double strands.

2. Plasmoids are not in a need of metabolic energy unless it happens that the temperature in F layer cools too much during night time from $T \sim 0.12$ eV. One might imagine that plasmoids suck metabolic energy from the biosphere during sleep (say brains which remain active): this would be a possible explanation for why we sleep. One can even imagine that during sleep magnetospheric collective levels of consciousness take command and life forms in the biosphere entangle to form kind of stereo consciousness providing a collective view what is to be human, member of species, or a part of biosphere.

4. About the interpretation of bio-photons?

Also the wave lengths of bio-photons are in the range of visible photons. Their spectrum is claimed to be featureless, which would suggest that identification in terms of photons resulting in dropping of electrons and protons to larger space-time sheets might not make sense. The variation of the geometric shape of space-time sheets, the possibility of surplus energy, and the clustering of the transition lines around the lower end of wave length spectrum might however give rise to effectively featureless spectrum.

Suppose that bio-photons correspond to superposition of ERE bands and thus reflect the presence of UV energy feed. Unless biological body is not able to generate the needed UV photons, they must arrive from Sun. Bio-photons or their dark counterparts with much longer wavelengths could indeed live at the flux quanta of the magnetic bodies and observed visible bio-photons could represent some kind of leakage.

5. Gariaev's experiments

Gariaev's experiments [149] involved the irradiation of DNA using visible laser light with photon energy 1.9595 eV. The irradiation induced emission of radio waves with same polarization with frequencies above kHz. Radio waves induced growth of potatoes. A possible interpretation is that 2 eV photons kicked electrons to a smaller space-time sheet and thus gave metabolic energy to DNA. The radio waves possibly resulting in the dropping of electrons back to the larger space-time sheets could have consisted of dark photons with same or smaller energy and could have been used as a metabolic energy by the potatoes. That the dropping can occur to several space-time sheets would explain why several radio wave frequencies were observed. The prediction would be sum of period doubling spectra discussed earlier since sequences of droppings are possible. The radio-wave signal would result from the de-coherence of dark radio-wave photons to a bundle of ordinary radio-wave photons.

6. Earth's interior as a living system?

For years ago I developed in detail the working hypothesis that entire magnetosphere is a living system. Even Earth's interior (and also solar surface) could contain plasmoid life [29, 40] . The temperature below the mantle of Earth does not differ too much from the surface temperature of Sun and metabolic energy could come from the radioactive decays from the interior of Earth. There would be UV shielding by Earth: UV light has energies above 3.1 eV whereas the temperature at the mantle-core boundary is 4300 K which corresponds to energy 2.2 eV energy at the maximum of thermal distribution. Metabolic energy quantum of 2 eV would be highly suggestive and might be directly used to kick protons and electrons to smaller space-time sheet.

The metabolism would not probably involve energy quantum of .5 eV. Magnetic flux tubes could also mediate metabolic energy from the biosphere and possibly also ionosphere and the plasmoid life in question could be at an evolutionary level not tolerating UV light and involve molecules in essential manner.

2.6 Exotic color and electro-weak interactions

The finding of a correct interpretation of long ranged electro-weak and color gauge fields predicted by classical TGD has been the basic stumbling block for the development of the understanding of TGD Universe and it took about 27 years before the time was ripe to see that TGD predicts entire fractal hierarchy of scaled down copies of standard model physics so that TGD Universe can be seen as a kind of inversion of Mandelbrot fractal for which each new bird eye of view reveals new structures assignable to higher levels in the hierarchy of consciousness.

2.6.1 Long range classical weak and color gauge fields as correlates for dark massless weak bosons

Long ranged electro-weak gauge fields are unavoidably present when the dimension D of the CP_2 projection of the space-time sheet is larger than 2. Classical color gauge fields are non-vanishing for all non-vacuum extremals. This poses deep interpretational problems. If ordinary quarks and leptons are assumed to carry weak charges feeded to larger space-time sheets within electro-weak length scale, large hadronic, nuclear, and atomic parity breaking effects, large contributions of the classical Z^0 force to Rutherford scattering, and strong isotopic effects, are expected. If weak charges are screened within electro-weak length scale, the question about the interpretation of long ranged classical weak fields remains.

Various interpretations for the long ranged classical electro-weak fields

During years I have discussed several solutions to the problems listed above.

Option I: The trivial solution of the constraints is that Z^0 charges are neutralized at electro-weak length scale. The problem is that this option leaves open the interpretation of classical long ranged electro-weak gauge fields unavoidably present in all length scales when the dimension for the CP_2 projection of the space-time surface satisfies $D > 2$.

Option II: Second option involves several variants but the basic assumption is that nuclei or even quarks feed their Z^0 charges to a space-time sheet with size of order neutrino Compton length. The large parity breaking effects in hadronic, atomic, and nuclear length scales is not the only difficulty. The scattering of electrons, neutrons and protons in the classical long range Z^0 force contributes to the Rutherford cross section and it is very difficult to see how neutrino screening could make these effects small enough. Strong isotopic effects in condensed matter due to the classical Z^0 interaction energy are expected. It is far from clear whether all these constraints can be satisfied by any assumptions about the structure of topological condensate.

Option III: During 2005 (27 years after the birth of TGD!) third option solving the problems emerged based on the progress in the understanding of the basic mathematics behind TGD.

In ordinary phase the Z^0 charges of elementary particles are indeed neutralized in intermediate boson length scale so that the problems related to the parity breaking, the large contributions of classical Z^0 force to Rutherford scattering, and large isotopic effects in condensed matter, trivialize.

Classical electro-weak gauge fields in macroscopic length scales are identified as space-time correlates for the gauge fields created by dark matter, which corresponds to a macroscopically quantum coherent phase for which elementary particles possess complex conformal weights such that the net conformal weight of the system is real.

In this phase $U(2)_{ew}$ symmetry is not broken below the scaled up weak scale except for fermions so that gauge bosons are massless below this length scale whereas fermion masses are essentially the same as for ordinary matter. By charge screening gauge bosons look massive in length scales much longer than the relevant p-adic length scale. The large parity breaking effects in living matter (chiral selection for bio-molecules) support the view that dark matter is what makes living matter living.

Classical color gauge fields

Classical long ranged color gauge fields always present for non-vacuum extremals are interpreted as space-time correlates of gluon fields associated with dark copies of hadron physics. It seems that this picture is indeed what TGD predicts. A very special feature of classical color fields is that the holonomy group is Abelian. This follows directly from the expression $g^A_{\alpha\beta} \propto H^A J_{\alpha\beta}$ of induced gluon fields in terms of Hamiltonians H^A of color isometries and induced Kähler form $J_{\alpha\beta}$. This means that classical color magnetic and electric fluxes reduce to the analogs of ordinary magnetic fluxes appearing in the construction of configuration space geometry [15] .

By a local color rotation the color field can be rotated to a fixed direction so that genuinely Abelian field would be in question apart from the possible presence of gauge singularities making impossible a global selection of color direction. These singularities could be present since Kähler form defines a magnetic monopole field. An interesting question inspired by quantum classical correspondence is what the Abelian holonomy tells about the sources of color gauge fields and color confinement.

For instance, could Abelian holonomy mean that colored gluons (and presumably also other colored particles) do not propagate in the p-adic length scale considered? Color neutral gluons would propagate but since also their sources must be color neutral, they should have vanishing net color electric fluxes. This form of confinement would allow those states of color multiplets which have vanishing color charges and obviously symmetry breaking down to $U(1) \times U(1)$ would be in question. This would serve as a signal for monopole confinement which would not exclude higher multipoles for the Abelian color fields. This kind of fields appear in the the TGD based model for nuclei as nuclear strings bound together by color flux tubes [69] . In the sequel the model for nuclear color force is briefly discussed in order to give an idea about how the dark color forces might act also in longer length scales.

2.6.2 Dark color force as a space-time correlate for the strong nuclear force?

Color confinement suggests a basic application of the basic criteria for the transition to large $\hbar$ phase. The obvious guess is that valence quarks are dark [24, 22] . Dark matter phase for quarks does not change the lowest order classical strong interaction cross sections but reduces dramatically higher order perturbative corrections and resolves the problems created by the large value of QCD coupling strength in the hadronic phase.

The challenge is to understand the strong binding solely in terms of dark QCD with large value of $\hbar$ reducing color coupling strength of valence quarks by factor $1/r \simeq 2^{-k_a}$. The best manner to introduce the basic ideas is as a series of not so frequently asked questions and answers.

Rubber band model of strong nuclear force as starting point

The first question is what is the vision for nuclear strong interaction that one can start from. The sticky toffee model of Chris Illert [4] is based on the paradox created by the fact alpha particles can tunnel from the nucleus but that the reversal of this process in nuclear collisions does not occur. Illert proposes a classical model for the tunnelling of alpha particles from nucleus based on dynamical electromagnetic charge. Illert is forced to assume that virtual pions inside nuclei have considerably larger size than predicted by QCD and the model. Strikingly, the model favors fractional alpha particle charges at the nuclear surface. The TGD based interpretation would be based on the identification of the rubber bands of Illert as long color bonds having exotic light quark and anti-quark at their ends and connecting escaping alpha particle to the mother nucleus. The challenge is to give meaning to the attribute "exotic".

How the darkness of valence quarks can be consistent with the known sizes of nuclei?

The assumption about darkness of valence quarks in the sense of of large $\hbar$ ($\hbar_s = \hbar/v_0$) is very natural if one takes the basic criterion for darkness seriously. The obvious question is how the dark color force can bind the nucleons to nuclei of ordinary size if the strength of color force is v_0 and color sizes of valence quarks are about $L(129)$?

It seems also obvious that $L(107)$ in some sense defines the size for nucleons, and somehow this should be consistent with scaled up size $L(k_{eff} = 129)$ implied by the valence quarks with large $\hbar$. The proposal of [24, 22] inspired by RHIC findings [7] is that valence quarks are dark in the sense of having large value of $\hbar$ and thus correspond to $k_{eff} = 129$ whereas sea quarks correspond to ordinary value for $\hbar$ and give rise to the QCD size $\sim L(107)$ of nucleon.

If one assumes that the typical distances between sea quark space-time sheets of nucleons is obtained by scaling down the size scale of valence quarks, the size scale of nuclei comes out correctly.

Valence quarks and exotic quarks cannot be identical

The hypothesis is that nucleons contain or there are associated with them pairs of exotic quarks and flux tubes of color field bodies of size $\sim L(129)$ connecting the exotic quark and anti-quark in separate nuclei. Nucleons would be structures with the size of ordinary nucleus formed as densely packed structures of size $L(129)$ identifiable as the size of color magnetic body.

The masses of exotic quarks must be however small so that they must differ from valence quarks. The simplest possibility is that exotic quarks are not dark but p-adically scaled down versions of sea quarks with ordinary value of $\hbar$ having $k = 127$ so that masses are scaled down by a factor 2^{-10}.

Energetic considerations favor the option that exotic quarks associate with nucleons via the $k_{eff} = 111$ space-time sheets containing nucleons and dark quarks. Encouragingly, the assumption that nucleons topologically condense at the weak $k_{eff} = 111$ space-time sheet of size $L(111) \simeq 10^{-14}$ m of exotic quarks predicts essentially correctly the mass number of the highest known super-massive nucleus. Neutron halos are outside this radius and can be understood in terms color Coulombic binding by dark gluons. Tetraneutron can be identified as alpha particle containing two negatively charged color bonds.

What determines the binding energy per nucleon?

The binding energies per nucleon for $A \geq 4$ to not vary too much from 7 MeV but the lighter nuclei have anomalously small binding energies. The color bond defined by a color magnetic flux tube of length $\sim L(k = 127)$ or $\sim L(k_{eff} = 129)$ connecting exotic quark and anti-quark in separate nucleons with scaled down masses $m_q(dark) \sim xm_q$, with $x = 2^{-10}$ for option for $k = 127$, is a good candidate in this respect. Color magnetic spin-spin interaction would give the dominant contribution to the interaction energy as in the case of hadrons. This interaction energy is expected to depend on exotic quark pair only. The large zero point kinetic energy of light nuclei topologically condensed at $k_{eff} = 111$ space-time sheet having possible identification as the dark variant of $k = 89$ weak space-time sheet explains why the binding energies of D and ^3He are anomalously small.

What can one assume about the color bonds?

Can one allow only quark anti-quark type color bonds? Can one allow the bonds to be also electromagnetically charged as the earlier model for tetra-neutron suggests (tetra-neutron would be alpha particle containing two negatively charged color bonds so that the problems with the Fermi statistics are circumvented). Can one apply Fermi statistics simultaneously to exotic quarks and anti-quarks and dark valence quarks?

Option I: Assume that exotic and dark valence quarks are identical in the sense of Fermi statistics. This assumption sounds somewhat non-convincing but is favored by p-adic mass calculations supporting the view that the p-adic mass scale of hadronic quarks can vary. If this hypothesis holds true at least effectively, very few color bonds from a given nucleon are allowed by statistics and there are good reasons to argue that nucleons are arranged to highly tangled string like structures filling nuclear volume with two nucleons being connected by color bonds having of length of order $L(129)$. The organization into closed strings is also favored by the conservation of magnetic flux.

The notion of nuclear string is strongly supported by the resulting model explaining the nuclear binding energies per nucleon. It is essential that nucleons form what might be called nuclear strings rather than more general tangles. Attractive p-p and n-n bonds must correspond to colored ρ_0 type bonds with spin one and attractive p-n type bonds to color singlet pion type bonds. The quantitative estimates for the spin-spin interaction energy of the lightest nuclei lead to more precise estimates for the lengths of color bonds. The resulting net color quantum numbers must be compensated by dark gluon condensate, the existence of which is suggested by RHIC experiments [7]. This option is strongly favored by the estimate of nuclear binding energies.

Option II: If Fermi statistics is not assumed to apply in the proposed manner, then color magnetic flux tubes bonds between any pair of nucleons are possible. The identification of color isospin as strong isospin still effective removes color degree of freedom. As many as 8 color tubes can leave the nucleus if exotic quarks and anti-quarks are in the same orbital state and a cubic lattice like structure would become possible. This picture would be consistent with the idea that in ordinary field theory all particle pairs contribute to the interaction energy. The large scale of the magnetic flux tubes would suggest that the contributions cannot depend much on particle pair. The behavior of the binding energies favors strongly the idea of nuclear string and reduces this option to the first one.

What is the origin of strong force and strong isospin?

Here the answer is motivated by the geometry of CP_2 allowing to identify the holonomy group of electro-weak spinor connection as U(2) subgroup of color group. Strong isospin group SU(2) is iden-

tified as subgroup of isotropy group U(2) for space-time surfaces in a sub-theory defined by $M^4 \times S^2$, S^2 a homologically non-trivial geodesic sphere of CP_2 and second factor of $U(1) \times U(1)$ subgroup of the holonomies for the induced Abelian gauge fields corresponds to strong isospin component I_3. The extremely tight correlations between various classical fields lead to the hypothesis that the strong isospin identifiable as color isospin I_3 of exotic quarks at the ends of color bonds attached to a given nucleon is identical with the weak isospin of the nucleon. Note that this does not require that exotic and valence quarks are identical particles in the sense of Fermi statistics.

Does the model explain the strong spin orbit coupling ($L \cdot S$ force)? This force can be identified as an effect due to the motion of fermion string containing the effectively color charged nucleons in the color magnetic field $v \times E$ induced by the motion of string in the color electric field at the dark $k = 107$ space-time sheet.

How the phenomenological shell model with harmonic oscillator potential emerges?

Nucleus can be seen as a collection of of long color magnetic flux tubes glued to nucleons with the mediation of exotic quarks and anti-quarks. If nuclei form closed string, as one expects in the case of Fermi statistics constraint, also this string defines a closed string or possibly a collection of linked and knotted closed strings. If Fermi statistics constraint is not applied, the nuclear strings form a more complex knotted and linked tangle. The stringy space-time sheets would be the color magnetic flux tubes connecting exotic quarks belonging to different nucleons.

The color bonds between the nucleons are indeed strings connecting them and the averaged interaction between neighboring nucleons in the nuclear string gives in the lowest order approximation 3-D harmonic oscillator potential although strings have $D = 2$ transversal degrees of freedom. Even in the case that nucleons for nuclear strings and thus have only two bonds to neighbors the average force around equilibrium position is expected to be a harmonic force in a good approximation. The nuclear wave functions fix the restrictions of stringy wave functionals to the positions of nucleons at the nuclear strings. Using M-theory language, nucleons would represent branes connected by color magnetic flux tubes representing strings whose ends co-move with branes.

Which nuclei are the most stable ones and what is the origin of magic numbers?

$P = N$ closed strings correspond to energy minima and their deformations obtained by adding or subtracting nucleons in general correspond to smaller binding energy per nucleon. Thus the observed strong correlation between P and N finds a natural explanation unlike in the harmonic oscillator model. For large values of A the generation of dark gluon condensate and corresponding color Coulombic binding energy favors the surplus of neutrons and the generation of neutron halos. The model explains also the spectrum of light nuclei, in particular the absence of pp, nn, ppp, and nnn nuclei.

In the standard framework spin-orbit coupling explains the magic nuclei and color Coulombic force gives rise to this kind of force in the same manner as in atomic physics context. Besides the standard magic numbers there are also non-standard ones (such as $Z, N = 6, 12$) if the maximum of binding energy is taken as a definition of magic, there are also other magic numbers than the standard ones. Hence can consider also alternative explanations for magic numbers. The geometric view about nucleus suggests that the five Platonic regular solids might defined favor nuclear configurations and it indeed turns that they explain non-standard magic numbers for light nuclei.

New magic nuclei might be obtained by linking strings representing doubly magic nuclei. An entire hierarchy of linkings becomes possible and could explain the new magic numbers 14, 16, 30, 32 discovered for neutrons [2] . Linking of the nuclear strings could be rather stable by Pauli Exclusion Principle. For instance, ^{16}O would corresponds to linked ^4He and ^{12}C nuclei. Higher magic numbers $28, 50, ...$ allow partitions to sums of lower magic numbers which encourages to consider the geometric interpretation as linked nuclei. p-Adic length scale hypothesis in turn suggest the existence of magic numbers coming as powers of 2^3.

2.6.3 How brain could deduce the position and velocity of an object of perceptive field?

The basic degrees of freedom for mind like space-time sheets can be regarded as parameters specifying color quantization axes and spin quantization axis. The parameters characterizing the choices of

the color quantization axes define 3+3-dimensional symplectic flag-manifold $F_3 = SU(3)/U(1) \times U(1)$ whereas the parameters fixing spin-quantization axes define two-dimensional flag-manifold $F_2 = SU(1)/U(1) = S^2$, which is identical to two-sphere and whose point characterizes some orientation vector. A mathematically attractive identification of the flag manifold F_3 is as a representation for the possible positions and velocities of an object of the perceptive field whereas F_2 could represent some orientation, say ear-to-ear orientation axis. This identification, if correct, provides additional support for the uniqueness of the choice of the imbedding space $H = M^4_+ \times CP_2$. Amazingly, the model of honeybee dance by Barbara Shipman leads to the identification of the flag manifold F_3 as a fundamental mathematical structure associated with the cognition of the honeybee.

Without a good physical justification this kind of identification is however ad hoc. Fortunately, the following argument makes it possible to understand why F_3 should code the position and the velocity of the objects of the perceptive field.

1. The time development by quantum self-organization is expected to lead to well defined asymptotic values of (P, Q) coordinates during each wake-up period of the mind like space-time sheet representing object of the perceptive field and in self-state.

2. The crucial observation is that classical em and Z^0 fields are accompanied by classical color fields in TGD. Color rotations rotate the color field in color space whereas induced Kähler form remains unchanged. Most importantly: classical em and Z^0 fields do not remain invariant under color rotations as they would remain in standard model. This leads to the idea that different (P, Q) values obtained by color rotations of cognitive and neuronal space-time sheets correspond to slightly different membrane potentials and that it is the dependence of the membrane potential on the position and velocity of the object of the perceptive field, which leads to (P, Q) coding.

3. An observation not directly related to (P, Q) coding is that classical em and color fields induce tiny color polarization at quark level leading to color polarization of nuclei: this color polarization could provide the quantum correlate for the color quale. The representation of color in this manner however requires that (P, Q) are same for all neurons in the perceptive field so that the coding of positions and velocities and color are mutually exclusive. Positions and velocities and color are indeed represented by different regions of cortex.

4. Color rotation induces motion in F_3 rotating color quantization axes and leaving the induced Kähler field invariant so that absolute minima of Kähler action are mapped to absolute minima and zero modes are not changed. Classical Z^0 and em fields are however *not* invariant under color rotations. How classical em and Z^0 depend on Kähler form becomes clear from the the following formulas:

$$\begin{aligned} \gamma &= 3J - \frac{1}{2} sin^2\theta_W Z^0 \ , \\ Z^0 &= 2J + 4e^0 \wedge e^3 \ , \\ J &= 2(e^0 \wedge e^3 + e^1 \wedge e^2) \ . \end{aligned} \tag{2.6.1}$$

Here J denotes Kähler form invariant under color rotations and e^k denote vierbein vectors of CP_2. $e^0 \wedge e^3$ denotes the part of Z^0, which is not invariant under color rotations. From these formulas it is evident that classical photon field is not in general invariant since it is a superposition of the induced Kähler field and classical Z^0 field and reduces to induced Kähler field only when the Weinberg angle vanishes: the physical value of the Weinberg angle is about $sin^2(\theta_W) = 1/4$. This means that various points (P, Q) of (3+3)-dimensional F_3 indeed correspond to different classical Z^0 fields and classical em fields.

5. There is however an important exception to this picture. If CP_2 projection belongs to geodesic sphere S^2, the field equations reduces to those for $X^4 \subset M^4 \times S^2$. For space-time sheets for which CP_2 projection is $r = \infty$ homologically non-trivial geodesic sphere of CP_2 one has

$$\gamma = (\frac{3}{4} - \frac{sin^2(\theta_W)}{2})Z^0 \simeq \frac{5Z^0}{8}$$

as the explicit study of $r = \infty$ geodesic sphere shows (see the appendix of the book). The induced W fields vanish in this case and they vanish also for all geodesic spheres obtained by $SU(3)$ rotation. There are excellent reasons to believe that also the relationship between Z^0 and γ is $SU(3)$ invariant so that there would be no mixing between em and Z^0 fields. For homologically trivial geodesic spheres γ and Z^0 vanish and only W fields are non-vanishing. This kind of MEs would naturally correspond to W MEs.

For $D >$ 2-dimensional CP_2 projection the situation changes. MEs have always 2-D CP_2 projection field equations and field equations are satisfied without assuming that CP_2 projection is a geodesic sphere and in this case one can hope of getting mixing of γ and Z^0 also in this case perhaps characterizable in terms of the value of the Weinberg angle. Also W fields can be present in this case.

6. Assuming that the values of (P, Q) coordinates are the same for the neuronal group representing an object of the perceptive field and the mind like space-time sheet associated with it (this could be forced by the wormhole contacts), (P, Q) coding for the positions and velocities for the objects of the perceptive field follows if these observables are coded into the properties of the classical Z^0 field associated with the neuronal membrane. This seems plausible since a change of the classical Z^0 field implies a change of the classical em field if the induced Kähler field remains invariant (as is natural). Thus the problem of understanding (P, Q) coding for position and velocity reduces to the problem of understanding why the position and velocity should affect some natural em field associated with cell membrane. Obviously membrane resting potential is an excellent candidate for this em field.

7. The dependence of the value of the membrane resting potential for the representation of an object of the perceptive field on the the position and velocity of the object is natural. For instance, it is advantageous for the neurons representing object near to the observer to be nearer to the criticality for firing. Thus the membrane potential must be reduced by a suitable color rotation and effective code position of the object to Q coordinates. Also, when the object moves towards/away from the observer, the resting potential should be reduced/increased and this means that velocity is coded to P value (note that there is infinite number of symplectic coordinates at use). From these correlations it is quite plausible that (P, Q) coding could be a result of natural selection. Of course, the coding of position and velocity to (P, Q) values need not be one-to-one. For instance, simple organisms are sensitive for velocity only and some organisms experience world as 2-dimensional.

2.7 Exotic representations of super-symplectic algebra

The unique feature of the Super Virasoro algebra is that it allows a fractal hierarchy of sub-algebras and one obtains hierarchy of exotic representations in p-adic sector. One must however assume that Super Virasoro gauge conditions allow arbitrary values of the super-symplectic scaling quantum number L_0 is non-vanishing. $L_0 = 0$ condition would be replaced by $L_0 \ mod \ p^n = 0$ condition in the p-adic context so that conformal invariance would become approximate in p-adic sense. The alternative interpretation would be as fractality in the sense that scalings would leave the states almost invariant.

One could however argue that exotic Super Virasoro representations can make sense only in the purely p-adic sense and the assumption that mass values values $M^2 \propto p^n$, which are gigantic in real sense, can be mapped by the canonical identification to $M^2 \propto p^{-n}$ is highly counter intuitive and has no physical basis. Also in p-adic mass calculations the canonical identification is applied only to fix the real probabilities as canonical images of the p-adic probabilities. Essentially the same predictions would result by using a real statistical ensemble defined by the real counterparts of the p-adic probabilities since the three lowest powers of p determine the outcome in an excellent approximation (that is only the states with $M^2 \propto n$, $n \in \{0, 1, 2\}$ are included).

The idea that the states $L_0 \ mod \ p^n = 0$ are light in some well-defined physical sense is however too beautiful to be given up immediately, and an analogy with condensed matter lattice systems comes in rescue. For a one-dimensional lattice with lattice constant a only a discrete sub-group of translations acts as symmetries and momentum cutoff emerges via the condition $p \equiv p + n\hbar/a$. Although the large momenta $p = n\hbar/a$ are still real, they correspond to the motion of the entire lattice.

By replacing the lattice obtained by translations with a lattice obtained by scalings one would obtain a highly analogous situation. More concretely, suppose that L_0 act as infinitesimal scaling of the imbedding space coordinates of the space-time surface. The action is almost trivial if the space-time surface has a fractal structure in the sense of being approximately invariant under the scaling of the points of M^4 by powers of p. Let a be a positive integer replacing e as the base of exponential so that a^{mL_0} defines an exponentiated scaling. The condition $a^{mL_0}\ mod\ p = 1$ states that the state remains invariant under this scaling and corresponds to the invariance of lattice state under translation by a multiple ma of the lattice vector. By Fermat's little theorem this condition is satisfied if one has $L_0\ mod\ p^n = 0$.

One can consider also the 2-based exponential of L_0 giving $2^{mL_0}\ mod\ p = 0$. p-Adic length scale hypothesis in its most general form stating $p \simeq 2^m$, m a positive integer, provides an approximate solution to this condition. Note that the fractal lattice picture suggests that p-adic cognitive codons corresponds to octaves of the p-adic frequency $f(n,k) = \hbar/T(n,k)$. In the case of memetic code this would mean that the frequency range $10 - 10^3$ Hz dictated by the time scale 1 ms of nerve pulse activity would contain 6 octaves meaning an effective reduction to genetic code with 6 bits. The prediction would be that the frequencies 10,20,40,80,160,320,640 Hz are in a special role in neural dynamics.

The idea p-adic local dynamics codes for the p-adic fractality of the long length scale real dynamics indeed leads to this kind of picture and leads to a concrete quantum model for intentional action allowing even to show that the S-matrix for intention-to-action transitions has the same general form as the ordinary S-matrix [72, 48] .

2.7.1 Exotic p-adic representations as representations for which states are almost p-adic fractals

When the value of L_0 is power of p: $L_0 \propto p^n$, $n = 1, 2, ..$, the real counterpart of the scaling quantum number is extremely small since it is proportional to $1/p^n$ in this case. In particular, the scalings a^{L_0} are p-adically very near to identity transformation for any integer by Fermat's theorem. Fractals are invariant under scalings and since the states of exotic representations are in good approximation invariant under the group of scalings one could say that they are fractals modulo $O(1/p)$, perhaps resulting as asymptotic states of self-organization processes. One can also say that Virasoro conditions are satisfied to order $O(1/p)$ and that approximate conformal invariance is realized ($L_0 = 0$ condition would completely trivialize the super-symplectic representations since mass squared operator is not involved now). Note that the subalgebra of super-symplectic algebra with conformal weights proportional to p^m emerges naturally as an algebra replacing the entire super-conformal algebra.

One could sharpen the notion of approximate super-conformal representation. The failure of L_0 to annihilate the states means that L_{mp^n} can generate zero norm state only in order $O(p^n)$. Thus only the generators L_{-mp^n}, $m \geq 0$, but not L_{mp^n} can annihilate the physical states. Same would hold true also for the super generators and super-symplectic generators. Also multi-p-adic exotic representations are possible since any integer $n = \prod_i p_i^{k_i}$ defines a sub-algebra spanned by the generators for which conformal weights are proportional to n.

The representations of the conformal algebra with a non-vanishing central charge could be in question. The central charge term in the commutators of the conformal generators, being proportional to $(c/12)(n^3 - n)$ (c is central charge) is of order $O(p^k)$ unless p divides 12 (,that is $p = 2$ or $p = 3$ holds true,) or p divides the denominator of c, which is in general rational number. The central extension term for the anti-commutator of the fermionic super-generators G_n and G_{-n} is $\frac{c}{12}(2n-1)(2n+1)$ and is *not* of order $O(p^k)$ for n multiple of p^k.

Semiclassical argument suggests that the lengths of MEs associated with these representations correspond to p-adic length scales and it turns out that corresponding fundamental frequencies correspond to important EEG frequencies in ELF frequency range. This encourages to think that the exotic representations of super-symplectic algebra might of special interest from the point of view of cognition.

Also quaternion conformal representations allow similar phenomenon and in this case p-adic mass squared proportional to L_0 has extremely small real counterpart. The mass squared associated with the corresponding real states is however astrophysical and, in contrast to the original working hypothesis, it will be assumed that these states are not important for consciousness. There are however indications

supporting the importance of these states in hadron physics: one could perhaps understand non-perturbative aspects of QCD in terms of exotic p-adic quaternion-conformal representations.

2.7.2 Mersenne primes and Gaussian Mersennes are special

Mersenne primes

One can also consider the milder requirement that the exponent $\lambda = 2^{\epsilon L_0}$ represents trivial scaling represented by unit in good approximation for some p-adic topology. Not surprisingly, this is the case for $L_0 = mp^k$ since by Fermat's theorem $a^p \ mod \ p = 1$ for any integer a, in particular $a = 2$. This is also the case for $L_0 = mk$ such that $2^k \ mod \ p = 1$ for p prime. This occurs if $2^k - 1$ is Mersenne prime: in this case one has $2^{L_0} = 1$ modulo p so that the sizes of the fractal sub-algebras are exponentially larger than the sizes of $L_0 \propto p^n$ algebras. Note that all scalings a^{L_0} are near to unity for $L_0 = p^n$ whereas now only $a = 2$ gives scalings near unity for Mersenne primes. Perhaps this extended fractality provides the fundamental explanation for the special importance of Mersenne primes.

In this case integrated scalings 2^{L_0} leave the states almost invariant so that even a stronger form of the breaking of the exact conformal invariance would be in question in the super-symplectic case. The representation would be defined by the generators for which conformal weights are odd multiples of n ($M_n = 2^n - 1$) and L_{-kn}, $k > 0$ would generate zero norm states only in order $O(1/M_n)$.

Especially interesting is the hierarchy of primes defined by the so called Combinatorial Hierarchy resulting from TGD based model for abstraction process. The primes are given by $2, 3, 7 = 2^3 - 1, 127 = 2^7 - 1, 2^{127} - 1$,..: $L_0 = n \times 127$ would correspond to M_{127}-adicity crucial for the memetic code.

Gaussian Mersennes are also special

If one allows also Gaussian primes then the notion of Mersenne prime generalizes: Gaussian Mersennes are of form $(1 \pm i)^n - 1$. In this case one could replace the scaling operations by scaling combined with a twist of $\pi/4$ around some symmetry axis: $1 + i = \sqrt{2}exp(i\pi/4)$ and generalized p-adic fractality would mean that for certain values of n the exponentiated operation consisting of n basic operations would be very near to unity.

1. The integers k associated with the lowest Gaussian Mersennes are following: $2, 3, 5, 7, 11, 19, 29, 47, 73, 79, 113$. $k = 113$ corresponds to the p-adic length scale associated with the atomic nucleus and muon. Thus all known charged leptons, rather than only e and τ, as well as nuclear physics length scale, correspond to Mersenne primes in the generalized sense.

2. The primes $k = 151, 157, 163, 167$ define perhaps the most fundamental biological length scales: $k = 151$ corresponds to the thickness of the cell membrane of about ten nanometers and $k = 167$ to cell size about 2.56 μm. This observation also suggests that cellular organisms have evolved to their present form through four basic evolutionary stages. This also encourages to think that $\sqrt{2}exp(i\pi/4)$ operation giving rise to logarithmic spirals abundant in living matter is fundamental dynamical symmetry in bio-matter.

   Logarithmic spiral provides the simplest model for biological growth as a repetition of the basic operation $\sqrt{2}exp(i\pi/4)$. The naive interpretation would be that growth processes consist of $k = 151, 157, 163, 167$ steps involving scaling by $\sqrt{2}$. This however requires the strange looking assumption that growth starts from a structure of size of order CP_2 length. Perhaps this exotic growth process is associated with pair of MEs or magnetic flux tubes of opposite time orientation and energy emergenging CP_2 sized region in a mini big bang type process and that the resulting structure serves as a template for the biological growth.

3. $k = 239, 241, 283, 353, 367, 379, 457$ associated with the next Gaussian Mersennes define astronomical length scales. $k = 239$ and $k = 241$ correspond to the p-adic time scales .55 ms and 1.1 ms: basic time scales associated with nerve pulse transmission are in question. $k = 283$ corresponds to the time scale of 38.6 min. An interesting question is whether this period could define a fundamental biological rhythm. The length scale $L(353)$ corresponds to about 2.6×10^6 light years, roughly the size scale of galaxies. The length scale $L(367) \simeq \times 3.3 \times 10^8$ light years is of same order of magnitude as the size scale of the large voids containing galaxies on

their boundaries (note the analogy with cells). $T(379) \simeq 2.1 \times 10^{10}$ years corresponds to the lower bound for the order of the age of the Universe. $T(457) \sim 10^{22}$ years defines a completely superastronomical time and length scale.

Connection with the em realization of genetic code and Gaussian Mersennes?

The considerations above suggest that $\sqrt{2} \times exp(i\pi/4)$ might code for a fundamental logarithmic spiral growth step in some sense. The powers of the phase factor $exp(i\pi/4)$ define 8-element cyclic group which should be thus fundamental for 2-adic logarithmic spiral growth process in which the diagonal of square becomes the side of the next square rotated by $\pi/4$ with respect to original one.

Perhaps it is worth of noticing that for 3-bit Boolean algebra with one statement excluded the maximal Boolean algebra corresponds to 2 bits of information, and is naturally associated with the predecessor of the genetic code in the hierarchy of codes predicted by the TGD based model for abstraction process. In this case the counterpart of 64 DNA triplets code for 4 statements and the 4 DNA nucleotides themselves might correspond to these "basic truths".

Second point perhaps worth of noticing is that the model of electromagnetic realization of the genetic code discussed in [48] , which was inspired by the observations Cyril Smith [204] about the coding of arithmetic operations to the sequences of 7 binary electromagnetic pulses, led to a guess for a 7-bit binary code for binary arithmetic operations of type $f = f(f_1, f_2) = Xf_1OYf_2$ giving output frequency as a function of two input frequencies f_1 and f_2. O codes for the arithmetic operation proper represented by single bit and the eight operations X and Y acting on the operands are represented by 3 bits each. Depending on context, $O = 0/1$ represents either $+/-$ or $\times//$.

There are eight different operations X (Y), which suggests an interpretation in terms of 8-element cyclic group. Perhaps the coding of the growth process might be achieved by this kind of coding. Each DNA triplet would code this kind of elementary growth process whereas conjugate triplet would code its time reversal. MEs would read genes to sequences of pulses of light-like vacuum current generating hologram realized in terms of coherent photons in turn coding the growth program and conjugate DNA would give rise to time reversed phase conjugate hologram coding for the time reversal of the growth step.

What remains to be understood is the meaning of the arithmetic operation in the growth process. The coding of growth process might reduce to coding of the growth of MEs and super-conducting magnetic flux tubes. If the eight rotations are accompanied by scalings, then multiplication and division of two growth steps would make sense since also the inverse of growth step makes sense. What remains however mysterious why DNA triplets would code the growth steps in this manner. An alternative interpretation is that a growth process of binary structures in question and that arithmetic operation $\pm$ tells something about the second member of the binary structure. For instance, pairs of mind like space-time sheets might be in question (pairs of spiralling MEs with light-like boundaries or wormhole magnetic fields) and $\pm$ might tell whether the other space-time sheet has positive or negative time orientation.

2.7.3 The huge degeneracies of the exotic states make them ideal for representational purposes

For a given eigenvalue of L_0 there is degeneracy of states given essentially by the exponent of L_0. The states with $L_0 = O(p^n)$ have enormous degeneracy since the degeneracy of states increases exponentially as function of mass (this in fact leads to Hagedorn temperature). Huge ground state degeneracy is just what also spin glass analogy suggests and effective information storage and processing requires. The huge (really!) information processing potential suggests that these states correspond to an infinite hierarchy of life forms. Thus matter or 'flesh' would correspond to states of super-symplectic algebra with $L_0 = 0$ whereas the 'spirit' would correspond to states with L_0 eigenvalue divisible by p^n, $n = 1, 2, .., p$ prime and to states with $L_0 \propto n$, $2^n - 1$ Mersenne prime. The identification of mind like space-time sheets as MEs which allow these sub-Super Virasoro representations, means that this hypothesis is consistent with TGD inspired theory of consciousness.

Thus one can conclude that life forms would be characterized by integer triplets

$$(p, m, n), \quad p \ \text{prime} \ .$$

This is a rather far-reaching prediction effectively promising a resolution to the riddle of life as a quantum physical phenomenon and gives a hint about the predictive and explanatory powers of geometrization of physics using p-adic numbers.

The Super Virasoro representations in question are associated with the algebra of super-symplectic transformations. There are two kinds of bosonic generators. The generators of first kind correspond to infinitesimal symplectic transformations of $E^2 \times CP_2$ localized with respect to the light-like coordinate S_+ of the light-like projection of the light-like boundary of ME. The coordinate lines of $S_\pm$ correspond in geometric optics picture curved light rays. E^2 denotes $S_+ = constant$ (or $S_- = constant$) 2-surface and can be obviously chosen in several manners. If ME is glued along a space-like section to some matter like 4-surface then this section most naturally corresponds to $S_+ = constant$ section. A tempting assumption is that sensory experience could be determined by the properties of the quantum state in this section. The generators of second type correspond to the radial Virasoro algebra (functions of S_+ coordinate) localized with respect to CP_2 coordinates so that they act as CP_2-local radial deformations of the light-like boundary. Fermionic generators are in one-one correspondence with the bosonic generators and correspond to configuration space gamma matrices. In the case of future light cone boundary similar algebra generates the isometries of the configuration space of 3-surfaces [15] .

As noticed super-symplectic and super-conformal degrees of freedom do not contribute to mass squared unlike quaternion conformal degrees of freedom. This means an immense degeneracy of states with respect to energy broken only by the non-commutativity of Poincare algebra and super-symplectic and super-conformal algebras. It is not at all obvious whether one can assing this degeneracy to elementary particles or only with the light-like boundaries of MEs.

Any function of $E^2 \times CP_2$ coordinates and of the radial coordinate S_+ of the light-like boundary (that is function of the coordinates of light-cone boundary δM^4_+) defines Hamiltonian and thus configuration space isometry. It is convenient to assume that Hamiltonians correspond to CP_2 partial waves with well defined color quantum numbers. In the case of S^2 one could assume angular momentum eigenstates but this choice is not practical. Generalized Super Virasoro algebra acts as CP_2-local conformal symmetries of light-cone boundary which by its metric 2-dimensionality indeed allows infinite-group of conformal symmetries. The functions of $E^2 \times CP_2$ coordinate having no dependence on the light-like coordinate E_+ of the light-cone boundary define the Hamiltonians of symplectic transformations of $E^2 \times CP_2$. The subset of Hamiltonians with vanishing color and angular momentum quantum numbers ((I_3, Y) and J_z) correspond to the zero modes in the proposed complexification of the configuration space tangent space [15] . The group of these symplectic transformations divided by the Cartan group of $U(1) \times SU(3)$ defines infinite-dimensional flag-manifold parametrizing all possible choices of quantization axes.

Super generators are expressible in terms of fermionic oscillator operators carrying quantum numbers of quarks and leptons. The Super Virasoro representations differ from the standard representations used in superstring models in that super generators are not Hermitian $G^\dagger_r \neq G_{-r}$) and carry fermion number [17] . In quaternion confromal case Super generators carry lepton number in the case of Ramond type representations and quark number in the case of Neveu-Schwartz type representations. super-symplectic representations are Ramond type representations. Both quaternion conformal and super-symplectic representations carry all possible quark/lepton numbers and thus spans what is very much like the Fock states of second quantized theory with configuration space degrees of freedom included as additional degrees of freedom and reflecting the fact that point like particles are replaces with 3-D surfaces.

2.7.4 Could one assign life-forms to the exotic Super-Virasoro representations?

First order life forms associated with elementary particles

Exotic representations are possible also in quaternion-conformal sector. In this case mass squared operator is of order $M^2 = O(p)$ p-adically so that the real counterpart of the p-adic mass would be of the order of elementary particle mass. Also now degeneracies of the states are gigantic. Unless p-adic and real string tensions are different, the mass of the corresponding real state is by a factor of order p higher ($\sim 10^{-4} \times \sqrt{p}$ Planck masses!). This can be seen as a strong objection either against the existence of light real counterparts of the exotic p-adic states or against the applicability of the canonical identification map outside the realm of p-adic thermodynamics.

It is not clear whether super-symplectic degeneracy is present for the quaternion conformal representations. In fact, it might be that quaternion conformal representations are associated with CP_2 type extremals representing elementary particles and cannot be assigned to the light-like boundaries of MEs. This would mean that the boundaries of MEs represent completely new form of light-like matter. Massless states with super-symplectic conformal weight $L_0 = O(p)$ are possible and momentum scale for these states is naturally determined by p. They define a more promising fractal hierarchy of life forms.

The lowest quaternion-conformal life form in the hierarchy are states having mass squared $M^2 \propto L_0 = O(p)$ could be called first order life[1]. These states have masses which are same order of magnitude as the masses of elementary particles with same value of p but have nothing to do with the elementary particles themselves. The extremely weak direct interaction between these these representations and ordinary elementary particles might mean that these life forms do not affect elementary particle physics directly. On the other hand, there is intriguing numerical evidence that non-perturbative aspects of hadron physics might be understood if transition from high energy hadron physics to low energy hadron physics corresponds to a phase transition replacing ordinary Super Virasoro representations with exotic Super Virasoro representations (Regge slope and pion mass are predicted with few percent accuracy: see the chapter [45] . This result is intriguing and forces to keep mind open for new interpretations of the p-adicity. Life requires also the presence of macroscopic quantum phases and one cannot therefore exclude the possibility of hadronic life when macroscopic quantum phases like Bose-Einstein condensates of pions or of super conducting neutron pairs are possible. Neutron super-conductivity is indeed believed to be possible in neutron stars.

To generate first order life forms in elementary particle length scales one would need MEs with wavelengths of order elementary particle Compton length. Presumably also temperature should be in interval around the energy defined by the secondary p-adic length scale. The Darwinian selection implied by self-organization should select some preferred p-adic primes as winners in the struggle for survival. Elementary particles are survivers at the lowest level and the first guess is that the primes corresponding to elementary particles provide good candidates for survivers at higher levels. The p-adic length scale $L(169) \simeq 5.1$ microns associated with neutrinos is especially interesting as far as first order life is considered and could (actually should, as the model of memetic code suggests) be an essential aspect of life in cell length scale.

Also the other primary p-adic lengths scales seem to be important for the structure of bio-matter, which suggests that first order life in these length scales is important for the understanding of living matter.

Higher order life forms in biologically interesting length scales

$L_0 = O(p^n)$ $n \geq 1$, representations of p-adic super-symplectic algebra defining 'n:th order life' are especially interesting as far as living matter is considered. The reason is that the energy scale for these excitations is so small that the 'matter-mind interaction' with low frequency classical fields associated with MEs becomes possible. There seems to be no obvious difference between life forms with different values of n having p-adic length scales $L(n,k)$ of same order of magnitude as far as degeneracy of states is considered. However, if the negentropy gain in single quantum jump is limited by $log(p)$ or $plog(p)$ as the simplest scenario suggests [44]), then first order life forms have potential for more information rich conscious experiences than higher order life forms with roughly the same p-adic length scale. Also the estimate for the maximal number of primary qualia allows more primary qualia for first order life forms.

What makes the hypothesis so interesting is that the number of interesting-to-us p-adic length scales associated with the exotic representations is rather small. Especially interesting are the secondary p-adic length- and time scales defined by Mersenne primes. Mersenne primes M_{89}, M_{107} and M_{127} define fundamental p-adic length scale in elementary particle physics and correspond to intermediate gauge bosons, hadrons and electron. M_{61} could correspond also to new ultra high energy physics. The natural guess is that secondary p-adic length scales, and those associated with Mersenne primes in particular, are especially important for consciousness and life.

1. Higher order life in nanoscales

[1]Note that also Super Virasoro representations associated with ordinary particles allow light excitations with $L_0 - n_0 = O(p)$.

The secondary p-adic length associated with M_{61} is $L(127)/2^{3/2}$ and is slightly below electron length scale. Besides primary p-adic length scales $L(k)$, $k = 127, 131, 137, 139$ listed in table below, also the secondary p-adic length scales $L_2(k) = L(2k)$, $k = 67, 71, 73$ and even the tertiary length scales $L_3(43) = L(129)$ and $L_3(47) = L(141)$ could have been important for the evolution of bio-intelligence. $L_2(67)$ is .28 Angstroms, $L_3(47) = 3.1$ Angstroms, $L_2(71) = 4.4$ Angstroms and $L_2(73) = 1.8$ nanometers might be crucial for self-organization and intelligence at level of DNA and proteins. Thus the miracles of biochemical self-organization would not be reducible to standard chemistry but would involve in absolutely essential manner the symbiosis with higher life forms. The energy scale involved is in nanometer length scales of order keV and seems quite too high for life: room temperature which corresponds to 10^{-2} eV or at least the energy scale of atomic transitions seems to be the natural energy scale in protein length scales.

k	127	131	67_2	137	139	71_2	73_2
$L(k,n)/10^{-10}m$	.025	.1	.28	.8	1.6	4.5	18.0

Table 1. p-Adic length scales $L(k, n)$ possibly relevant to consciousness and life in atomic and nanolength scales. The length scale $L(151)$ is taken to be the thickness of cell membrane, which is 10^{-8} meters in a good approximation.

2. Higher order life forms in subcellular length scales and retina as living creature

First order life forms in subcellular length scales correspond to $k = 149, 151, 157, 163, 167$ and 169: corresponding p-adic length scales vary in the range of 5 nanometers and 5 micrometers and are given in the table below. Second order life forms associated with $L_2(79) = L(158) = 113$ nanometers, $L_2(83) = L(166) = 1.8$ micrometers as well as third order life form associated with $L_3(53) = L(159) = 160$ nanometers could also be important for self-organization and intelligence at subcellular levels. The energies for the secondary excitations of $k = 83$ Super Virasoro are in the region of visible light and an interesting possibility is that that these excitations might be excited when photons are absorbed by retina and that retina could be regarded as an intelligent conscious living being. This would also partially explain why our vision is just in this particular wavelength range. To decide whether interaction between photons and secondary Super Virasoro excitations is strong enough one should be able to device a model for this interaction.

k	149	151	157	79_2	53_3	163	83_2	167	169
$L_p/10^{-8}m$	.5	1	8	11.3	16	64	181	256	512

Table 2. p-Adic length scales $L(k, n)$ possibly relevant to consciousness and life between cell membrane and cellular length scales.

3. Higher order life in submillimeter length scales

The length scale range between $k = 169$ and $k = 191$ contains primary length scales $k = 173, 179, 181$ given in table below, secondary length scale $L_2(89) = L(178) = 1.1 \times 10^{-4}$ meters, and tertiary length scale $L_3(59) = L(177) = .8 \times 10^{-4}$ meters. The special importance of Mersenne primes suggests M_{89} second order life have managed to survive and might have meant a breakthrough in evolution. The size scale of largest neurons, say pyramidal neurons in cortex is indeed of order $L_2(M_{89})$. The fact that the lengths of micro-tubuli inside axons have length of order 10^{-4} meters suggests that they are accompanied by MEs corresponding to M_{89}. This hypothesis is inspired also by quantum antenna hypothesis and by the notion that MEs associated with axons serve as neural windows. The frequency scale associated with M_{89} is 3.3×10^{12} Hz and in infrared range. The energies involved correspond to 10^{-12} eV which is the thermal energy associated with the room temperature. This might explain the crucial importance of temperature for biolife. In too low temperatures secondary Super Virasoro excitations would be frozen whereas in too high temperatures situation would be thermalized.

k	173	59_3	89_2	179	181
$L_p/10^{-4}m$	.2	.8	1.1	1.6	3.2

Table 4. p-Adic length scales $L(k,n)$ possibly relevant to consciousness and life between cellular and submillimeter length scales.

IR radiation is known to be important for odor perception of at least insects [118] : the energies of $k = 89$ Super Virasoro are in this energy range. The structure of olfactory receptors also resembles the structure of the photoreceptors in retina. This would suggest that odor (and possibly also taste) perception might be regarded basically as IR vision with various odors playing the role of colors. The large number of different odors suggests that the number of different 'cones' is much higher than in the case of vision. The secondary p-adic length scale associated with M_{89} could give rise to secondary excitations of electro-weak fields with huge degeneracies. If the size of the 'pixel' characterizing sensory experience corresponds to the p-adic length scale of Super Virasoro associated with primary sensory organ, then one must conclude that also tactile senses could correspond to M_{89} or some smaller prime. Quite generally, vision, olfaction (and possibly also tastes) and tactile senses could thus be related with the secondary p-adic length scales $L_2(83)$ and $L_2(89)$ and/or with the primary length scales $L(169)$ and $L(173)$ and $L(179) = \sqrt{2}L_2(89)$. Note that the classical gauge fields associated with MEs could be used to generate secondary sensory experiences in longer p-adic length scales.

4. Higher order life forms in human length scales

The length scale range relevant to the structures of human brain contains the primary length scales corresponding to $k = 191, 193, 197$ and 199 varying in the range of 1-16 cm and are listed in the table below. The secondary and tertiary length scales $L_2(97) = 2.8$ cm, $L_3(67) = .32$ meters, $L_2(101) = .45$ meters and $L_2(103) = 1.81$ meters covers length scale range between brain nuclei and human body size. The fact that these primes correspond to the p-adic length scales associated with elementary particles (quarks) suggest that also second order life in these length scales is winner in the fight for survival. $L_2(97)$ corresponds to the size scale of brain nuclei which suggests that single pixel now provides a summary about sensory experience of brain nucleus. For instance, 'amygdalar emotions' might be in question.

It could be that the mind like space-times sheet with the size of brain and other body parts and entire body correspond carries exotic representations of $k = 67_3$, $k = 101_2$ and $k = 103_2$ Super Virasoro. The hypothesis that these levels correspond to emotions understood as generalized sensory experiences about the state of body solve the puzzles why emotions are 'single pixel' emotions and determined by the state of body. Secondary p-adic length scale should determine the size of the pixel in the bitmap provided by generalized sensory experience: since the size of pixel is of order human brain or even body, one could understand why emotions are 'single-pixel' emotions. Note that 'our experience' about these emotions probably does not correspond to this experience but experience coded to ELF level of self hierarchy. Body length scale would be associated with 'body-consciousness' quite different from our consciousness which corresponds to much higher level of the hierarchy.

k	191	193	97_2	197	199	67_3	101_2	103_2
L_p/m	.01	.02	2.8	.08	.16	.32	.45	1.8

Table 5. p-Adic length scales $L(k,n)$ possibly relevant to consciousness and life at length scales relevant to human brain and body.

5. Higher order life above body length scale

The primary p-adic length scales $k = 211, 223, 227,\ 229, 233, 239,\ 241$ and 251 between body size and $L_2(127)$ (quite near to Earth's circumference), and also longer p-adic length scales are listed in the table above. This range contains the secondary length scales $k = 107, 113$ and $k = 127$ correspond to a hierarchy of collective consciousness from the point of view of body (but, as it seems, not from our point of view!). The reader is encouraged to find the tertiary length scales in this range.

k	211	71_3	107_2	109_2	223
L_p/m	10	20	28.3	113	640
$T_p/\mu s$	3.3E-2	6.6E-2	9.2E-2	.37	2.1
k	113_2	227	229	233	79_3
L_p/m	1.8E+3	$2.5E+3$	$5E+3$	$2E+4$	8E+4
$T_p/\mu s$	6.1	8.6	17	69	276
k	239	241	$3^5 = 243$	83_3	2_2^5
L_p/m	$1.6E+5$	$3.2E+5$	6.4E+5	5.1E+6	7.2E+6
T_p/ms	.55	1.1	2.2	17.6	24.9
k	251	127_2	257	131_2	263
L_p/m	$E+7$	2.8E+7	$8E+7$	44.8	$6.4E+8$
T_p	35 ms	.1 s	.28 s	1.6 s	2.26 s
k	269	271	137_2	277	139_2
L_p/m	$5E+9$	$E+10$	2.8E+10	$7.7E+10$	11.2E+10
T_p	18.1 s	36.2 s	1.7 min	4.3 min	6.1 min
k	281	283	289	97_3	293
L_p/m	3.2E+11	6.4E+11	$5.2E+12$	1.1E+13	$2.1E+13$
T_p	17.3 min	34.6 min	4.6 h	6.3 h	18.5 h
k	149_2	151_2	101_3	307	103_3
L_p/ld	4.9	19.5	27.6	98.6	197.2
T_p/d	4.9	19.5	27.6	98.6	197.2

Table 6. p-Adic length and time scales above length scale $L(211) = 10$ meters possibly relevant to life and consciousness.

The emergence of Mersenne prime M_{107} could perhaps be associated with the emergence of social groups. Amusingly, M_{107} is hadronic length scale and associated with the emergence of color confined many-quark states, kind of societies also these! More seriously, color confinement should make sense also for the exotic Super Virasoro representations and might have some counterpart at the level of consciousness. For M_{107} the p-adic length scale is about 29.0 meters, which is between $L(211) = 10.2$ meters and $L(223) = 655$ meters. The corresponding frequency scale is 6 MHz. $L_2(113) \simeq 1853$ meters is the length scale associated with the next secondary Super Virasoro.

The tertiary length scales $L_3(83) = L(249)$, $L_2(k = 5^3 = 125) = L(250)$; secondary length scale $L_2(127)$, and the primary p-adic length scales $L(251), L_2(127), L(2^{2^8}) = L(256)$ and $L(257)$ correspond to the sequence of fundamental Super Virasoro frequencies

$$\frac{f(1,0)}{Hz} \in \{56.4, 40, 28.2, 10.0, 5.0, 3.5\} \ ,$$

which are important resonance frequencies of EEG which strongly encouratges the view that exotic Super Virasoro are involved with our qualia.

M_{127} corresponds to Earth size and to frequency of 10 Hz which is in EEG range. Next Mersenne prime corresponds to a completetely super-astronomical length scale. Uncertainty Principle suggests that if EEG frequencies stimulate the quantum transitions giving rise to our conscious experiences, then our mental images should correspond to MEs with $k = 127$ and 131. $k = 131$ indeed corresponds to frequencies above .63 Hz (1.6 seconds) covering delta, theta and alpha frequencies up to 10 Hz where the range of $k = 127$ frequencies begins (note however that the difference of M_{127} energies can be also below 10 Hz). Also the basic rhythms of body (heart beat and respiration) could correspond to $k = 131$ time scales.

The next secondary p-adic time scales corresponding to $k = 137, 139, 149$ and $k = 151$. $T_2(137)$ is are 1 minute 40 seconds, $T_2(139)$ is 6 minutes 40 seconds, $T_2(149)$ is 4.2 days roughly, $T_2(151)$ is 16.8 days roughly. $T_2(157)$ is roughly 1078.5 days (roughly three years). $T_2(163)$ is roughly 69024 days which makes roughly 189 years. These time scales could be important for human life cycle and the secondary excitations of these Super Virasoros could define important biological rhythms.

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Chapter 3

Topological Quantum Computation in TGD Universe

3.1 Introduction

Quantum computation is perhaps one of the most rapidly evolving branches of theoretical physics. TGD inspired theory of consciousness has led to new insights about quantum computation and in this chapter I want to discuss these ideas in a more organized manner.

There are three mathematically equivalent approaches to quantum computation [3] : quantum Turing machines, quantum circuits, and topological quantum computation (TQC). In fact, the realization that TGD Universe seems to be ideal place to perform TQC [21] , [8] served as the stimulus for writing this chapter.

Quite generally, quantum computation allows to solve problems which are NP hard, that is the time required to solve the problem increases exponentially with the number of variables using classical computer but only polynomially using quantum computer. The topological realization of the computer program using so called braids resulting when threads are weaved to 2-dimensional patterns is very robust so that de-coherence, which is the basic nuisance of quantum computation, ceases to be a problem. More precisely, the error probability is proportional to $exp(-\alpha l)$, where l is the length scale characterizing the distance between strands of the braid [21] .

3.1.1 Evolution of basic ideas of quantum computation

The notion of quantum computation goes back to Feynman [11] who demonstrated that some computational tasks boil down to problems of solving quantum evolution of some physical system, say electrons scattering from each other. Many of these computations are NP hard, which means that the number of computational steps required grows exponentially with the number of variables involved so that they become quickly unsolvable using ordinary computers. A quicker manner to do the computation is to make a physical experiment. A further bonus is that if you can solve one NP hard problem, you can solve many equivalent NP hard problems. What is new that quantum computation is not deterministic so that computation must be carried out several times and probability distribution for the outcomes allows to deduce the answer. Often however the situation is such that it is easy to check whether the outcome provides the sought for solution.

Years later David Deutch [8] transformed Feynman's ideas into a detailed theory of quantum computation demonstrating how to encode quantum computation in a quantum system and researchers started to develop applications. One of the key factors in the computer security is cryptography which relies on the fact that the factorization of large integers to primes is a NP hard problem. Peter Shor [26] discovered an algorithm, which allows to carry out the factorization in time, which is exponentially shorter than by using ordinary computers. A second example is problem of searching a particular from a set of N items, which requires time proportional to N classically but quantally only a time proportional to $\sqrt{N}$.

The key notion is quantum entanglement which allows to store information in the relationship between systems, qubits in the simplest situation. This means that information storage capacity

increases exponentially as a function of number of qubits rather than only linearly. This explains why NP hard problems which require time increasing exponentially with the number of variables can be solved using quantum computers. It also means exponentially larger information storage capacity than possible classically.

Recall that there are three equivalent approaches to quantum computation: quantum Turing machine, quantum circuits, and topology based unitary modular functor approach. In quantum circuit approach the unitary time evolution defining the quantum computation is assumed to be decomposable to a product of more elementary operations defined by unitary operators associated with quantum gates. The number of different gates needed is surprisingly small: only 1-gates generating unitary transformations of single qubit, and a 2-gate representing a transformation which together with 1-gates is able to generate entanglement are needed to generate a dense subgroup of unitary group $U(2^n)$ in the case of n-qubit system. 2-gate could be conditional NOT (CNOT). The first 1-gate can induce a phase factor to the qubit 0 and do nothing for qubit 1. Second 1-gate could form orthogonal square roots of bits 1 and 0 as superposition of 1 and 0 with identical probabilities.

The formal definition of the quantum computation using quantum circuit is as a computation of the value of a Boolean function of n Boolean arguments, for instance the k:th bit of the largest prime factor of a given integer. The unitary operator U is constructed as a product of operators associated with the basic gates. It is said that the function coding the problem belongs to the class BQP (function is computable with a bounded error in polynomial time) if there exists a classical polynomial-time (in string length) algorithm for specifying the quantum circuit. The first qubit of the outgoing n-qubit is measured and the probability that the the value is 0 determines the value of the bit to be calculated. For instance, for $p(0) \geq 2/3$ the bit is 0 and for $p(0) \geq 1/3$ the bit is 1. The evaluation of the outcome is probabilistic and requires a repeat the computation sufficiently many times.

The basic problem of quantum computation is the extremely fragility of the physical qubit (say spin). The fragility can be avoided by mapping q-bits to logical qubits realized as highly entangled states of many qubits and quantum error-correcting codes and fault tolerant methods [24, 27, 14] rely on this.

The space W of the logical qubits is known as a code space. The sub-space W of physical states of space $Y = V \otimes V..... \otimes V$ is called k-code if the effect of any k-local operator (affecting only k tensor factors of Y linearly but leaving the remaining factors invariant) followed by an orthogonal projection to W is multiplication by scalar. This means that k-local operator modify the states only in directions orthogonal to W.

These spaces indeed exist and it can be shown that the quantum information coded in W is not affected by the errors operating in fewer than $k/2$ of the n particles. Note that $k = 3$ is enough to guarantee stability with respect to 1-local errors. In this manner it is possible to correct the errors by repeated quantum measurements and by a suitable choice of the sub-space eliminate the errors due to the local changes of qubits by just performing a projection of the state back to the subspace (quantum measurement).

If the the error magnitude is below so called accuracy threshold, arbitrary long quantum computations are reliable. The estimates for this constant vary between 10^{-5} and 10^{-3}. This is beyond current technologies. Error correction is based on the representation of qubit as a logical qubit defined as a state in a linear sub-space of the tensor product of several qubits.

Topological quantum computation [21] provides an alternative approach to minimize the errors caused by de-coherence. Conceptually the modular functor approach [21, 20] is considerably more abstract than quantum circuit approach. Unitary modular functor is the S-matrix of a topological quantum field theory. It defines a unitary evolution realizing the quantum computation in macroscopic topological ground states degrees of freedom. The nice feature of this approach is that the notion of physical qubit becomes redundant and the code space defined by the logical qubits can be represented in terms topological and thus non-local degrees of freedom which are stable against local perturbations as required.

3.1.2 Quantum computation and TGD

Concerning quantum computation [3] in general, TGD TGD inspired theory of consciousness provides several new insights.

Quantum jump as elementary particle of consciousness and cognition

Quantum jump is interpreted as a fundamental cognitive process leading from creative confusion via analysis to an experience of understanding, and involves TGD counterpart of the unitary process followed by state function reduction and state preparation. One can say that quantum jump is the elementary particle of consciousness and that selves consists of sequences of quantum jump just like hadrons, nuclei, atoms, molecules,... consist basically of elementary particles. Self loses its consciousness when it generates bound state entanglement with environment. The conscious experience of self is in a well-defined sense a statistical average over the quantum jump during which self exists. During macro-temporal quantum coherence during macro-temporal quantum coherence a sequence of quantum jumps integrates effectively to a single moment of consciousness and effectively defines single unitary time evolution followed by state function reduction and preparation. This means a fractal hierarchy of consciousness very closely related to the corresponding hierarchy for bound states of elementary particles and structure formed from them.

Negentropy Maximization Principle guarantees maximal entanglement

Negentropy Maximization Principle is the basic dynamical principle constraining what happens in state reduction and self measurement steps of state preparation. Each self measurement involves a decomposition of system into two parts. The decomposition is dictated by the requirement that the reduction of entanglement entropy in self measurement is maximal. Self measurement can lead to either unentangled state or to entangled state with density matrix which is proportional to unit matrix (density matrix is the observable measured). In the latter case maximally entangled state typically involved with quantum computers results as an outcome. Hence Nature itself would favor maximally entangling 2-gates. Note however that self measurement occurs only if it increases the entanglement negentropy.

Number theoretical information measures and extended rational entanglement as bound state entanglement

The emerging number theoretical notion of information allows to interpret the entanglement for which entanglement probabilities are rational (or belong to an extension of rational numbers defining a finite extension of p-adic numbers) as bound state entanglement with positive information content. Macro-temporal quantum coherence corresponds to a formation of bound entanglement stable against state function reduction and preparation processes.

Spin glass degeneracy, which is the basic characteristic of the variational principle defining space-time dynamics, implies a huge number of vacuum degrees of freedom, and is the key mechanism behind macro-temporal quantum coherence. Spin glass degrees of freedom are also ideal candidates qubit degrees of freedom. As a matter fact, p-adic length scale hierarchy suggests that qubit represents only the lowest level in the hierarchy of qupits defining p-dimensional state spaces, p prime.

Time mirror mechanism and negative energies

The new view about time, in particular the possibility of communications with and control of geometric past, suggests the possibility of circumventing the restrictions posed by time for quantum computation. Iteration based on initiation of quantum computation again and again in geometric past would make possible practically instantaneous information processing.

Space-time sheets with negative time orientation carry negative energies. Also the possibility of phase conjugation of fermions is strongly suggestive. It is also possible that anti-fermions possess negative energies in phases corresponding to macroscopic length scales. This would explain matter-antimatter asymmetry in elegant manner. Zero energy states would be ideal for quantum computation purposes and could be even created intentionally by first generating a p-adic surface representing the state and then transforming it to a real surface.

The most predictive and elegant cosmology assumes that the net quantum numbers of the Universe vanish so that quantum jumps would occur between different kinds of vacua. Crossing symmetry makes this option almost consistent with the idea about objective reality with definite conserved total quantum numbers but requires that quantum states of 3-dimensional quantum theory represent S-matrices of 2-dimensional quantum field theory. These quantum states are thus about something. The

boundaries of space-time surface are most naturally light-like 3-surfaces space-time surface and are limiting cases of space-like 3-surface and time evolution of 2-surface. Hence they would act naturally as space-time correlates for the reflective level of consciousness.

3.1.3 TGD and the new physics associated with TQC

TGD predicts the new physics making possible to realized braids as entangled flux tubes and also provides a detailed model explaing basic facts about anyons.

Topologically quantized magnetic flux tube structures as braids

Quantum classical correspondence suggests that the absolute minimization of Kähler action corresponds to a space-time representation of second law and that the 4-surfaces approach asymptotically space-time representations of systems which do not dissipate anymore. The correlate for the absence of dissipation is the vanishing of Lorentz 4-force associated with the induced Kähler field. This condition can be regarded as a generalization of Beltrami condition for magnetic fields and leads to very explicit general solutions of field equations [8] .

The outcome is a general classification of solutions based on the dimension of CP_2 projection. The most unstable phase corresponds to $D = 2$-dimensional projection and is analogous to a ferromagnetic phase. $D = 4$ projection corresponds to chaotic demagnetized phase and $D = 3$ is the extremely complex but ordered phase at the boundary between chaos and order. This phase was identified as the phase responsible for the main characteristics of living systems [52, 53] . It is also ideal for quantum computations since magnetic field lines form extremely complex linked and knotted structures.

The flux tube structures representing topologically quantized fields, which have $D = 3$ -dimensional CP_2 projection, are knotted, linked and braided, and carry an infinite number of conserved topological charges labelled by representations of color group. They seem to be tailor-made for defining the braid structure needed by TQC. The boundaries of the magnetic flux tubes correspond to light-like 3-surfaces with respect to the induced metric (being thus metrically 2-dimensional and allowing conformal invariance) and can be interpreted either as 3-surfaces or time-evolutions of 2-dimensional systems so that S-matrix of 2-D system can be coded into the quantum state of conformally invariant 3-D system.

Anyons in TGD

TGD suggests a many-sheeted model for anyons used in the modelling of quantum Hall effect [12, 18, 15] . Quantum-classical correspondence requires that dissipation has space-time correlates. Hence a periodic motion should create a permanent track in space-time. This kind of track would be naturally magnetic flux tube like structure surrounding the Bohr orbit of the charged particle in the magnetic field. Anyon would be electron plus its track.

The magnetic field inside magnetic flux tubes impels the anyons to the surface of the magnetic flux tube and a highly conductive state results. The partial fusion of the flux tubes along their boundaries makes possible delocalization of valence anyons localized at the boundaries of flux tubes and implies a dramatic increase of longitudinal conductivity. When magnetic field is gradually increased the radii of flux tubes and the increase of the net flux brings in new flux tubes. The competition of these effects leads to the emergence of quantum Hall plateaus and sudden increase of the longitudinal conductivity σ_{xx}.

The simplest model explains only the filling fractions $\nu = 1/m$, m odd. The filling fractions $\nu = N/m$, m odd, require a more complex model. The transition to chaos means that periodic orbits become gradually more and more non-periodic: closed orbits fail to close after the first turn and do so only after N 2π rotations. Tracks would become N-branched surfaces. In N-branched space-time the single-valued analytic two particle wave functions $(\xi_k - \xi_l)^m$ of Laughlin [15] correspond to multiple valued wave functions $(z_k - z_l)^{m/N}$ at its M^4_+ projection and give rise to a filling fraction $\nu = N/m$. The filling fraction $\nu = N/m$, m even, requires composite fermions [5] . Anyon tracks can indeed contain up to $2N$ electrons if both directions of spin are allowed so that a rich spectroscopy is predicted: in particular anyonic super-conductivity becomes possible by 2-fermion composites. The branching gives rise to Z_N-valued topological charge.

One might think that fractional charges could be only apparent and result from the multi-branched character as charges associated with a single branch. This does not seem to be the case. Rather, the fractional charges result from the additional contribution of the vacuum Kähler charge of the anyonic flux tube to the charge of anyon. For $D = 3$ Kähler charge is topologized in the sense that the charge density is proportional to the Chern-Simons. Also anyon spin could become genuinely fractional due to the vacuum contribution of the Kähler field to the spin. Besides electronic anyons also anyons associated with various ions are predicted and certain strange experimental findings about fractional Larmor frequencies of proton in water environment [24] , [42] have an elegant explanation in terms of protonic anyons with $\nu = 3/5$. In this case however the magnetic field was weaker than the Earth's magnetic field so that the belief that anyons are possible only in systems carrying very strong magnetic fields would be wrong.

In TGD framework anyons as punctures of plane would be replaced by wormhole like tubes connecting different points of the boundary of the magnetic flux tube and are predicted to always appear as pairs as they indeed do. Detailed arguments demonstrate that TGD anyons are for $N = 4$ ($\nu = 4/m$) ideal for realizing the scenario of [21] for TQC.

The TGD inspired model of non-Abelian anyons is consistent with the model of anyons based on spontaneous symmetry breaking of a gauge symmetry G to a discrete sub-group H dynamically [10] . The breaking of electro-weak gauge symmetry for classical electro-weak gauge fields occurs at the space-time sheets associated with the magnetic flux tubes defining the strands of braid. Symmetry breaking implies that elements of holonomy group span H. This group is also a discrete subgroup of color group acting as isotropy group of the many-branched surface describing anyon track inside the magnetic flux tube. Thus the elements of the holonomy group are mapped to a elements of discrete subgroup of the isometry group leading from branch to another one but leaving many-branched surface invariant.

Witten-Chern-Simons action and light-like 3-surfaces

The magnetic field inside magnetic flux tube expels anyons at the boundary of the flux tube. In quantum TGD framework light-like 3-surfaces of space-time surface and future light cone are in key role since they define causal determinants for Kähler action. They also provide a universal manner to satisfy boundary conditions. Hence also the boundaries of magnetic flux tube structures could be light like surfaces with respect to the induced metric of space-time sheet and would be somewhat like black hole horizons. By their metric 2-dimensionality they allow conformal invariance and due the vanishing of the metric determinant the only coordinate invariant action is Chern-Simons action associated Kähler gauge potential or with the induced electro-weak gauge potentials.

The quantum states associated with the light-like boundaries would be naturally "self-reflective" states in the sense that they correspond to S-matrix elements of the Witten-Chern-Simons topological field theory. Modular functors could results as restriction of the S-matrix to ground state degrees of freedom and Chern-Simons topological quantum field theory is a promising candidate for defining the modular functors [38, 35] .

Braid group B_n is isomorphic to the first homotopy group of the configuration space $C_n(R^2)$ of n particles. $C_n(R^2)$ is $((R^2)_n - D)/S_n$, where D is the singularity represented by the configurations in which the positions of 2 or more particles. and be regarded also as the configuration associated with plane with $n + 1$ punctures with $n + 1$:th particle regarded as inert. The infinite order of the braid group is solely due to the 2-dimensionality. Hence the dimension $D = 4$ for space-time is unique also in the sense that it makes possible TQC.

3.1.4 TGD and TQC

Many-sheeted space-time concept, the possibility of negative energies, and Negentropy Maximization Principle inspire rather concrete ideas about TQC. NMP gives good hopes that the laws of Nature could take care of building fine-tuned entanglement generating 2-gates whereas 1-gates could be reduced to 2-gates for logical qubits realized using physical qubits realized as Z^4 charges and not existing as free qubits.

Only 2-gates are needed

The entanglement of qubits is algebraic which corresponds in TGD Universe to bound state entanglement. Negentropy Maximization Principle implies that maximal entanglement results automatically in quantum jump. This might saves from the fine-tuning of the 2-gates. In particular, the maximally entangling Yang-Baxter R-matrix is consistent with NMP.

TGD suggests a rather detailed physical realization of the model of [21] for anyonic quantum computation. The findings about strong correlation between quantum entanglement and topological entanglement are apparently contradicted by the Temperley-Lie representations for braid groups using only single qubit. The resolution of the paradox is based on the observation that in TGD framework batches containing anyon Cooper pair (AA) and single anyon (instead of two anyons as in the model of [21]) allow to represent single qubit as a logical qubit, and that mixing gate and phase gate can be represented as swap operations s_1 and s_2. Hence also 1-gates are induced by the purely topological 2-gate action, and since NMP maximizes quantum entanglement, Nature itself would take care of the fine-tuning also in this case. The quantum group representation based on $q = exp(i2\pi/5)$ is the simplest representation satisfying various constraints and is also physically very attractive. [21, 20] .

TGD makes possible zero energy TQC

TGD allows also negative energies: besides phase conjugate photons also phase conjugate fermions and anti-fermions are possible, and matter-antimatter asymmetry might be only apparent and due to the ground state for which fermion energies are positive and anti-fermion energies negative.

This would make in principle possible zero energy topological quantum computations. The least one could hope wold be the performance of TQC in doubles of positive and negative energy computations making possible error detection by comparison. The TGD based model for anyon computation however leads to expect that negative energies play much more important role.

The idea is that the quantum states of light-like 3-surfaces represent 2-dimensional time evolutions (in particular modular functors) and that braid operations correspond to zero energy states with initial state represented by positive energy anyons and final state represented by negative energy anyons. The simplest manner to realize braid operations is by putting positive *resp.* negative energy anyons near the boundary of tube T_1 *resp.* T_2. Opposite topological charges are at the ends of the magnetic threads connecting the positive energy anyons at T_1 with the negative energy anyons at T_2. The braiding for the threads would code the quantum gates physically.

Before continuing a humble confession is in order: I am not a professional in the area of quantum information science. Despite this, my hope is that the speculations below might serve as an inspiration for real professionals in the field and help them to realize that TGD Universe provides an ideal arena for quantum information processing, and that the new view about time, space-time, and information suggests a generalization of the existing paradigm to a much more powerful one.

3.2 Existing view about topological quantum computation

In the sequel the evolution of ideas related to topological quantum computation, dance metaphor, and the idea about realizing the computation using a system exhibiting so called non-Abelian Quantum Hall effect, are discussed.

3.2.1 Evolution of ideas about TQC

The history of the TQC paradigm is as old as that of QC and involves the contribution of several Fields Medalists. At 1987 to-be Fields Medalist Vaughan Jones [20] demonstrated that the von Neumann algebras encountered in quantum theory are related to the theory of knots and allow to distinguish between very complex knots. Vaughan also demonstrated that a given knot can be characterized in terms an array of bits. The knot is oriented by assigning an arrow to each of its points and projected to a plane. The bit sequence is determined by a sequence of bits defined by the self-intersections of the knot's projection to plane. The value of the bit in a given intersection changes when the orientation of either line changes or when the line on top of another is moved under it. Since the logic operations performed by the gates of computer can be coded to matrices consisting of 0s and 1s, this means that tying a know can encode the logic operations necessary for computation.

String theorist Edward Witten [38] , also a Fields Medalist, connected the work of Jones to quantum physics by showing that performing measurements to a system described by a 3-dimensional topological quantum field theory defined by non-Abelian Chern-Simons action is equivalent with performing the computation that a particular braid encodes. The braids are determined by linked word lines of the particles of the topological quantum field theory. What makes braids and quantum computation so special is that the coding of the braiding pattern to a bit sequence gives rise to a code, which corresponds to a code solving NP hard problem using classical computer.

1989 computer scientist Alexei Kitaev [17] demonstrated that Witten's topological quantum field theory could form a basis for a computer. Then Fields Medalist Michael Freedman entered the scene and in collaboration with Kitaev, Michael Larson and Zhenghan Wang developed a vision of how to build a topological quantum computer [21, 20] using system exhibiting so called non-Abelian quantum Hall effect [20] .

The key notion is Z_4 valued topological charge which has values 1 and 3 for anyons and 0 and 2 for their Cooper pairs. For a system of $2n$ non-Abelian anyon pairs created from vacuum there are n-1 anyon qubits analogous to spin . The notion of physical qubit is not needed at all and logical qubit is coded to the topological charge of the anyon Cooper pair. The basic idea is to utilize entanglement between Z_4 valued topological charges to achieve quantum information storage stable against decoherence. The swap of neighboring strands of the braid is the topological correlate of a 2-gate which as such does not generate entanglement but can give rise to a transformation such as CNOT. When combined with 1-gates taking square root of qubit and relative phase, this 2-gate is able to generate $U(2^n)$.

The swap can be represented as the so called braid Yang-Baxter R-matrix characterizing also the deviation of quantum groups from ordinary groups [16] . Quite generally, all unitary Yang-Baxter R-matrices are entangling when combined with square root gate except for special values of parameters characterizing them and thus there is a rich repertoire of topologically realized quantum gates. Temperley-Lieb representation provides a 1-qubit representation for swaps in 3-braid system [16, 20] . The measurement of qubit reduces to the measurement of the topological charge of the anyon Cooper pair: in the case that it vanishes (qubit 0) the anyon Cooper pair can annihilate and this serves as the physical signature.

3.2.2 Topological quantum computation as quantum dance

Although topological quantum computation involves very abstract and technical mathematical thinking, it is possible to illustrate how it occurs by a very elegant metaphor. With tongue in cheek one could say that topological quantum computation occurs like a dance. Dancers form couples and in this dancing floor the partners can be also of same sex. Dancers can change their partners. If the partners are of the same sex, they define bit 1 and if they are of opposite sex they define bit 0.

To simplify things one can arrange dancers into a row or several rows such that neighboring partners along the row form a couple. The simplest situation corresponds to a single row of dancers able to make twists of 180 degrees permuting the dancers and able to change the partner to a new one any time. Dance corresponds to a pattern of tracks of dancers at the floor. This pattern can be lifted to a three-dimensional pattern introducing time as a third dimension. When one looks the tracks of a row of dancers in this 2+1-dimensional space-time, one finds that the tracks of the dancers form a complex weaved pattern known as braiding. The braid codes for the computation. The braiding consists of primitive swap operations in which two neighboring word lines twist around each other.

The values of the bits giving the result of the final state of the calculation can be detected since there is something very special which partners with opposite sex can do and do it sooner or later. Just by looking which pairs do it allows to deduce the values of the bits. The alert reader has of course guessed already now that the physical characterization for the sex is as a Z^4 valued topological charge, which is of opposite sign for the different sexes forming Cooper pairs, and that the thing that partners of opposite sex can do is to annihilate! All that is needed to look for those pairs which annihilate after the dance evening to detect the 0s in the row of bits. The coding of the sex to the sign of the topological charge implies also robustness.

It is however essential that the value of topological charge for a given particle in the final state is not completely definite (this is completely general feature of all quantum computations). One can tell only with certain probability that given couple in the final state is male-female or male-male or

female-female and the probabilities in question code for the braid pattern in turn coding for quantum logic circuit. Hence one must consider an ensemble of braid calculations to deduce these probabilities.

The basic computational operation permuting the neighboring topological charges is topological so that the program represented by the braiding pattern is very stable against perturbations. The values of the topological charges are also stable. Hence the topological quantum computation is a very robust process and immune to quantum de-coherence even in the standard physics context.

3.2.3 Braids and gates

In order to understand better how braids define gates one must introduce some mathematical notions related to the braids.

Braid groups

Artin introduced the braid groups bearing his name as groups generated by the elements, which correspond to the cross section between neighboring strands of the braid. The definition of these groups is discussed in detail in [16] . For a braid having $n+1$ strands the Artin group B_{n1} has n generators s_i. The generators satisfy certain relations. Depending on whether the line coming from left is above the the line coming from right one has s_i or s_i^{-1}. The elements s_i and s_j commute for $i < j$ and $i > j+1$: $s_i s_j = s_j s_i$, which only says that two swaps which do not have common lines commute. For $i = j$ and $i = j+1$ commutativity is not assumed and this correspond to the situation in which the swaps act on common lines.

As already mentioned, Artin's braid group B_n is isomorphic with the homotopy group $\pi_1((R^2)^n/S_{n+1})$ of plane with $n+1$ punctures. B_n is infinite-dimensional because the conditions $s_i^2 = 1$ added to the defining relations in the case of permutation group S_n are not included. The infinite-dimensionality of homotopy groups reflects the very special topological role of 2-dimensional spaces.

One must consider also variants of braid groups encountered when all particles in question are not identical particles. The reason is that braid operation must be replaced by a 2π rotation of particle A around B when the particles are not identical.

1. Consider first the situation in which all particles are non-identical. The first homotopy group of $R^2)^n - D$, where D represents points configurations for which two or more points are identical is identical with the colored braid group B_n^c defined by $n+1$ punctures in plane such that $n+1$:th is passive (punctures are usually imagined to be located on line). Since particles are not identical the braid operation must be replaced by monodromy in which i:th particle makes 2π rotation around j:th particle. This group has generators

$$\gamma_{ij} = s_i ... s_{j-2} s_{j-1}^2 s_{j-2} ... s_i^{-1} \quad , i < j \quad , \tag{3.2.1}$$

   and can be regarded as a subgroup of the braid group.

2. When several representatives of a given particle species are present the so called partially colored braid group B_n^{pc} is believed to describe the situation. For pairs of identical particles the generators are braid generators and for non-identical particles monodromies appear as generators. It will be found later that in case of anyon bound states, the ordinary braid group with the assumption that braid operation can lead to a temporary decay and recombination of anyons to a bound state, might be a more appropriate model for what happens in braiding.

3. When all particles are identical, one has the braid group B_n, which corresponds to the fundamental group of $C_n(R^2) = ((R^2)^n - D)/S_n$. Division by S_n expresses the identicality of particles.

Extended Artin's group

Artin's group can be extended by introducing any group G and forming its tensor power $G^{\otimes^n} = G \otimes ... \otimes G$ by assigning to every strand of the braid group G. The extended group is formed from elements of $g_1 \otimes g_2 .... \otimes g_n$ and s_i by posing additional relations $g_i s_j = s_j g_i$ for $i < j$ and $i > j + 1$. The interpretation of these relations is completely analogous to the corresponding one for the Artin's group.

If G allows representation in some space V one can look for the representations of the extended Artin's group in the space $V^{\otimes^n}$. In particular, unitary representations are possible. The space in question can also represent physical states of for instance anyonic system and the element g_i associated with the lines of the braid can represent the unitary operators characterizing the time development of the strand between up to the moment when it experiences a swap operation represented by s_i after this operation g_i becomes $s_i g_i s_i^{-1}$.

Braids, Yang-Baxter relations, and quantum groups

Artin's braid groups can be related directly to the so called quantum groups and Yang-Baxter relations. Yang-Baxter relations follow from the relation $s_1 s_2 s_1 = s_2 s_1 s_2$ by noticing that these operations permute the lines 123 of the braid to the order 321. By assigning to a swap operation permuting i:th and j:th line group element R_{ij} when i:th line goes over the j:th line, and noticing that $R_{ij} i$ acts in the tensor product $V_i \otimes V_j$, one can write the relation for braids in a form

$$R_{32} R_{13} R_{12} = R_{12} R_{13} R_{23} \ .$$

Braid Yang-Baxter relations are equivalent with the so called algebraic Yang-Baxter relations encountered in quantum group theory. Algebraic R can be written as $R_a = RS$, where S is the matrix representing swap operation as a mere permutation. For a suitable choice R_a provides the fundamental representations for the elements of the quantum group $SL(n)_q$ when V is n-dimensional.

The equations represent n^6 equations for n^4 unknowns and are highly over-determined so that solving the equations is a difficult challenge. Equations have symmetries which are obvious on basis of the topological interpretation. Scaling and automorphism induced by linear transformations of V act as symmetries, and the exchange of tensor factors in $V \otimes V$ and transposition are symmetries as also shift of all indices by a constant amount (using modulo N arithmetics).

Unitary R-matrices

Quite a lot is known about the general solutions of the Yang-Baxter equations and for $n = 2$ the general unitary solutions of equations is known [9] . All of these solutions are entangling and define thus universal 1-gates except for certain parameter values.

The first solution is

$$R = \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & \cdot & \cdot & 1 \\ \cdot & 1 & -1 & \cdot \\ \cdot & 1 & 1 & \cdot \\ -1 & \cdot & \cdot & 1 \end{pmatrix} \tag{3.2.2}$$

and contains no free parameters (dots denote zeros). This R-matrix is strongly entangling. Note that the condition $R^8 = 1$ is satisfied. The defining relations for Artin's braid group allow also more general solutions obtained by multiplying R with an arbitrary phase factor. This would mean that $R^8 = 1$ constraint is not satisfied anymore. One can argue that over-all phase does not matter: on the other hand, the over all phase is visible in knot invariants defined by the trace of R.

The second and third solution come as families labelled four phases a, b, c and d:

$$R'(a,b,c,d) = \frac{1}{\sqrt{2}} \begin{pmatrix} a & \cdot & \cdot & \cdot \\ \cdot & & b & \cdot \\ \cdot & c & \cdot & \cdot \\ \cdot & \cdot & \cdot & d \end{pmatrix}$$

$$R''(a,b,c,d) = \frac{1}{\sqrt{2}} \begin{pmatrix} \cdot & \cdot & \cdot & a \\ \cdot & b & \cdot & \cdot \\ \cdot & \cdot & c & \cdot \\ d & \cdot & \cdot & \cdot \end{pmatrix} \tag{3.2.3}$$

These matrices are not as such entangling. The products $U_1 \otimes U_2 R V_1 \otimes V_2$, where U_i and V_i are 2×2 unitary matrices, are however entangling matrices and thus act as universal gates for $ad - bc \neq 0$ guaranteeing that the state $a|11\rangle + b|10\rangle + |01\rangle + |00\rangle$ is entangled.

It deserves to be noticed that the swap matrix

$$S = R'(1,1,1,1) = \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & \cdot & \cdot & \cdot \\ \cdot & & 1 & \cdot \\ \cdot & 1 & 1 & \cdot \\ \cdot & \cdot & \cdot & 1 \end{pmatrix} \tag{3.2.4}$$

permuting the qubits does not define universal gate. This is understandable since in this representation of braid group reduces it to permutation group and situation becomes completely classical.

One can write all solutions R of braid Yang-Baxter equation in the form $R = R_a$, where R_a is the solution of so called algebraic Yang-Baxter equation. The interpretation is that the swap matrix S represents the completely classical part of the swap operation since it acts as a mere permutation whereas R_a represents genuine quantum effects related to the swap operation.

In the article of Kauffman [16] its is demonstrated explicitly how to construct CNOT gate as a product MRN, where M and N are products of single particle gates. This article contains also a beautiful discussion about how the traces of the unitary matrices defined by the braids define knot invariants. For instance, the matrix R satisfies $R^8 = 1$ so that the invariants constructed using R as 2-gate cannot distinguish between knots containing n and $n + 8k$ sub-sequent swaps. Note however that the multiplication of R with a phase factor allows to get rid of the 8-periodicity.

Knots, links, braids, and quantum 2-gates

In [16] basic facts about knots, links, and their relation to braids are discussed. Knot diagrams are introduced, the so called Reidermeister moves and homeomorphisms of plane as isotopies of knots and links are discussed. Also the notion of braid closure producing knots or links is introduced together with the theorem of Markov stating that any knot and link corresponds to some (not unique) braid. Markov moves as braid deformations leaving corresponding knots and links invariant are discussed and it the immediate implication is that traces of the braid matrices define knot invariants. In particular, the traces of the unitary matrices defined by R-matrix define invariants having same value for the knots and links resulting in the braid closure.

In [16] the state preparation and quantum measurement allowing to deduce the absolute value of the trace of the unitary matrix associated with the braid defining the quantum computer is discussed as an example how quantum computations could occur in practice. The braid in question is product of the braid defining the invariant and trivial braid with same number n of strands. The incoming state is maximally entangled state formed $\sum_n |n\rangle \otimes |n\rangle$, where n runs over all possible bit sequences defined by the tensor product of n qubits. Quantum measurement performs a projection to this state and from the measurements it is possible to deduce the absolute value of the trace defining the knot invariant.

3.2.4 About quantum Hall effect and theories of quantum Hall effect

Using the dance metaphor for TQC, the system must be such that it is possible to distinguish between the different sexes of dancers. The proposal of [21] is that the system exhibiting so called non-Abelian Quantum Hall effect [18, 21] could make possible realization of the topological computation.

The most elegant models of quantum Hall effect are in terms of anyons regarded as singularities due to the symmetry breaking of gauge group G down to a finite sub-group H, which can be also non-Abelian. Concerning the description of the dynamics of topological degrees of freedom topological quantum field theories based on Chern-Simons action are the most promising approach.

Quantum Hall effect

Quantum Hall effect [12, 18] occurs in 2-dimensional systems, typically a slab carrying a longitudinal voltage V causing longitudinal current j. A magnetic field orthogonal to the slab generates a transversal current component j_T by Lorentz force. j_T is proportional to the voltage V along the slab and the dimensionless coefficient is known as transversal conductivity. Classically the coefficients is proportional ne/B, where n is 2-dimensional electron density and should have a continuous spectrum. The finding that came as surprise was that the change of the coefficient as a function of parameters like magnetic field strength and temperature occurred as discrete steps of same size. In integer quantum Hall effect the coefficient is quantized to $2\nu\alpha$, $\alpha = e^2/4\pi$, such that ν is integer.

Later came the finding that also smaller steps corresponding to the filling fraction $\nu = 1/3$ of the basic step were present and could be understood if the charge of electron would have been replaced with $\nu = 1/3$ of its ordinary value. Later also QH effect with wide large range of filling fractions of form $\nu = k/m$ was observed.

The model explaining the QH effect is based on pseudo particles known as anyons [10] , [18] . According to the general argument of [12] anyons have fractional charge νe. Also the TGD based model for fractionization to be discussed later suggests that the anyon charge should be νe quite generally. The braid statistics of anyon is believed to be fractional so that anyons are neither bosons nor fermions. Non-fractional statistics is absolutely essential for the vacuum degeneracy used to represent logical qubits.

In the case of Abelian anyons the gauge potential corresponds to the vector potential of the divergence free velocity field or equivalently of incompressible anyon current. For non-Abelian anyons the field theory defined by Chern-Simons action is free field theory and in well-defined sense trivial although it defines knot invariants. For non-Abelian anyons situation would be different. They would carry non-Abelian gauge charges possibly related to a symmetry breaking to a discrete subgroup H of gauge group [10] each of them defining an incompressible hydrodynamical flow. Non-Abelian QH effect has not yet been convincingly demonstrated experimentally. According to [21] the anyons associated with the filling fraction $\nu = 5/2$ are a good candidate for non-Abelian anyons and in this case the charge of electron is reduced to $Q = 1/4$ rather than being $Q = \nu e$.

Non-Abelian anyons [18, 20] are always created in pairs since they carry a conserved topological charge. In the model of [21] this charge should have values in 4-element group Z_4 so that it is conserved only modulo 4 so that charges +2 and -2 are equivalent as are also charges 3 and -1. The state of n anyon pairs created from vacuum can be show to possess 2^{n-1}-dimensional vacuum degeneracy [21] : later a TGD based argument for why this is the case is constructed. When two anyons fuse the 2^{n-1}-dimensional state space decomposes to 2^{n-2}-dimensional tensor factors corresponding to anyon Cooper pairs with topological charges 2 and 0. The topological "spin" is ideal for representing logical qubits. Since free topological charges are not possible the notion of physical qubit does not make sense (note the analogy with quarks). The measurement of topological qubit reduces to a measurement of whether anyon Cooper pair has vanishing topological charge or not.

Quantum Hall effect as a spontaneous symmetry breaking down to a discrete subgroup of the gauge group

The system exhibiting quantum Hall effect is effectively 2-dimensional. Fractional statistics suggests that topological defects, anyons, allowing a description in terms of the representations of the homotopy group of $((R^2)^n - D)/S_n$. The gauge theory description would be in terms of spontaneous symmetry breaking of the gauge group G to a finite subgroup H by a Higgs mechanism [10] , [18] . This would make all gauge degrees of freedom massive and leave only topological degrees of freedom. What is

unexpected that also non-Abelian topological degrees of freedom are in principle possible. Quantum Hall effect is Abelian or non-Abelian depending on whether the group H has this property.

In the symmetry breaking $G \to H$ the non-Abelian gauge fluxes defined as non-integrable phase factors $Pexp(i \oint A_\mu dx^\mu)$ around large circles (surrounding singularities (so that field approaches a pure gauge configuration) are elements of the first homotopy group of G/H, which is H in the case that H is discrete group and G is simple. An idealized manner to model the situation [18] is to assume that the connection is pure gauge and defined by an H-valued function which is many-valued such that the values for different branches are related by a gauge transformation in H. In the general case a gauge transformation of a non-trivial gauge field by a multi-valued element of the gauge group would give rise to a similar situation.

One can characterize a given topological singularity magnetically by an element in conjugacy class C of H representing the transformation of H induced by a 2π rotation around singularity. The elements of C define states in given magnetic representation. Electrically the particles are characterized by an irreducible representations of the subgroup of $H_C \subset H$ which commutes with an arbitrarily chosen element of the conjugacy class C.

The action of $h(B)$ resulting on particle A when it makes a closed turn around B reduces in magnetic degrees of freedom to translation in conjugacy class combined with the action of element of H_C in electric degrees of freedom. Closed paths correspond to elements of the braid group $B_n(X^2)$ identifiable as the mapping class group of the punctured 2-surface X^2 and this means that symmetry breaking $G \to H$ defines a representation of the braid group. The construction of these representations is discussed in [18] and leads naturally via the group algebra of H to the so called quantum double $D(H)$ of H, which is a quasi-triangular Hopf algebra allowing non-trivial representations of braid group.

Anyons could be singularities of gauge fields, perhaps even non-Abelian gauge fields, and the latter ones could be modelled by these representations. In particular, braid operations could be represented using anyons.

Witten-Chern-Simons action and topological quantum field theories

The Wess-Zumino-Witten action used to model 2-dimensional critical systems consists of a 2-dimensional conformally invariant term for the chiral field having values in group G combined with 2+1-dimensional term defined as the integral of Chern-Simons 3-form over a 3-space containing 2-D space as its boundary. This term is purely topological and identifiable as winding number for the map from 3-dimensional space to G. The coefficient of this term is integer k in suitable normalization. k gives the value of central extension of the Kac-Moody algebra defined by the theory.

One can couple the chiral field $g(x)$ to gauge potential defined for some subgroup of G_1 of G. If the G_1 coincides with G, the chiral field can be gauged away by a suitable gauge transformation and the theory becomes purely topological Witten-Chern-Simons theory. Pure gauge field configuration represented either as flat gauge fields with non-trivial holonomy over homotopically non-trivial paths or as multi-valued gauge group elements however remain and the remaining degrees of freedom correspond to the topological degrees of freedom.

Witten-Chern-Simons theories are labelled by a positive integer k giving the value of central extension of the Kac-Moody algebra defined by the theory. The connection with Wess-Zumino-Witten theory come from the fact that the highest weight states associated with the representations of the Kac-Moody algebra of WZW theory are in one-one correspondence with the representations R_i possible for Wilson loops in the topological quantum field theory.

In the Abelian case case 2+1-dimensional Chern-Simons action density is essentially the inner product $A \wedge dA$ of the vector potential and magnetic field known as helicity density and the theory in question is a free field theory. In the non-Abelian case the action is defined by the 3-form

$$\frac{k}{4\pi} Tr\left(A \wedge (dA + \frac{2}{3} A \wedge A) \right)$$

and contains also interaction term so that the field theory defined by the exponential of the interaction term is non-trivial.

In topological quantum field theory the usual n-point correlation functions defined by the functional integral are replaced by the functional averages for $Diff^3$ invariant quantities defined in terms of non-integrable phase factors defined by ordered exponentials over closed loops. One can consider

arbitrary number of loops which can be knotted, linked, and braided. These quantities define both knot and 3-manifold invariants (the functional integral for zero link in particular). The perturbative calculation of the quantum averages leads directly to the Gaussian linking numbers and infinite number of perturbative link and not invariants.

The experience gained from topological quantum field theories defined by Chern-Simons action has led to a very elegant and surprisingly simple category theoretical approach to the topological quantum field theory [21, 29] allowing to assign invariants to knots, links, braids, and tangles and also to 3-manifolds for which braids as morphisms are replaced with cobordisms. The so called modular Hopf algebras, in particular quantum groups $Sl(2)_q$ with q a root of unity, are in key role in this approach. Also the connection between links and 3-manifolds can be understood since closed, oriented, 3-manifolds can be constructed from each other by surgery based on links.

Witten's article [38] "Quantum Field Theory and the Jones Polynomial" is full of ingenious constructions, and for a physicist it is the easiest and certainly highly enjoyable manner to learn about knots and 3-manifolds. For these reasons a little bit more detailed sum up is perhaps in order.

1. Witten discusses first the quantization of Chern-Simons action at the weak coupling limit $k \to \infty$. First it is shown how the functional integration around flat connections defines a topological invariant for 3-manifolds in the case of a trivial Wilson loop. Next a canonical quantization is performed in the case $X^3 = \Sigma^2 \times R^1$: in the Coulomb gauge $A_3 = 0$ the action reduces to a sum of $n = dim(G)$ Abelian Chern-Simons actions with a non-linear constraint expressing the vanishing of the gauge field. The configuration space consists thus of flat non-Abelian connections, which are characterized by their holonomy groups and allows Kähler manifold structure.

2. Perhaps the most elegant quantal element of the approach is the decomposition of the 3-manifold to two pieces glued together along 2-manifold implying the decomposition of the functional integral to a product of functional integrals over the pieces. This together with the basic properties of Hilbert of complex numbers (to which the partition functions defined by the functional integrals over the two pieces belong) allows almost a miracle like deduction of the basic results about the behavior of 3-manifold and link invariants under a connected sum, and leads to the crucial skein relations allowing to calculate the invariants by decomposing the link step by step to a union of unknotted, unlinked Wilson loops, which can be calculated exactly for $SU(N)$. The decomposition by skein relations gives rise to a partition function like representation of invariants and allows to understand the connection between knot theory and statistical [9]. A direct relationship with conformal field theories and Wess-Zumino-Witten model emerges via Wilson loops associated with the highest weight representations for Kac Moody algebras.

3. A similar decomposition procedure applies also to the calculation of 3-manifold invariants using link surgery to transform 3-manifolds to each other, with 3-manifold invariants being defined as Wilson loops associated with the homology generators of these (solid) tori using representations R_i appearing as highest weight representations of the loop algebra of torus. Surgery operations are represented as mapping class group operations acting in the Hilbert space defined by the invariants for representations R_i for the original 3-manifold. The outcome is explicit formulas for the invariants of trivial knots and 3-manifold invariant of S^3 for $G = SU(N)$, in terms of which more complex invariants are expressible.

4. For $SU(N)$ the invariants are expressible as functions of the phase $q = exp(i2\pi/(k+N))$ associated with quantum groups. Note that for $SU(2)$ and $k = 3$, the invariants are expressible in terms of Golden Ratio. The central charge $k = 3$ is in a special position since it gives rise to $k + 1 = 4$-vertex representing naturally 2-gate physically. Witten-Chern-Simons theories define universal unitary modular functors characterizing quantum computations [20] .

Chern-Simons action for anyons

In the case of quantum Hall effect the Chern-Simons action has been deduced from a model of electrons as a 2-dimensional incompressible fluid [15] . Incompressibility requires that the electron current has a vanishing divergence, which makes it analogous to a magnetic field. The expressibility of the current as a curl of a vector potential b, and a detailed study of the interaction Lagrangian leads to the identification of an Abelian Chern-Simons for b as a low energy effective action. This action

is Abelian, whereas the anyonic realization of quantum computation would suggest a non-Abelian Chern-Simons action.

Non-Abelian Chern-Simons action could result in the symmetry breaking of a non-Abelian gauge group G, most naturally electro-weak gauge group, to a non-Abelian discrete subgroup H [10] so that states would be labelled by representations of H and anyons would be characterized magnetically H-valued non-Abelian magnetic fluxes each of them defining its own incompressible hydro-dynamical flow. As will be found, TGD predicts a non-Abelian Chern-Simons term associated with electroweak long range classical fields.

3.2.5 Topological quantum computation using braids and anyons

By the general mathematical results braids are able to code all quantum logic operations [18] . In particular, braids allow to realize any quantum circuit consisting of single particle gates acting on qubits and two particle gates acting on pairs of qubits. The coding of braid requires a classical computation which can be done in polynomial time. The coding requires that each dancer is able to remember its dancing history by coding it into its own state.

The general ideas are following.

1. The ground states of anyonic system characterize the logical qubits, One assumes non-Abelian anyons with Z_4 -valued topological charge so that a system of n anyon pairs created from vacuum allows 2^{n-1}-fold anyon degeneracy [21] . The system is decomposed into blocks containing one anyonic Cooper pair with $Q_T \in \{2, 0\}$ and two anyons with such topological charges that the net topological charge vanishes. One can say that the states $(0, 1-1)$ and $(0, -1, +1))$ represent logical qubit 0 whereas the states $(2, -1, -1)$ and $(2, +1, +1)$ represent logical qubit 1. This would suggest 2^2-fold degeneracy but actually the degeneracy is 2-fold.

   Free physical qubits are not possible and at least four particles are indeed necessarily in order to represent logical qubit. The reason is that the conservation of Z^4 charge would not allow mixing of qubits 1 and 0, in particular the Hadamard 1-gate generating square root of qubit would break the conservation of topological charge. The square root of qubit can be generated only if 2 units of topological charge is transferred between anyon and anyon Cooper pair. Thus qubits can be represented as entangled states of anyon Cooper pair and anyon and the fourth anyon is needed to achieve vanishing total topological charge in the batch.

2. In the initial state of the system the anyonic Cooper pairs have $Q_T = 0$ and the two anyons have opposite topological charges inside each block. The initial state codes no information unlike in ordinary computation but the information is represented by the braid. Of course, also more general configurations are possible. Anyons are assumed to evolve like free particles except during swap operations and their time evolution is described by single particle Hamiltonians.

   Free particle approximation fails when the anyons are too near to each other as during braid operations. The space of logical qubits is realized as k-code defined by the 2^{n-1} ground states, which are stable against local single particle perturbations for $k = 3$ Witten-Chern-Simons action. In the more general case the stability against n-particle perturbations with $n < [k/2]$ is achieved but the gates would become $[k/2]$-particle gates (for $k = 5$ this would give 6-particle vertices).

3. Anyonic system provides a unitary modular functor as the S-matrix associated with the anyon system whose time evolution is fixed by the pre-existing braid structure. What this means that the S-matrices associated with the braids can be multiplied and thus a unitary representation for the group formed by braids results. The vacuum degeneracy of anyon system makes this representation non-trivial. By the NP complexity of braids it is possible to code any quantum logic operation by a particular braid [12] . There exists a powerful approximation theorem allowing to achieve this coding classically in polynomial time [18] . From the properties of the R-matrices inducing gate operations it is indeed clear that two gates can be realized. The Hadamard 1-gate could be realized as 2-gate in the system formed by anyon Cooper pair and anyon.

4. In [21] the time evolution is regarded as a discrete sequence of modifications of single anyon Hamiltonians induced by swaps [13] . If the modifications define a closed loop in the space

of Hamiltonians the resulting unitary operators define a representation of braid group in a dense discrete sub-group of $U(2^n)$. The swap operation is 2-local operation acting like a 2-gate and induces quantum logical operation modifying also single particle Hamiltonians. What is important that this modification maps the space of the ground states to a new one and only if the modifications correspond to a closed loop the final state is in the same code space as the initial state. What time evolution does is to affect the topological charges of anyon Cooper pairs representing qubits inside the 4-anyon batches defined by the braids.

In quantum field theory the analog but not equivalent of this description would be following. Quite generally, a given particle in the final state has suffered a unitary transformation, which is an ordered product consisting of two kinds of unitary operators. Unitary single particle operators $U_n = Pexp(i \int_{t_n}^{t_{n+1}} H_0 dt)$ are analogs of operators describing single qubit gate and play the role of anyon propagators during no-swap periods. Two-particle unitary operators $U_{swap} = Pexp(i \int H_{swap} dt)$ are analogous to four-particle interactions and describe the effect of braid operations inducing entanglement of states having opposite values of topological charge but conserving the net topological charge of the anyon pair. This entanglement is completely analogous to spin entanglement. In particular, the braid operation mixes different states of the anyon. The unitary time development operator generating entangled state of anyons and defined by the braid structure represents the operation performed by the quantum circuit and the quantum measurement in the final state selects a particular final state.

5. Formally the computation halts with a measurement of the topological charge of the left-most anyon Cooper pair when the outcome is just single bit. If decay occurs with sufficiently high probability it is concluded that the value of the computed bit is 0, otherwise 1.

3.3 General implications of TGD for quantum computation

TGD based view about time and space-time could have rather dramatic implications for quantum computation in general and these implications deserve to be discussed briefly.

3.3.1 Time need not be a problem for quantum computations in TGD Universe

Communication with and control of the geometric past is the basic mechanism of intentional action, sensory perception, and long term memory in TGD inspired theory of consciousness. The possibility to send negative energy signals to the geometric past allows also instantaneous computations with respect to subjective time defined by a sequence of quantum jumps. The outcome of computation back to the past where it defines initial values of the next round of iteration. Time would cease to be a limiting factor to computation.

3.3.2 New view about information

The notion of information is very problematic even in the classical physics and in quantum realm this concept becomes even more enigmatic. TGD inspired theory consciousness has inspired number theoretic ideas about quantum information which are still developing. The standard definition of entanglement entropy relies on the Shannon's formula: $S = -\sum_k p_k log(p_k)$. This entropy is always non-negative and tells that the best one can achieve is entanglement with zero entropy.

The generalization of the notion of entanglement entropy to the p-adic context however led to realization that entanglement for which entanglement probabilities are rational or in an extension of rational numbers defining a finite extension of p-adics allows a hierarchy of entanglement entropies S_p labelled by primes. These entropies are defined as $S_p = -\sum_k p_k log(|p_k|_p)$, where $|p_k|_p$ denotes the p-adic norm of probability. S_p can be negative and in this case defines a genuine information measure. For given entanglement probabilities S_p has a minimum for some value p_0 of prime p, and S_{p_0} could be taken as a measure for the information carried by the entanglement in question whereas entanglement in real and p-adic continua would be entropic. The entanglement with negative entanglement entropy is identified as bound state entanglement.

Since quantum computers by definition apply states for which entanglement coefficients belong to a finite algebraic extension of rational numbers, the resulting states, if ideal, should be bound states. Also finite-dimensional extensions of p-adic numbers by transcendentals are possible. For instance, the extension by the $p-1$ first powers of e (e^p is ordinary p-adic number in R_p). As an extension of rationals this extension would be discrete but infinite-dimensional. Macro-temporal quantum coherence can be identified as being due to bound state formation in appropriate degrees of freedom and implying that state preparation and state function reduction effectively ceases to occur in these degrees of freedom.

Macro-temporal quantum coherence effectively binds a sequence of quantum jumps to single quantum jump so that the effective duration of unitary evolution is stretched from about 10^4 Planck times to arbitrary long time span. Also quantum computations can be regarded as this kind of extended moments of consciousness.

3.3.3 Number theoretic vision about quantum jump as a building block of conscious experience

The generalization of number concept resulting when reals and various p-adic number fields are fused to a book like structure obtaining by gluing them along rational numbers common to all these number fields leads to an extremely general view about what happens in quantum jump identified as basic building block of conscious experience. First of all, the unitary process U generates a formal superposition of states belonging to different number fields including their extensions. Negentropy Maximization Principle [44] constrains the dynamics of state preparation and state function reduction following U so that the final state contains only rational or extended rational entanglement with positive information content. At the level of conscious experience this process can be interpreted as a cognitive process or analysis leading to a state containing only bound state entanglement serving as a correlate for the experience of understanding. Thus quantum information science and quantum theory of consciousness seem to meet each other.

In the standard approach to quantum computing entanglement is not bound state entanglement. If bound state entanglement is really the entanglement which is possible for quantum computer, the entanglement of qubits might not serve as a universal entanglement currency. That is, the reduction of the general two-particle entanglement to entanglement between N qubits might not be possible in TGD framework.

The conclusion that only bound state entanglement is possible in quantum computation in human time scales is however based on the somewhat questionable heuristic assumption that subjective time has the same universal rate, that is the average increment Δt of the geometric time in single quantum jump does not depend on the space-time sheet, and is of order CP_2 time about 10^4 Planck times. The conclusion could be circumvented if one assumes that Δt depends on the space-time sheet involved: for instance, instead of CP_2 time Δt could be of order p-adic time scale T_p for a space-time sheet labelled by p-adic prime p and increase like $\sqrt{p}$. In this case the unitary operator defining quantum computation would be simply that defining the unitary process U.

3.3.4 Dissipative quantum parallelism?

The new view about quantum jump implies that state function reduction and preparation process decomposes into a hierarchy of these processes occurring in various scales: dissipation would occur in quantum parallel manner with each p-adic scale defining one level in the hierarchy. At space-time level this would correspond to almost independent quantum dynamics at parallel space-time sheets labelled by p-adic primes. In particular, dissipative processes can occur in short scales while the dynamics in longer scales is non-dissipative. This would explain why the description of hadrons as dissipative systems consisting of quarks and gluons in short scales is consistent with the description of hadrons as genuine quantum systems in long scales. Dissipative quantum parallelism would also mean that thermodynamics at shorter length scales would stabilize the dynamics at longer length scales and in this manner favor scaled up quantum coherence.

NMR systems [3] might represent an example about dissipative quantum parallelism. Room temperature NMR (nuclear magnetic resonance) systems use highly redundant replicas of qubits which have very long coherence times. Quantum gates using radio frequency pulses to modify the spin evolution have been implemented, and even effective Hamiltonians have been synthesized. Quantum

computations and dynamics of other quantum systems have been simulated and quantum error protocols have been realized. These successes are unexpected since the energy scale of cyclotron states is much below the thermal energy. This has raised fundamental questions about the power of quantum information processing in highly mixed states, and it might be that dissipative quantum parallelism is needed to explain the successes.

Magnetized systems could realize quite concretely the renormalization group philosophy in the sense that the magnetic fields due to the magnetization at the atomic space-time sheets could define a return flux along larger space-time sheets as magnetic flux quanta (by topological flux quantization) defining effective block spins serving as thermally stabilized qubits for a long length scale quantum parallel dynamics. For an external magnetic field $B \sim 10$ Tesla the magnetic length is $L \sim 10$ nm and corresponds to the p-adic length scale $L(k = 151)$. The induced magnetization is $M \sim n\mu^2 B/T$, where n is the density of nuclei and $\mu = ge/2m_p$ is the magnetic moment of nucleus. For solid matter density the magnetization is by a factor ~ 10 weaker than the Earth's magnetic field and corresponds to a magnetic length $L \sim 15$ μm: the p-adic length scale is around $L(171)$. For 10^{22} spins per block spin used for NMR simulations the size of block spin should be $\sim$ 1mm solid matter density so that single block spin would contain roughly 10^6 magnetization flux quanta containing 10^{16} spins each. The magnetization flux quanta serving as logical qubits could allow to circumvent the standard physics upper bound for scaling up of about 10 logical qubits [3] .

3.3.5 Negative energies and quantum computation

In TGD universe space-times are 4-surfaces so that negative energies are possible due to the fact that the sign of energy depends on time orientation (energy momentum tensor is replaced by a collection of conserved momentum currents). This has several implications. Negative energy photons having phase conjugate photons as physical correlates of photons play a key role in TGD inspired theory of consciousness and living matter and there are also indications that magnetic flux tubes structures with negative energies are important.

Negative energies makes possible communications to the geometric past, and time mirror mechanism involving generation of negative energy photons is the key mechanism of intentional action and plays central role in the model for the functioning of bio-systems. In principle this could allow to circumvent the problems due to the time required by computation by initiating computation in the geometric past and iterating this process. The most elegant and predictive cosmology is that for which the net conserved quantities of the universe vanish due the natural boundary condition that nothing flows into the future light cone through its boundaries representing the moment of big bang.

Also topological quantum field theories describe systems for which conserved quantities associated with the isometries of space-time, such as energy and momentum, vanish. Hence the natural question is whether negative energies making possible zero energy states might also make possible also zero energy quantum computations.

Crossing symmetry and Eastern and Western views about what happens in scattering

The hypothesis that all physical states have vanishing net quantum numbers (Eastern view) forces to interpret the scattering events of particle physics as quantum jumps between different vacua. This interpretation is in a satisfactory consistency with the assumption about existence of objective reality characterized by a positive energy (Western view) if crossing symmetry holds so that configuration space spinor fields can be regarded as S-matrix elements between initial state defined by positive energy particles and negative energy state defined by negative energy particles. As a matter fact, the proposal for the S-matrix of TGD at elementary particle level relies on this idea: the amplitudes for the transition from vacuum to states having vanishing net quantum numbers with positive and negative energy states interpreted as incoming and outgoing states are assumed to be interpretable as S-matrix elements.

More generally, one could require that scattering between any pair of states with zero net energies and representing S-matrix allows interpretation as a scattering between positive energy states. This requirement is satisfied if their exists an entire self-reflective hierarchy of S-matrices in the sense that the S-matrix between states representing S-matrices S_1 and S_2 would be the tensor product $S_1 \otimes S_2$. At the observational level the experience the usual sequence of observations $|m_1\rangle \to |m_2\rangle ..... \to |m_n\rangle ...$ based on belief about objective reality with non-vanishing conserved net quantum numbers would

correspond to a sequence $(|m_1 \to m_2\rangle \to |m_2 \to m_3\rangle ...$ between "self-reflective" zero energy states. These sequences are expected to be of special importance since the contribution of the unit matrix to S-matrix $S = 1+iT$ gives dominating contribution unless interactions are strong. This sequence would result in the approximation that $S_2 = 1 + iT_2$ in $S = S_1 \otimes S_2$ is diagonal. The fact that the scattering for macroscopic systems tends to be in forward direction would help to create the materialistic illusion about unique objective reality.

It should be possible to test whether the Eastern or Western view is correct by looking what happens strong interacting systems where the western view should fail. The Eastern view is consistent with the basic vision about quantum jumps between quantum histories having as a counterpart the change of the geometric past at space-time level.

Negative energy anti-fermions and matter-antimatter asymmetry

The assumption that space-time is 4-surface means that the sign of energy depends on time orientation so that negative energies are possible. Phase conjugate photons [25] are excellent candidates for negative energy photons propagating into geometric past.

Also the phase conjugate fermions make in principle sense and one can indeed perform Dirac quantization in four manners such that a) both fermions and anti-fermions have positive/negative energies, b) fermions (anti-fermions) have positive energies and anti-fermions (fermions) have negative energies. The corresponding ground state correspond to Dirac seas obtained by applying the product of a) all fermionic and anti-fermionic annihilation (creation) operators to vacuum, b) all fermionic creation (annihilation) operators and anti-fermionic annihilation (creation) operators to vacuum. The ground states of a) have infinite vacuum energy which is either negative or positive whereas the ground states of b) have vanishing vacuum energy. The case b) with positive fermionic and negative anti-fermionic energies could correspond to long length scales in which are matter-antisymmetric due to the effective absence of anti-fermions ("effective" meaning that no-one has tried to detect the negative energy anti-fermions). The case a) with positive energies could naturally correspond to the phase studied in elementary particle physics.

If gravitational and inertial masses have same magnitude and same sign, consistency with empirical facts requires that positive and negative energy matter must have been separated in cosmological length scales. Gravitational repulsion might be the mechanism causing this. Applying naively Newton's equations to a system of two bodies with energies $E_1 > 0$ and $-E_2 < 0$ and assuming only gravitational force, one finds that the sign of force for the motion in relative coordinates is determined by the sign of the reduced mass $-E_1E_2/(E_1 - E_2)$, which is negative for $E_1 > |E_2|$: positive masses would act repulsively on smaller negative masses. For $E_1 = -E_2$ the motion in the relative coordinate becomes free motion and both systems experience same acceleration which for E_1 corresponds to a repulsive force. The reader has probably already asked whether the observed acceleration of the cosmological expansion interpreted in terms of cosmological constant due to vacuum energy could actually correspond to a repulsive force between positive and negative energy matter.

It is possible to create pairs of positive energy fermions and negative energy fermions from vacuum. For instance, annihilation of photons and phase conjugate photons could create electron and negative energy positron pairs with a vanishing net energy. Magnetic flux tubes having positive and negative energies carrying fermions and negative energy positrons pairs of photons and their phase conjugates via fermion anti-fermion annihilation. The obvious idea is to perform zero energy topological quantum computations by using anyons of positive energy and anti-anyons of negative energy plus their Cooper pairs. This idea will be discussed later in more detail.

3.4 TGD based new physics related to topological quantum computation

For a long the belief was that absolute minimum property defines the basic dynamical principle of space-time physics. The reduction of the theory to the level of modified Dirac action [28] made it however clear that the preferred extremals defining the analogs of Bohr orbits must be critical in the sense of having an infinite number of deformations for which the second variation of Kähler action vanishes. The criticality of Kähler action would thus the basic dynamical principle of space-time dynamics. Purely number theoretic conditions in turn lead to the conclusion that space-time surfaces must be

hyper-quaternionic in the sense that the modified gamma matrices span hyper-quaternionic (asociative) or co-hyper-quaternionic (co-associative) plane at each point of the spacce-time surface. "Co-" means that the orthogonal complement of this plane is hyper-quaternionic (associative). Whether criticality and associativity (co-associativity) are consistent is not clear.

For a long time it remained an open question whether the known solutions of field equations are building blocks of preferred extremals of Kähler action or represent only the simplest extremals one can imagine and perhaps devoid of any real significance. Quantum-classical correspondence meant a great progress in the understanding the solution spectrum of field equations. Among other things, this principle requires that the dissipative quantum dynamics leading to non-dissipating asymptotic self-organization patterns should have the vanishing of the Lorentz 4-force as space-time correlate. The absence of dissipation in the sense of vanishing of Lorentz 4-force is a natural correlate for the absence of dissipation in quantum computations.

The vanishing of Lorentz 4-force generalizes the so called Beltrami conditions [19, 25] stating the vanishing of Lorentz force for purely magnetic field configurations and these conditions reduce in many cases to topological conditions. The study of classical field equations predicts three phases corresponding to non-vacuum solutions of field equations possessing vanishing Lorentz force. The dimension D of CP_2 projection of the space-time sheet serves as classifier of the phases.

1. $D = 2$ phase is analogous to ferro-magnetic phase possible in low temperatures and relatively simple, $D = 4$ phase is in turn analogous to a chaotic de-magnetized high temperature phase.

2. $D = 3$ phase represents spin glass phase, kind of boundary region between order and chaos possible in a finite temperature range and is an ideal candidate for the field body serving as a template for living systems. $D = 3$ phase allows infinite number of conserved topological charges having interpretation as invariants describing the linking of the magnetic field lines. This phase is also the phase in which topological quantum computations are possible.

3.4.1 Topologically quantized generalized Beltrami fields and braiding

From the construction of the solutions of field equations in terms topologically quantized fields it is obvious that TGD Universe is tailor made for TQC.

$D = 3$ phase allows infinite number of topological charges characterizing the linking of magnetic field lines

When space-time sheet possesses a $D = 3$-dimensional CP_2 projection, one can assign to it a non-vanishing and conserved topological charge characterizing the linking of the magnetic field lines defined by Chern-Simons action density $A \wedge dA/4\pi$ for induced Kähler form. This charge can be seen as classical topological invariant of the linked structure formed by magnetic field lines. For $D = 2$ the topological charge densities vanish identically, for $D = 3$ they are in general non-vanishing and conserved, whereas for $D = 4$ they are not conserved. The transition to $D = 4$ phase can thus be used to erase quantum computer programs realized as braids. The 3-dimensional CP_2 projection provides an economical manner to represent the braided world line pattern of dancers and would be the space where the 3-dimensional quantum field theory would be defined.

The topological charge can also vanish for $D = 3$ space-time sheets. In Darboux coordinates for which Kähler gauge potential reads as $A = P_k dQ^k$, the surfaces of this kind result if one has $Q^2 = f(Q^1)$ implying $A = f dQ^1$, $f = P_1 + P_2 \partial_{Q_1} Q^2$, which implies the condition $A \wedge dA = 0$. For these space-time sheets one can introduce Q^1 as a global coordinate along field lines of A and define the phase factor $exp(i \int A_\mu dx^\mu)$ as a wave function defined for the entire space-time sheet. This function could be interpreted as a phase of an order order parameter of super-conductor like state and there is a high temptation to assume that quantum coherence in this sense is lost for more general $D = 3$ solutions. Note however that in boundaries can still remain super-conducting and it seems that this occurs in the case of anyons.

Chern-Simons action is known as helicity in electrodynamics [22] . Helicity indeed describes the linking of magnetic flux lines as is easy to see by interpreting magnetic field as incompressible fluid flow having A as vector potential: $B = \nabla \times A$. One can write A using the inverse of $\nabla\times$ as $A = (1/\nabla\times)B$. The inverse is non-local operator expressible as

$$\frac{1}{\nabla\times}B(r) = \int dV' \frac{(r-r')}{|r-r'|^3} \times B(r') \quad ,$$

as a little calculation shows. This allows to write $\int A \cdot B$ as

$$\int dV A \cdot B = \int dV dV' B(r) \cdot \left(\frac{(r-r')}{|r-r'|^3} \times B(r') \right) \quad ,$$

which is completely analogous to the Gauss formula for linking number when linked curves are replaced by a distribution of linked curves and an average is taken.

For $D = 3$ field equations imply that Kähler current is proportional to the helicity current by a factor which depends on CP_2 coordinates, which implies that the current is automatically divergence free and defines a conserved charge for $D = 3$-dimensional CP_2 projection for which the instanton density vanishes identically. Kähler charge is not equal to the helicity defined by the inner product of magnetic field and vector potential but to a more general topological charge.

The number of conserved topological charges is infinite since the product of any function of CP_2 coordinates with the helicity current has vanishing divergence and defines a topological charge. A very natural function basis is provided by the scalar spherical harmonics of $SU(3)$ defining Hamiltonians of CP_2 canonical transformations and possessing well defined color quantum numbers. These functions define and infinite number of conserved charges which are also classical knot invariants in the sense that they are not affected at all when the 3-surface interpreted as a map from CP_2 projection to M^4_+ is deformed in M^4_+ degrees of freedom. Also canonical transformations induced by Hamiltonians in irreducible representations of color group affect these invariants via Poisson bracket action when the $U(1)$ gauge transformation induced by the canonical transformation corresponds to a single valued scalar function. These link invariants are additive in union whereas the quantum invariants defined by topological quantum field theories are multiplicative.

Also non-Abelian topological charges are well-defined. One can generalize the topological current associated with the Kähler form to a corresponding current associated with the induced electro-weak gauge fields whereas for classical color gauge fields the Chern-Simons form vanishes identically. Also in this case one can multiply the current by CP_2 color harmonics to obtain an infinite number of invariants in $D = 3$ case. The only difference is that $A \wedge dA$ is replaced by $Tr(A \wedge (dA + 2A \wedge A/3))$.

There is a strong temptation to assume that these conserved charges characterize colored quantum states of the conformally invariant quantum theory as a functional of the light-like 3-surface defining boundary of space-time sheet or elementary particle horizon surrounding wormhole contacts. They would be TGD analogs of the states of the topological quantum field theory defined by Chern-Simons action as highest weight states associated with corresponding Wess-Zumino-Witten theory. These charges could be interpreted as topological counterparts of the isometry charges of configuration space of 3-surfaces defined by the algebra of canonical transformations of CP_2.

The interpretation of these charges as contributions of light-like boundaries to configuration space Hamiltonians would be natural. The dynamics of the induced second quantized spinor fields relates to that of Kähler action by a super-symmetry, so that it should define super-symmetric counterparts of these knot invariants. The anti-commutators of these super charges would contribute to configuration space metric a part which would define a Kähler magnetic knot invariant. These Hamiltonians and their super-charge counterparts would be responsible for the topological sector of quantum TGD.

The color partial wave degeneracy of topological charges inspires the idea that also anyons could move in color partial waves identifiable in terms of "rigid body rotation" of the magnetic flux tube of anyon in CP_2 degrees of freedom. Their presence could explain non-Abelianity of Chern-Simons action and bring in new kind bits increasing the computational capacity of the topological quantum computer. The idea about the importance of macroscopic color is not new in TGD context. The fact that non-vanishing Kähler field is always accompanied by a classical color field (proportional to it) has motivated the proposal that colored excitations in macroscopic length scales are important in living matter and that colors as visual qualia correspond to increments of color quantum numbers in quantum phase transitions giving rise to visual sensations.

Knot theory, 3-manifold topology, and $D = 3$ solutions of field equations

Topological quantum field theory (TQFT) [29] demonstrates a deep connection between links and 3-topology, and one might hope that this connection could be re-interpreted in terms of imbeddings

of 3-manifolds to $H = M^4_+ \times CP_2$ as surfaces having 3-dimensional CP_2 projection, call it X^3 in the sequel. $D = 3$ suggests itself because in this case Chern-Simons action density for the induced Kähler field is generically non-vanishing and defines an infinite number of classical charges identifiable as Kähler magnetic canonical covariants invariant under $Diff(M^4_+)$. The field topology of Kähler magnetic field should be in a key role in the understanding of these invariants.

1. Could 3-D CP_2 projection of 3-surface provide a representation of 3-topology?

Witten-Chern-Simons theory for a given 3-manifold defines invariants which characterize both the topology of 3-manifold and the link. Why this is the case can be understood from the construction of 3-manifolds by drilling a tubular neighborhood of a link in S^3 and by gluing the tori back to get a new 3-manifolds. The links with some moves defining link equivalences are known to be in one-one correspondence with closed 3-manifolds and the axiomatic formulation of TQFT [29] as a modular functor clarifies this correspondence. The question is whether the CP_2 projection of the 3-surface could under some assumptions be represented by a link so that one could understand the connection between the links and topology of 3-manifolds.

In order to get some idea about what might happen consider the CP_2 projection X^3 of 3-surface. Assume that X^3 is obtained from S^3 represented as a 3-surface in CP_2 by removing from S^3 a tubular link consisting of linked and knotted solid tori $D^2 \times S^1$. Since the 3-surface is closed, it must have folds at the boundaries being thus representable as a two-valued map $S^3 \to M^4_+$ near the folds. Assume that this is the case everywhere. The two halves of the 3-surface corresponding to the two branches of the map would be glued together along the boundary of the tubular link by identification maps which are in the general case characterized by the mapping class group of 2-torus. The gluing maps are defined inside the overlapping coordinate batches containing the boundary $S^1 \times S^1$ and are maps between the pairs (Ψ_i, Φ_i), $i = 1, 2$ of the angular coordinates parameterizing the tori.

Define longitude as a representative for the $a + nb$ of the homology group of the 2-torus. The integer n defines so called framing and means that the longitude twists n times around torus. As a matter fact, TQFT requires bi-framing: at the level of Chern-Simons perturbation theory bi-framing is necessary in order to define self linking numbers. Define meridian as the generator of the homology group of the complement of solid torus in S^3. It is enough to glue the carved torus back in such a manner that meridian is mapped to longitude and longitude to minus meridian. This map corresponds to the $SL(2, C)$ element

$$\begin{pmatrix} 0 & 1 \\ -1 & 0 \end{pmatrix} .$$

Also other identification maps defined by $SL(2, Z)$ matrices are possible but one can do using only this. Note that the two component $SL(2, Z)$ spinors defined as superpositions of the generators (a, b) of the homology group of torus are candidates for the topological correlates of spinors. In the gluing process the tori become knotted and linked when seen in the coordinates of the complement of the solid tori.

This construction would represent the link surgery of 3-manifolds in terms of CP_2 projections of 3-surfaces of H. Unfortunately this representation does not seem to be the only one. One can construct closed three-manifolds also by the so called Heegaard splitting. Remove from S^3 D_g, a solid sphere with g handles having boundary S_g, and glue the resulting surface with its oppositely oriented copy along boundaries. The gluing maps are classified by the mapping class group of S_g. Any closed orientable 3-manifold can be obtained by this kind of procedure for some value of g. Also this construction could be interpreted in terms of a fold at the boundary of the CP_2 projection for a 2-valued graph $S^3 \to M^4_+$. Whether link surgery representation and Heegaard splitting could be transformed to each other by say pinching D_g to separate tori is not clear to me.

When the graph $CP_2 \to M^4_+$ is at most 2-valued, the intricacies due to the imbedding of the 3-manifold are at minimum, and the link associated with the projection should give information about 3-topology and perhaps even characterize it. Also the classical topological charges associated with Kähler Chern-Simons action could give this kind of information.

2. Knotting and linking for 3-surfaces

The intricacies related to imbedding become important in small co-dimensions and it is of considerable interest to find what can happen in the case of 3-surfaces. For 1-dimensional links and knots the projection to a plane, the shadow of the knot, characterizes the link/knot and allows to deduce

link and knot invariants purely combinatorially by gradually removing the intersection points and writing a contribution to the link invariant determined by the orientations of intersecting strands and by which of them is above the other. Thus also the generalization of knot and link diagrams is of interest.

Linking of m- and n-dimensional sub-manifolds of D-dimensional manifold H_D occurs when the condition $m+n=D-1$ holds true. The n-dimensional sub-manifold intersects $m+1$-dimensional surfaces having m-dimensional manifold as its boundary at discrete points, and it is usually not possible to remove these points by deforming the surfaces without intersections in some intermediate stage. The generalization of the link diagram results as a projection $D-1$-dimensional disk D^{D-1} of H_D.

3-surfaces link in dimension $D=7$ so that the linking of 3-surfaces occurs quite generally in time=constant section of the imbedding space. A link diagram would result as a projection to $E^2 \times CP_2$, E^2 a 2-dimensional plane: putting CP_2 coordinates constant gives ordinary link diagram in E^2. For magnetic flux tubes the reduction to 2-dimensional linking by idealizing flux tubes with 1-dimensional strings makes sense.

Knotting occurs in codimension 2 that is for an n-manifold imbedded in $D=n+2$-dimensional manifold. Knotting can be understood as follows. Knotted surface spans locally $n+1$-dimensional 2-sided n+1-disk D^{n+1} (disk for ordinary knot). The portion of surface going through D^{n+1} can be idealized with a 1-dimensional thread going through it and by $n+2=D$ knotting is locally linking of this 1-dimensional thread with n-dimensional manifold. N-dimensional knots define n+1-dimensional knots by so called spinning. Take an n-knot with the topology of sphere S^n such that the knotted part is above $n+1$-plane of $n+2$-dimensional space R^{n+2} ($z \geq 0$), cut off the part below plane ($z<0$), introduce an additional dimension (t) and make a 2π rotation for the resulting knot in $z-t$ plane. The resulting manifold is a knotted S^{n+1}. The counterpart of the knot diagram would be a projection to $n+1$-dimensional sub-manifold, most naturally disk D^{n+1}, of the imbedding space.

3-surfaces could become knotted under some conditions. Vacuum extremals correspond to 4-surfaces $X^4 \subset M^4_+ \times Y^2$ whereas the four-surfaces $X^4 \subset M^4_+ \times S^2$, S^2 homologically non-trivial geodesic sphere, define their own "sub-theory". In both cases 3-surfaces in time=constant section of imbedding space can get knotted in the sense that un-knotting requires giving up the defining condition temporarily. The counterpart of the knot diagram is the projection to $E^2 \times X^2$, $X^2=Y^2$ or S^2, where E^2 is plane of M^4_+. For constant values of CP_2 coordinates ordinary knot diagram would result. Reduction to ordinary knot diagrams would naturally occur for $D=2$ magnetic flux tubes. The knotting occurs also for 4-surfaces themselves in $M^4_+ \times X^2$: knot diagram is now defined as projection to $E^3 \times X^2$.

3. Could the magnetic field topology of 3-manifold be able to mimic other 3-topologies?

In $D=3$ case the topological charges associated with Kähler Chern-Simons term characterize the linking of the field lines of the Kähler gauge potential A. What $dA \wedge A \neq 0$ means that field lines are linked and it is not possible to define a coordinate varying along the field lines of A. This is impossible even locally since the $dA \wedge A \neq 0$ condition is equivalent with non existence of a scalar functions k and Φ such that $\nabla\Phi = kA$ guaranteing that Φ would be the sought for global coordinate.

One can idealize the situation a little bit and think of a field configuration for which magnetic flux is concentrated at one-dimensional closed lines. The vector potential would in this case be simply $A=\nabla(k\Psi+l\Phi)$, where Ψ is an angle coordinate around the singular line and Φ a coordinate along the singular circle. In this idealized situation the failure to have a global coordinate would be due to the singularities of otherwise global coordinates along one-dimensional linked and knotted circles. The reason is that the field lines of A and B rotate helically around the singular circle and the points (x,y,z) with constant values of x,y are on a helix which becomes singular at z-axis. Since the replacement of a field configuration with a non-singular field configuration but having same field line topology does not affect the global field line topology, one might hope of characterizing the field topology by its singularities along linked and knotted circles also in the general case.

Just similar linked and knotted circles are used to construct 3-manifolds in the link surgery which would suggest that the singularities of the field line topology of X^3 code the non-trivial 3-topology resulting when the singularities are removed by link surgery. Physically the longitude defining the framing $a+nb$ would correspond to the field line of A making an $n2\pi$ twist along the singular circle. Meridian would correspond to a circle in the plane of B. The bi-framing necessitated by TQFT would have a physical interpretation in terms of the helical field lines of A and B rotating around the singular

circle. At the level of fields the gluing operation would mean a gauge transformation such that the meridians would become the field lines of the gauge transformed A and being non-helical could be continued to the the interior of the glued torus without singularities. Simple non-helical magnetic torus would be in question.

This means that the magnetic field patterns of a given 3-manifold could mimic the topologies of other 3-manifolds. The topological mimicry of this kind would be a very robust manner to represent information and might be directly relevant to TQC. For instance, the computation of topological invariants of 3-manifold Y^3 could be coded by the field pattern of X^3 representing the link surgery producing the 3-manifold from S^3, and the physical realization of TQC program could directly utilize the singularities of this field pattern. Topological magnetized flux tubes glued to the back-ground 3-surface along the singular field lines of A could provide the braiding.

This mimicry could also induce transitions to the new topology and relate directly to 3-manifold surgery performed by a physical system. This transition would quite concretely mean gluing of simple $D = 2$ magnetic flux tubes along their boundaries to the larger $D = 3$ space-time sheet from which similar flux tube has been cut away.

4. A connection with anyons?

There is also a possible connection with anyons. Anyons are thought to correspond to singularities of gauge fields resulting in a symmetry breaking of gauge group to a finite subgroup H and are associated with homotopically non-trivial loops of $C_n = ((R^2)^n - D)/S_n$ represented as elements of H. Could the singularities of gauge fields relate to the singularities of the link surgery so that the singularities would be more or less identifiable as anyons? Could N-branched anyons be identified in terms of framings $a + Nb$ associated with the gluing map? $D = 3$ solutions allow the so called contact structure [8] , which means a decomposition of the coordinates of CP_2 projection to a longitudinal coordinate s and a complex coordinate w. Could this decomposition generalize the notion of effective 2-dimensionality crucial for the notion of anyon?

5. What about Witten's quantal link invariants?

Witten's quantal link invariants define natural multiplicative factors of configuration space spinor fields identifiable as representations of two 2-dimensional topological evolution. In Witten's approach these invariants are defined as functional averages of non-integrable phase factors associated with a given link in a given 3-manifold. TGD does not allow any natural functional integral over gauge field configurations for a fixed 3-surface unless one is willing to introduce fictive non-Abelian gauge fields. Although this is not a problem as such, the representation of the invariants in terms of inherent properties of the 3-surface or corresponding 4-surfaces would be highly desirable.

Functional integral representation is not the only possibility. Quantum classical correspondence combined with topological field quantization implied by the preferred extremal property generalizing Bohr rules to the field context gives hopes that the 3-surfaces themselves might be able to represent 3-manifold invariants classically. In $D = 3$ case the quantized exponents of Kähler-Chern-Simons action and $SU(2)_L$ Chern-Simons action could define 3-manifold invariants. These invariants would satisfy the obvious multiplicativity conditions and could correspond to the phase factors due to the framing dependence of Witten's invariants identifying the loops of surgery link as Wilson loops. These phase factors are powers of $U = exp(i2\pi c/24)$, where c is the central charge of the Virasoro representation defined by Kac Moody representation. One has $c = k \times dim(g)/(k + c_g/2)$, which gives $U = exp(i2\pi k/8(k+2))$ for $SU(2)$. The dependence on k differs from what one might naively expect. For this reason, and also because the classical Wilson loops do not depend explicitly on k, the value of k appearing in Chern-Simons action should be fixed by the internal consistency and be a constant of Nature according to TGD. The guess is that k possesses the minimal value $k = 3$ allowing a universal modular functor for $SU(2)$ with $q = exp(i2\pi/5)$.

The loops associated with the topological singularities of the Kähler gauge potential (typically the center lines of helical field configurations) would in turn define natural Wilson loops, and since the holonomies around these loops are also topologically quantized, they could define invariants of 3-manifolds obtained by performing surgery around these lines. The behavior of the induced gauge fields should be universal near the singularities in the sense that the holonomies associated with the CP_2 projections of the singularities to CP_2 would be universal. This expectation is encouraged by the notion of quantum criticality in general and in particular, by the interpretation of $D = 3$ phase as a critical system analogous to spin glass.

The exponent of Chern-Simons action can explain only the phase factors due to the framing, which are usually regarded as an unavoidable nuisance. This might be however all that is needed. For the manifolds of type $X^2 \times S^1$ all link invariants are either equal to unity or vanish. Surgery would allow to build 3-manifold invariants from those of $S^2 \times S^1$. For instance, surgery gives the invariant $Z(S^3)$ in terms of $Z(S^2 \times S^1, R_i)$ and mapping class group action coded into the linking of the field lines.

Holonomies can be also seen as multi-valued $SU(2)_L$ gauge transformations and can be mapped to a multi-valued transformations in the $SU(2)$ subgroup of $SU(3)$ acting on 3-surface as a geometric transformations and making it multi-branched. This makes sense if the holonomies define a finite group so that the gauge transformation is finitely many-valued. This description might apply to the 3-manifold resulting in a surgery defined by the Wilson loops identifiable as branched covering of the initial manifold.

The construction makes also sense for the holonomies defined by the classical $SU(3)$ gauge fields defined by the projections of the isometry currents. Furthermore, the fact that any CP_2 Hamiltonian defines a conserved topological charge in $D = 3$ phase should have a deep significance. At the level of the configuration space geometry the finite-dimensional group defining Kac Moody algebra is replaced with the group of canonical transformations of CP_2. Perhaps one could extend the notion of Wilson loop for the algebra of canonical transformations of CP_2 so that the representations R_i of the gauge group would be replaced by matrix representations of the canonical algebra. That the trace of the identity matrix is infinite in this case need not be a problem since one can simply redefine the trace to have value one.

Braids as topologically quantized magnetic fields

$D = 3$ space-time sheets would define complex braiding structures with flux tubes possessing infinite number of topological charges characterizing the linking of field lines. The world lines of the quantum computing dancers could thus correspond to the flux tubes that can get knotted, linked, and braided. This idea conforms with the earlier idea that the various knotted and linked structures formed by linear bio-molecules define some kind of computer programs.

1. Boundaries of magnetic flux tubes as light-like 3-surfaces

Field equations for Kähler action are satisfied identically at boundaries if the boundaries of magnetic flux tubes (and space-time sheet in general) are light-like in the induced metric. In M^4_+ metric the flux tubes could look static structures. Light-likeness allows an interpretation of the boundary state either as a 3-dimensional quantum state or as a time-evolution of a 2-dimensional quantum state. This conforms with the idea that quantum computation is cognitive, self reflective process so that quantum state is about something rather than something. There would be no need to force particles to flow through the braid structure to build up time-like braid whereas for time-like boundaries of magnetic flux tubes a time-like braid results only if the topologically charged particles flow through the flux tubes with the same average velocity so that the length along flux tubes is mapped to time.

Using the terminology of consciousness theory, one could say that during quantum dance the dancers are in trance being entangled to a single macro-temporally coherent state which represents single collective consciousness, and wake up to individual dancers when the dance ends. Quantum classical correspondence suggests that the generation of bound state entanglement between dancers requires tangled join along boundaries bonds connecting the space-time sheets of anyons (braid of flux tubes again!): dancers share mental images whereas direct contact between magnetic flux tubes defining the braid is not necessary. The bound state entanglement between sub-systems of unentangled systems is made possible by the many-sheeted space-time. This kind of entanglement could be interpreted as entanglement not visible in scales of larger flux tubes so that the notion is natural in the philosophy based on the idea of length scale resolution.

2. How braids are generated?

The encoding of the program to a braid could be a mechanical process: a bundle of magnetic flux tubes with one end fixed would be gradually weaved to a braid by stretching and performing the needed elementary twists. The time to perform the braiding mechanically requires classical computer program and the time needed to carry out the braiding depends polynomially on the number of strands.

The process could also occur by a quantum jump generating the braided flux tubes in single flash

and perhaps even intentionally in living systems (flux tubes with negative topological charge could have negative energy so that it would require no energy to generate the structure from vacuum). The interaction with environment could be used to select the desired braids. Also ensembles of braids might be imagined. Living matter might have discovered this mechanism and used int intentionally.

3. Topological quantization, many-sheetedness, and localization

Localization of modular functors is one of the key problems in topological quantum computation (see the article of Freedman [13] . For anyonic computation this would mean in the ideal case a decomposition of the system into batches containing 4 anyons each so that these anyon groups interact only during swap operations.

The role of topological quantization would be to select of a portion of the magnetic field defining the braid as a macroscopic structure. Topological field quantization realizes elegantly the requirement that single particle time evolutions between swaps involve no interaction with other anyons.

Also many-sheetedness is important. The (AA) pair and two anyons would correspond braids inside braids and as it turns out this gives more flexibility in construction of quantum computation since the 1-gates associated with logical qubits of 4-batch can belong to different representation of braid group than that associated with braiding of the batches.

3.4.2 Quantum Hall effect and fractional charges in TGD

In fractional QH effect anyons possess fractional electromagnetic charges. Also fractional spin is possible. TGD explains fractional charges as being due to multi-branched character of space-time sheets. Also the Z_n-valued topological charge associated with anyons has natural explanation.

Basic TGD inspired ideas about quantum Hall effect

Quantum Hall effect is observed in low temperature systems when the intensity of a strong magnetic field perpendicular to the current carrying slab is varied adiabatically. Classically quantum Hall effect can be understood as a generation of a transversal electric field, which exactly cancels the magnetic Lorentz force. This gives $E = -j \times B/ne$. The resulting current can be also understood as due to a drift velocity proportional to $E \times B$ generated in electric and magnetic fields orthogonal to each other and allowing to cancel Lorentz force. This picture leads to the classical expression for transversal Hall conductivity as $\sigma_{xy} = ne/B$. σ_{xy} should vary continuously as a function of the magnetic field and 2-dimensional electron density n.

In quantum Hall effect σ_{xy} is piece-wise constant and quantized with relative precision of about 10^{-10}. The second remarkable feature is that the longitudinal conductivity σ_{xx} is very high at plateaus: variations by 13 orders of magnitude are observed. The system is also very sensitive to small perturbations.

Consider now what these qualitative observations might mean in TGD context.

1. Sensitivity to small perturbations means criticality. TGD Universe is quantum critical and quantum criticality reduces to the spin glass degeneracy due to the enormous vacuum degeneracy of the theory. The $D = 2$ and $D = 3$ non-vacuum phases predicted by the generalized Beltrami ansatz are this in-stability might play important role in the effect.

2. The magnetic fields are genuinely classical fields in TGD framework, and for $D = 2$ proportional to induced Kähler magnetic field. The canonical symmetries of CP_2 act like $U(1)$ gauge transformations on the induced gauge field but are not gauge symmetries since canonical transformations change the shape of 3-surface and affect both classical gravitational fields and electro-weak and color gauge fields. Hence different gauges for classical Kähler field represent magnetic fields for which topological field quanta can have widely differing and physically non-equivalent shapes. For instance, tube like quanta act effectively as insulators whereas magnetic walls parallel to the slab act as conducting wires.

   Wall like flux tubes parallel to the slab perhaps formed by a partial fusion of magnetic flux tubes along their boundaries would give rise to high longitudinal conductivity. For disjoint flux tubes the motion would be around the flux tubes and the electrons would get stuck inside these tubes. By quantum criticality and by $D < 4$ property the magnetic flux tube structures are

unstable against perturbations, in particular the variation of the magnetic field strength itself. The transitions from a plateau to a new one would correspond to the decay of the magnetic walls back to disjoint flux tubes followed by a generation of walls again so that conductivity is very high outside transition regions. The variation of any parameter, such as temperature, is expected to be able to cause similar effects implying dramatic changes in Hall conductivity.

The percolation model for the quantum Hall effect represents slab as a landscape with mountains and valleys and the varied external parameter, say B or free electron density, as the sea level. For the critical values of sea level narrow regions carrying so called edge states allow liquid to fill large regions appear and implies increase of conductivity. Obviously percolation model differs from the model based on criticality for which the landscape itself is highly fragile and a small perturbation can develop new valleys and mountains.

3. The effective 2-dimensionality implies that the solutions of Schrödinger equation of electron in external magnetic field are products of any analytic function with a Gaussian representing the ground state of a harmonic oscillator. Analyticity means that the kinetic energy is completely degenerate for these solutions. The Lauhglin ansatz for the state functions of electron in the external magnetic field is many-electron generalization of these solutions: the wave functions consists of products of terms of form $(z_i - z_j)^m$, m odd integer from Fermi statistics.

   The N-particle variant of Laughlin's ansatz allows to deduce that the system is incompressible. The key observation is that the probability density for the many-particle state has an interpretation as a Boltzmann factor for a fictive two-dimensional plasma in electric field created by constant charge density [12, 15] . The probability density is extremely sensitive to the changes of the positions of electrons giving rise to the constant electron density. The screening of charge in this fictive plasma implies the filling fraction $\nu = 1/m$, m odd integer and requires charge fractionization $e \to e/m$. The explanation of the filling fractions $\nu = N/m$ would require multi-valued wave functions $(z_i - z_j)^{N/m}$. In single-sheeted space-time this leads to problems. TGD suggests that these wave functions are single valued but defined on N-branched surface.

   The degeneracy with respect to kinetic energy brings in mind the spin glass degeneracy induced by the vacuum degeneracy of the Kähler action. The Dirac equation for the induced spinors is not ordinary Dirac equation but super-symmetrically related to the field equations associated with Kähler action. Also it allows vacuum degeneracy. One cannot exclude the possibility that also this aspect is involved at deeper level.

4. The fractionization of charge in quantum Hall effect challenges the idea that charged particles of the incompressible liquid are electrons and this leads to the notion of anyon. Quantum-classical correspondence inspires the idea that although dissipation is absent, it has left its signature as a track associated with electron. This track is magnetic flux tube surrounding the classical orbit of electron and electron is confined inside it. This reduces the dissipative effects and explains the increase of conductivity. The rule that there is single electron state per magnetic flux quantum follows if Bohr quantization is applied to the radii of the orbits. The fractional charge of anyon would result from a contribution of classical Kähler charge of anyon flux tube to the charge of the anyon. This charge is topologized in $D = 3$ phase.

Anyons as multi-branched flux tubes representing charged particle plus its track

Electrons (in fact, any charged particles) moving inside magnetic flux tubes move along circular paths classically. The solutions of the field equations with vanishing Lorentz 4-force correspond to asymptotic patterns for which dissipation has already done its job and is absent. Dissipation has however definite effects on the final state of the system, and one can argue that the periodic motion of the charged particle has created what might called its "track". The track would be realized as a circular or helical flux tube rotating around field lines of the magnetic field. The corresponding cyclotron states would be localized inside tracks. Simplest tracks are circular ones and correspond to absence of motion in the direction of the magnetic field. Anyons could be identified as systems formed as particles plus the tracks containing them.

1. *Many-branched tracks and approach to chaos*

When the system approaches chaos one expects the the periodic circular tracks become non-periodic. One however expects that this process occurs in steps so that the tracks are periodic in the sense that they close after N 2π rotations with the value of N increasing gradually. The requirement that Kähler energy stays finite suggests also this. A basic example of this kind of track is obtained when the phase angles Ψ and Φ of complex CP_2 coordinates (ξ^1, ξ^2) have finitely multi-valued dependence on the coordinate ϕ of cylindrical coordinates: $(\Psi, \Phi) = (m_1/N, m_2/N)\phi$). The space-sheet would be many-branched and it would take N turns of 2π to get back to the point were one started. The phase factors behave as a phase of a spinning particle having effective fractional spin $1/N$. I have proposed this kind of mechanism as an explanation of so called hydrino atoms claimed to have the spectrum of hydrogen atom but with energies scaled up by N^2 [76] , [10] . The first guess that N corresponds to m in $\nu = 1/m$ is wrong. Rather, N corresponds to N in $\nu = N/m$ which means many-valued Laughlin wave functions in single branched space-time.

Similar argument applies also in CP_2 degrees of freedom. Only the N-multiples of 2π rotations by CP_2 isometries corresponding to color hyper charge and color iso-spin would affect trivially the point of multi-branched surface. Since the contribution of Kähler charge to electromagnetic charge corresponds also to anomalous hyper-charge of spinor field in question, an additional geometric contribution to the anomalous hypercharge would mean anomalous electromagnetic charge.

It must be emphasized the fractionization of the isometry charges is only effective and results from the interpretation of isometries as space-time transformations rather than transformation rotating entire space-time sheet in imbedding space. Also classical charges are effectively fractionized in the sense that single branch gives in a symmetric situation a fraction of $1/n$ of the entire charge. Later it will be found that also a genuine fractionization occurs and is due to the classical topologized Kähler charge of the anyon track.

2. Modelling anyons in terms of gauge group and isometry group

Anyons can be modelled in terms of the gauge symmetry breaking $SU(2)_L \to H$, where H is discrete sub-group. The breaking of gauge symmetry results by the action of multi-valued gauge transformation $g(x)$ such that different branches of the multi-valued map are related by the action of H.

1. The standard description of anyons is based on spontaneous symmetry breaking of a gauge symmetry G to a discrete sub-group H dynamically [10] . The gauge field has suffered multi-valued gauge transformation such that the elements of H permute the different branches of $g(x)$. The puncture is characterized by the element of the H associated with the loop surrounding puncture. In the idealized situation that gauge field vanishes, the parallel translation of a particle around puncture affects the particle state, itself a representation of G, by the element of the homotopy $\pi_1(G/H) = H$ identifiable as non-Abelian magnetic charge. Thus holonomy group corresponds to homotopy group of G/H which in turn equals to H. This in turn implies that the infinite-dimensional braid group whose elements define holonomies in turn is represented in H.

2. In TGD framework the multi-valuedness of $g(x)$ corresponds to a many-branched character of 4-surface. This in turn induces a branching of both magnetic flux tube and anyon tracks describable in terms of $H \subset SU(2)_L$ acting as an isotropy group for the boundaries of the magnetic flux tubes. H can correspond only to a non-Abelian subgroup $SU(2)_L$ of the electro-weak gauge group for the induced (classical) electro-weak gauge fields since the Chern-Simons action associated with the classical color gauge fields vanishes identically. The electro-weak holonomy group would reduce to a discrete group H around loops defined by anyonic flux tubes surrounding magnetic field lines inside the magnetic flux tubes containing anyons. The reduction to H need to occur only at the boundaries of the space-time sheet where conducting anyons would reside: boundaries indeed correspond to asymptotia in well-defined sense. Electro-weak symmetry group can be regarded as a sub-group of color group of isometries in a well-defined sense so that H can be regarded also as a subgroup of color group acting as isotropies of the multi-branched surface at least in the in regions where gauge field vanishes.

3. For branched surfaces the points obtained by moving around the puncture correspond in a good approximation to some elements of $h \in H$ leading to a new branch but the 2-surface as a whole however remains invariant. The braid group of the punctured 2-surface would be also

now represented as transformations of H. The simplest situation is obtained when H is a cyclic group Z_N of the $U(1)$ group of CP_2 geodesic in such a manner that 2π rotation around symmetry axis corresponds to the generating element $exp(i2\pi/N)$ of Z_N.

Dihedral group D_n having order $2n$ and acting as symmetries of n-polygon of the plane is especially interesting candidate for H. For $n = 2$ the group is Abelian group $Z_2 \times Z_2$ whereas for $n > 2$ D_n is a non-Abelian sub-group of the permutation group S_n. The cyclic group Z_4 crucial for TQC is a sub-group of D_4 acting as symmetries of square. D_4 has a 2-dimensional faithful representation. The numbers of elements for the conjugacy classes are 1,1,2,2,2. The sub-group commuting with a fixed element of a conjugacy class is D_4 for the 1-element conjugacy classes and cyclic group Z_4 for 2-element conjugacy classes. Hence 2-valued magnetic flux would be accompanied by Z_4 valued "electric charge" identifiable as a cyclic group permuting the branches.

3. Can one understand the increase in conductivity and filling fractions at plateaus?

Quantum Hall effect involves the increase of longitudinal conductivity by a factor of order 10^{13} [12] . The reduction of dissipation could be understood as being caused by the fact that anyonic electrons are closed inside the magnetic flux tubes representing their tracks so that their interactions with matter and thus also dissipation are reduced.

Laughlin's theory [12, 15] gives almost universal description of many aspects of quantum Hall effect and the question arises whether Laughlin's wave functions are defined on possibly multi-branched space-time sheet X^4 or at projection of X^4 to M^4_+. Since most theoreticians that I know still live in single sheeted space-time, one can start with the most conservative assumption that they are defined at the projection to M^4_+. The wave functions of one-electron state giving rise filling fraction $\nu = 1/m$ are constructed of $(z_i - z_j)^m$, where m is odd by Fermi statistics.

Also rational filling fractions of form $\nu = 1/m = N/n$ have been observed. These could relate to the presence of states whose projections to M^4 are multi-valued and which thus do not have any "classical" counterpart. For N-branched surface the single-valued wave functions $(\xi_i - \xi_j)^n$, n odd by Fermi statistics, correspond to apparently multi-valued wave functions $(z_i - z_j)^{n/N}$ at M^4 projection with fractional relative angular momenta $m = n/N$. The filling fraction would be $\nu = N/n$, n odd. All filling fractions reported in [12] have n odd with n varying in the range $1 - 7$. N has the values $1, 2, 3, 4, 5, 7, 9$. Also values $N = 12, 13$ for which $n = 5$ are reported [21] .

The filling fractions $\nu = N/n = 5/2, 3/8, 3/10$ reported in [5] would require even values of n conflicting with Fermi statistics. Obviously Lauhglin's model fails in this case and the question is whether one these fractions could correspond to bosonic anyons, perhaps Cooper pairs of electrons inside track flux tubes. The Z_N valued charge associated with N-branched surfaces indeed allows the maximum $2N$ electrons per anyon. Bosonic anyons are indeed the building block of the TQC model of [21] . The anyon Cooper pairs could be this kind of states and their BE condensation would make possible genuine super-conductivity rather than only exceptionally high value of conductivity.

One can imagine also more complex multi-electron wave functions than those of Laughlin. The so called conformal blocks representing correlation functions of conformal quantum field theories are natural candidates for the wave functions [21] and they appear naturally as state functions of in topological quantum field theories. For instance, wave functions which are products of factors $(z^k - z^l)^2$ with the Pfaffian $Pf(A_{kl})$ of the matrix $A_{kl} = 1/(z_k - z_l)$ guaranteing anti-symmetrization have been used to explain even values of m [21] .

4. N-branched space-time surfaces make possible Z_N valued topological charge

According to [21] that $2n$ non-Abelian anyon pairs with charge 1/4 created from vacuum gives rise to a 2^{n-1}-fold degenerate ground state. It is also argued that filling fraction 5/2 could correspond to this charge [21] . TGD suggests somewhat different interpretation. 4-fold branching implies automatically the Z_4-valued topological charge crucial for anyonic quantum computation. For 4-branched space-time surface the contribution of a single branch to electron's charge is indeed 1/4 units but this has nothing to do with the actual charge fractionization. The value of ν is of form $\nu = /m$ and electromagnetic charge equals to $\nu = 4e/m$ in this kind of situation.

If anyons (electron plus flux tube representing its track) have Z_4 charges 1 and 3, their Cooper pairs have charges 0 and 2. The double-fold degeneracy for anyon's topological charge means that it possesses topological spin conserved modulo 4. In presence of $2n$ anyon pairs one would expect

2^n-fold degeneracy. The requirement that the net topological charge vanishes modulo 4 however fixes the topological charge of n:th pair so that 2^{n-1} fold degeneracy results.

A possible interpretation for Z_N-valued topological charge is as fractional angular momenta k/N associated with the phases $exp(ik2\pi/N)$, $k = 0, 1, ..., n-1$ of particles in multi-branched surfaces. The projections of these wave functions to single-branched space-time would be many-valued. If electroweak gauge group breaks down to a discrete subgroup H for magnetic flux tubes carrying anyonic "tracks", this symmetry breakdown could induce their multi-branched property in the sense rotation by 2π would correspond to H isometry leading to a different branch.

Topologization of Kähler charge as an explanation for charge fractionization

The argument based on what happens when one adds one anyon to the anyon system by utilizing Faraday's law [12] leads to the conclusion that anyon charge is fractional and given by νe. The anyonic flux tube along boundary of the flux tube corresponds to the left hand side in the Faraday's equation

$$\oint E \cdot dl = -\frac{d\Phi}{dt} \quad .$$

By expressing E in turns of current using transversal conductivity and integrating with respect to time, one obtains

$$Q = \nu e$$

for the charge associated with a single anyon. Hence the addition of the anyon means an addition of a fractional charge νe to the system. This argument should survive as such the 1-branched situation so that at least in this case the fractional charges should be real.

In N-branched case the closed loop $\oint E \cdot dl$ around magnetic flux tube corresponds to N-branched anyon and surrounds the magnetic flux tube N times. This would suggest so that net magnetic flux should be N times the one associated with single but unclosed 2π rotation. Hence the formula would seem to hold true as such also now for the total charge of the anyon and the conclusion is that charge fractionization is real and cannot be an effective effect due to fractionization of charge at single branch of anyon flux tube.

One of the basic differences between TGD and Maxwell's theory is the possibility of vacuum charges and this provides an explanation of the effect is in terms of vacuum Kähler charge. Kähler charge contributes $e/2$ to the charge of electron. Anyon flux tube can generate vacuum Kähler charge changing the net charge of the anyon. If the anyon charge equals to νe the conclusions are following.

1. The vacuum Kähler charge of the anyon track is $q = (\nu - 1)e$.

2. The dimension of the CP_2 projection of the anyon flux tube must be $D = 3$ since only in this case the topologization of anyon charge becomes possible so that the charge density is proportional to the Chern-Simons term $A \wedge dA/4\pi$. Anyon flux tubes cannot be super-conducting in the sense that non-integrable phase factor $exp(\int A \cdot dl)$ would define global order parameter. The boundaries of anyonic flux tubes could however remain potentially super-conducting and anyon Cooper pairs would be expelled there by Meissner effect. This gives super-conductivity in length scale of single flux tube. Conductivity and super-conductivity in long length scales requires that magnetic flux tubes are glued together along their boundaries partially.

3. By Bohr quantization anyon tracks can have $r_n = \sqrt{n} \times r_B$, $n \leq m$, where r_m corresponds to the radius of the magnetic flux tube carrying m flux quanta. Only the tracks with radius r_m contribute to boundary conductivity and super-conductivity giving $\nu = 1/m$ for singly branched surfaces.

   The states with $\nu = N/m$ cannot correspond to non-super-conducting anyonic tracks with radii r_n, $n < m$, n odd, since these cannot contribute to boundary conductivity. The many-branched character however allows an N-fold degeneracy corresponding to the fractional angular momentum states $exp(ik\phi/N)$, $k = 0, ..., N-1$ of electron inside anyon flux tubes of radius r_m. k is obviously a an excellent candidate for the Z_N-valued topological charge crucial for anyonic quantum computation. Z_4 is uniquely selected by the braid matrix R.

Only part of the anyonic Fermi sea need to be filled so that filling fractions $\nu = k/m$, $k = 1, ..., N$ are possible. Charges νe are possible if each electron inside anyon track contributes $1/m$ units to the fractional vacuum Kähler charge. This is achieved if the radius of the anyonic flux tube grows as $\sqrt{k/m}$ when electrons are added. The anyon tracks containing several electrons give rise to composite fermions with fermion number up to $2N$ if both directions of electron spin are allowed.

4. Charge fractionization requires vacuum Kähler charge has rational values $Q_K = (\nu - 1)e$. The quantization indeed occurs for the helicity defined by Chern-Simons term $A \wedge dA/4\pi$. For compact 3-spaces without boundary the helicity can be interpreted as an integer valued invariant characterizing the linking of two disjoint closed curves defined by the magnetic field lines. This topological charge can be also related to the asymptotic Hopf invariant proposed by Arnold [4] , which in non-compact case has a continuum of values. Vacuum Kähler current is obtained from the topological current $A \wedge dA/4\pi$ by multiplying it with a function of CP_2 coordinates completely fixed by the field equations. There are thus reasons to expect that vacuum Kähler charge and also the topological charges obtained by multiplying Chern Simons current by $SU(3)$ Hamiltonians are quantized for compact 3-surfaces but that the presence of boundaries replaces integers by rationals.

What happens in quantum Hall system when the strength of the external magnetic field is increased?

The proposed mechanism of anyonic conducitivity allows to understand what occurs in quantum Hall system when the intensity of the magnetic field is gradually increased.

1. Percolation picture encourages to think that magnetic flux tubes fuse partially along their boundaries in a transition to anyon conductivity so that the anyonic states localized at the boundaries of flux tubes become delocalized much like electrons in metals. Laughlin's states provide an idealized description for these states. Also anyons, whose tracks have Bohr radii r_m smaller than the radius r_B of the magnetic flux tube could be present but they would not participate in this localization. Clearly, the anyons at the boundaries of magnetic flux tubes are highly analogous to valence electrons in atomic physics.

2. As the intensity of the magnetic field B increases, the areas a of the flux tubes decreases as $a \propto 1/B$: this means that the existing contacts between neighboring flux tubes tend to be destroyed so that anyon conductivity is reduced. On the other hand, new magnetic flux tubes must emerge by the constancy of the average magnetic flux implying $dn/da \propto B$ for the average density of flux tubes. This increases the probability that the newly generated flux tubes can partially fuse with the existing flux tubes.

3. If the flux tubes are not completely free to move and change their shape by area preserving transformations, one can imagine that for certain value ranges of B the generation of new magnetic flux tubes is not favored since there is simply no room for the newcomers. The Fermi statistics of the anyonic electrons at the boundaries of flux tubes might relate to this non-hospitable behavior. At certain critical values of the magnetic field the sizes of flux tubes become however so small that the situation changes and the new flux tubes penetrate the system and via the partial fusion with the existing flux tubes increase dramatically the conductivity.

Also protonic anyons are possible

According to the TGD based model, any charged particle can form anyons and the strength of the magnetic field does not seem to be crucial for the occurrence of the effect and it could occur even in the Earth's magnetic field. The change of the cyclotron and Larmor frequencies of the charged particle in an external magnetic field to a value corresponding to the fractional charge provides a clear experimental signature for both the presence of anyons and for their the fractional charge.

Interestingly, water displays a strange scaling of proton's cyclotron frequency in an external magnetic field [24] , [42] . In an alternating magnetic field of .1551 Gauss (Eearth's field has a nominal value of .58 Gauss) a strong absorption at frequency $f = 156$ Hz was observed. The frequency was

halved when D_2O was used and varied linearly with the field strength. The resonance frequency however deviated from proton's Larmor frequency, which suggests that a protonic anyon is in question. The Larmor frequency would be in this case $f_L = r \times \nu eB/2m_p$, where $r = \mu_p/\mu_B = 2.2792743$ is the ratio of proton's actual magnetic moment to its value for a point like proton. The experimental data gives $\nu = .6003 = 3/5$ with the accuracy of 5×10^{-4} so that 3-branched protonic anyons with $m = 5$ would be responsible for the effect.

If this interpretation is correct, entire p-adic hierarchy of anyonic NMR spectroscopies associated with various atomic nuclei would become possible. Bosonic anyon atoms and Cooper pairs of fermionic anyon atom could also form macroscopic quantum phases making possible super-conductivity very sensitive to the value of the average magnetic field and bio-systems and brain could utilize this feature.

3.4.3 Does the quantization of Planck constant transform integer quantum Hall effect to fractional quantum Hall effect?

The model for topological quantum computation inspired the idea that Planck constant might be dynamical and quantized. The work of Nottale [10] gave a strong boost to concrete development of the idea and it took year and half to end up with a proposal about how basic quantum TGD could allow quantization Planck constant associated with M^4 and CP_2 degrees of freedom such that the scaling factor of the metric in M^4 degrees of freedom corresponds to the scaling of $\hbar$ in CP_2 degrees of freedom and vice versa [27] . The dynamical character of the scaling factors of M^4 and CP_2 metrics makes sense if space-time and imbedding space, and in fact the entire quantum TGD, emerge from a local version of an infinite-dimensional Clifford algebra existing only in dimension $D = 8$ [83] .

The predicted scaling factors of Planck constant correspond to the integers n defining the quantum phases $q = exp(i\pi/n)$ characterizing Jones inclusions. A more precise characterization of Jones inclusion is in terms of group $G_b \subset SU(2) \subset SU(3)$ in CP_2 degrees of freedom and $G_a \subset SL(2, C)$ in M^4 degrees of freedom. In quantum group phase space-time surfaces have exact symmetry such that to a given point of M^4 corresponds an entire G_b orbit of CP_2 points and vice versa. Thus space-time sheet becomes $N(G_a)$ fold covering of CP_2 and $N(G_b)$-fold covering of M^4. This allows an elegant topological interpretation for the fractionization of quantum numbers. The integer n corresponds to the order of maximal cyclic subgroup of G.

In the scaling $\hbar_0 \to n\hbar_0$ of M^4 Planck constant fine structure constant would scale as

$$\alpha = \frac{e^2}{4\pi\hbar c} \to \frac{\alpha}{n} \quad ,$$

and the formula for Hall conductance would transform to

$$\sigma_H \to \frac{\nu}{n}\alpha \quad .$$

Fractional quantum Hall effect would be integer quantum Hall effect but with scaled down α. The apparent fractional filling fraction $\nu = m/n$ would directly code the quantum phase $q = exp(i\pi/n)$ in the case that m obtains all possible values. A complete classification for possible phase transitions yielding fractional quantum Hall effect in terms of finite subgroups $G \subset SU(2) \subset SU(3)$ given by ADE diagrams would emerge (A_n, D_{2n}, E_6 and E_8 are possible). What would be also nice that CP_2 would make itself directly manifest at the level of condensed matter physics.

3.4.4 Why 2+1-dimensional conformally invariant Witten-Chern-Simons theory should work for anyons?

Wess-Zumino-Witten theories are 2-dimensional conformally invariant quantum field theories with dynamical variables in some group G. The action contains the usual 2-dimensional kinetic term for group variables allowing conformal group action as a dynamical symmetry plus winding number defined associated with the mapping of 3-surface to G which is $Diff^4$ invariant. The coefficient of this term is quantized to integer.

If one couples this theory to a gauge potential, the original chiral field can be transformed away and only a Chern-Simons term defined for the 3-manifold having the 2-dimensional space as boundary remains. Also the coefficient k of Chern-Simons term is quantized to integer. Chern-Simons-Witten

action has close connection with Wess-Zumino-Witten theory. In particular, the states of the topological quantum field theory are in one-one correspondence with highest weights of the WZW action.

The appearance of 2+1-dimensional $Diff^3$ invariant action can be understood from the fundamentals of TGD.

1. Light-like 3-surfaces of both future light-cone M^4_+ and of space-time surface X^4 itself are in a key role in the construction of quantum TGD since they define causal determinants for Kähler action.

2. At the space-time level both the boundaries of X^4 and elementary particle horizons surrounding the orbits of wormhole contacts define light-like 3-surfaces. The field equations are satisfied identically at light-like boundaries. Of course, the projections of the the light-like surfaces of X^4 to Minkowski space need not look light-like at all, and even boundaries of magnetic flux tubes could be light-like.

   Light-like 3-surfaces are metrically 2-dimensional and allow a generalized conformal invariance crucial for the construction of quantum TGD. At the level of imbedding space conformal supersymplectic invariance results. At the space-time level the outcome is conformal invariance highly analogous to the Kac Moody symmetry of super string models [15, 73] . In fact, there are good reasons to believe that the three-dimensional Chern-Simons action appears even in the construction of configuration space metric and give an additional contribution to the configuration space metric when the light-like boundaries of 3-surface have 3-dimensional CP_2 projection.

3. By the effective two-dimensionality the Wess-Zumino-Witten action containing Chern-Simons term is an excellent candidate for the quantum description of S-matrix associated with the light-like 3-surfaces since by the vanishing of the metric determinant one cannot define any general coordinate invariant 3-dimensional action other than Chern-Simons action. The boundaries of the braid formed by the magnetic flux tubes having light-like boundaries, perhaps having join along boundaries bonds between swapped flux tubes would define the 2+1-dimensional space-time associated with a braid, would define the arena of Witten-Chern-Simons theory describing anyons. This S-matrix can be interpreted also as characterizing either a 3-dimensional quantum state since light-like boundaries are limiting cases of space-like 3-surfaces.

4. Kähler action defines an Abelian Chern-Simons term and the induced electroweak gauge fields define a non-Abelian variant of this term. The Chern-Simons action associated with the classical color degrees of freedom vanishes as is easy to find. The classical color fields are identified as projections of Killing vector fields of color group: $A^c_\alpha = j^A_k \partial_\alpha s^k \tau_A = J_k{}^r \partial_r H^A \partial_\alpha s^k$. The classical color gauge field is proportional to the induced Kähler form: $F^c_{\alpha\beta} = H^A J_{\alpha\beta} \tau_A$. A little calculation shows that the instanton density vanishes by the identity $H_A H^A = 1$ (this identity is forced by the necessary color-singletness of the YM action density and is easy to check in the simpler case of S^2.

5. Since qubit realizes the fundamental representation of the quantum group $SU(2)_q$, $SU(2)$ is in a unique role concerning the construction of modular functors and quantum computation using Chern-Simons action. The quantum group corresponding to $q = exp(i2\pi/r)$, $r = 5$ is realized for the level $k = 3$ Chern-Simons action and satisfies the constraint $r = k + c_g$, where $c_g = 2$ is the so called dual Coxeter number of $SU(2)$ [21, 20, 12] .

   The exponent non-Abelian $SU(2)_L \times U(1)$ Chern-Simons action combined with the corresponding action for Kähler form so that effective reduction to $SU(2)_L$ occurs, could appear as a multiplicative factor of the configuration space spinor fields defined in the configuration space of 3-surfaces. Since 3-dimensional quantum state would represent a 2-dimensional time evolution the role of these phase factor would be very analogous to the role of ordinary Chern-Simons action.

3.5 Topological quantum computation in TGD Universe

The general philosophy behind TQC inspires the dream that the existence of basic gates, in particular the maximally entangling 2-gate R, is guaranteed by the laws of Nature so that no fine tuning would

be needed to build the gates. Negentropy Maximization Principle, originally developed in context of TGD inspired theory of consciousness, is a natural candidate for this kind of Law of Nature.

3.5.1 Concrete realization of quantum gates

The bold dream is that besides 2-gates also 1-gates are realized by the basic laws of Nature. The topological realization of the 3-braid representation in terms of Temperley-Lie algebra allows the reduction of 1-gates to 2-gates.

NMP and TQC

Quantum jump involves a cascade of self measurements in which the system under consideration can be though of as decomposing to two parts which are either un-entangled or possess rational or extended rational entanglement in the final state. The sub-system is selected by the requirement that entanglement negentropy gain is maximal in the measurement of the density matrix characterizing the entanglement of the sub-system with its complement.

In the case case that the density matrix before the self measurement decomposes into a direct sum of matrices of dimensions N_i , such that $N_i > 1$ holds true for some values of i, say i_0, the final state is a rationally entangled and thus a bound state. i_0 is fixed by the requirement that the number theoretic entropy for the final state maximally negative and equals to $klog(p)$, where p^k is the largest power of prime dividing N_{i_0}. This means that maximally entangled state results and the density matrix is proportional to a unit matrix as it is also for the entanglement produced by R. In case of R the density matrix is $1/2$ times 2-dimensional unit matrix so that bound state entanglement negentropy is 1 bit.

The question is what occurs if the density matrix contains a part for which entanglement probabilities are extended rational but not identical. In this case the entanglement negentropy is positive and one could argue that no self-measurement occurs for this state and it remains entangled. If so then the measurement of the density matrix would occur only when it increases entanglement negentropy. This looks the only sensible option since otherwise only bound state entanglement with identical entanglement probabilities would be possible. This question is relevant also because Temperley-Lieb representation using $(AA) - A - A$ system involves entanglement with entanglement probabilities which are not identical.

In the case that the 2-gate itself is not directly entangling as in case of R' and R'', NMP should select just the quantum history, that single particle gates at it guarantee maximum entanglement negentropy. Thus NMP would come in rescue and give hopes that various gates are realized by Nature.

Non-Abelian anyon systems are modelled in terms of punctures of plane and Chern-Simons action for the incompressible vector potential of hydrodynamical flow. It is interesting to find how these ideas relate to the TGD description.

Non-Abelian anyons reside at boundaries of magnetic flux tubes in TGD

In [21] anyons are modelled in terms of punctures of plane defined by the slab carrying Hall current. In TGD the punctures correspond naturally to magnetic flux tubes defining the braid. It is now however obvious under what conditions the braid containing the TGD counterpart of (AA)-A-A system can be described as a punctured disk if the flux tubes describing the tracks of valence anyons are very near to the boundaries of the magnetic flux tubes. Rather, the punctured disk is replaced with the closed boundary of the magnetic flux tube or of the structure formed by the partial fusion of several magnetic flux tubes. This microscopic description and is consistent with Laughlin's model only if it is understood as a long length scale description.

Non-Abelian charges require singularities and punctures but a two-surface which is boundary does not allow punctures. The punctures assigned with an anyon pair would become narrow wormhole threads traversing through the interior of the magnetic flux tube and connecting the punctures like wormholes connect two points of an apple. It is also possible that the threads connect the surfaces of two nearby magnetic flux tubes. The wormhole like character conforms with the fact that non-Abelian anyons appear always in pairs.

The case in which which the ends of the wormhole thread belong to different neighboring magnetic flux tubes, call them T_1 and T_2, is especially interesting as far as the model for TQC is considered. The state of $(AA)-A-A$ system before (after) the 3-braid operation would be identifiable as anyons near the surface of T_1 (T_2). If only sufficiently local operations are allowed, the braid group would be same as for anyons inside disk. This means consistency with the anyon model of [21] for TQC requiring that the dimension for the space of ground states is 2^{n-1} in a system consisting of n anyon pairs.

The possibility of negative energies allows inspires the idea that the anyons at T_2 have negative energies so that the anyon system would have a vanishing net energy. This would conform with the idea that the scattering from initial to final state is equivalent with the creation of zero energy state for which initial (final) state particles have positive (negative) energies, and with the fact that the boundaries of magnetic flux tubes are light-like systems for which 3-D quantum state is representation for a 2-D time evolution.

Since the correlation between anyons at the ends of the wormhole thread is purely topological, the most plausible option is that they behave as free anyons dynamically. Assuming 4-branched anyon surfaces, the charges of anyons would be of form $Q=\nu_A e$, $\nu_A=4/m$, m odd.

Consider now the representation of 3-braid group. That the mapping class group for the 3-braid system should have a 2-dimensional representation is obvious from the fact that the group has same generators as the mapping class group for torus which is represented by as $SL(2,Z)$ matrices acting on the homology of torus having two generators a, b corresponding to the two non-contractible circles around torus. 3-braid group would be necessarily represented in Temperley-Lieb representation.

The character of the anyon bound state is important for braid representations.

1. If anyons form loosely bound states (AA), the electrons are at different tracks and the charge is additive in the process so that one has $Q_{AA}=2Q_A=8/m$, m odd, which is at odds with statistics. It might be that the naive rule of assigning fractional charge to the state does not hold true for loosely bound bosonic anyons. In this case $(AA)-A$ system with charge states $((1,-1),1)$ and $((1,1),-1)$ would be enough for realizing 1-gates in TQC. The braid operation s_2 of Temperley-Lieb representation represented $(A_1A_2)-A_3\rightarrow(A_1A_3)-A_2$ would correspond to an exchange of the dance partner by a temporary decay of (A_1A_2) followed by a recombination to a quantum superposition of (A_1A_2) and (A_1A_3) and could be regarded as an ordinary braid operation rather than monodromy. The relative phase 1-gate would correspond to s_1 represented as braid operation for A_1 and A_2 inside (A_1A_2).

2. If anyons form tightly bound states (AA) in the sense that single anyonic flux tube carries two electrons, charge need not be additive so that bound states could have charges $Q=4/2m_1$ so that the vacuum Kähler charge $Q_K=4(1/m_1-2/m)$ would be created in the process. This would stabilize (AA) state and would mean that the braid operation $(A_1A_2)-A_3\rightarrow(A_1A_3)-A_2$ cannot occur via a temporary decay to free anyons and it might be necessary to replace 3-braid group by a partially colored 3-braid group for $(AA)-A-A$ system which is sub-group of 3-braid group and has generators s_1^2 (two swaps for $(AA)-A$) and s_2 (swap for $A-A$) instead of s_1 and s_2. Also in this case a microscopic mechanism changing the value of (AA) Z^4 charge is needed and the situation might reduce to the case a) after all.

   The Temperley Lieb representation for this group is obtained by simply taking square of the generator inducing entanglement (s_2 rather than s_1 in the notation used!). The topological charge assignments for $(AA)-A-A$ system are $((1,-1),1,-1)$ and $((1,1),-1,-1)$. s_1^2 would correspond to the group element generating $(AA)-A$ entanglement and s_2 acting on $A-A$ pair would correspond to phase generating group element.

Braid representations and 4-branched anyon surfaces

Some comments about braid representations in relation to Z_N- valued topological charges are in order.

1. Yang-Baxter braid representation using the maximally entangling braid matrix R is especially attractive option. For anyonic computation with Z_4-valued topological charge R is the unique 2-gate conserving the net topological charge (note that the mixing of the $|1,1\rangle$ and $|-1,-1\rangle$ is allowed). On the other, R allows only the conservation of Z_4 value topological charge. This suggests that the the entanglement between logical qubits represented by $(AA)-A-A$ batches

is is generated by R. The physical implication is that only $\nu = 4/n$ 4-branched anyons could be used for TQC.

2. In TGD framework the entangling braid representation inside batches responsible for 1-gates need not be the same since batches correspond to magnetic flux tubes. In standard physics context it would be harder to defend this kind of assumption. As will be found 3-braid Temperley-Lieb representation is very natural for 1-gates. The implication is that the n-braid system with braids represented as 4-batches would have 2^n-dimensional space of logical qubits in fact identical with the space of realizable qubits.

3. Also n-braid Temperley-Lieb representations are possible and the explicit expressions of the braiding matrices for 6-braid case suggest that Z_4 topological charge is conserved also now [20] . In this case the dimension of the space of logical qubits is for highly favored value of quantum group parameter $q = exp(i\pi/5)$ given by the Fibonacci number $F(n)$ for n-braid case and behaves as Φ^{4n} asymptotically so that this option would be more effective. From $\Phi^4 = 1 + 3\Phi \simeq 8.03$ one can say that single 4-batch carries 3 bits of information instead of one. This is as it must be since topological charge is not conserved inside batches separately for this option.

4. $(AA) - A$ representation based on Z_4-valued topological charge is unique in that the space of logical qubits would be the space of topologically realizable qubits. Quantum superposition of logical qubits could could be represented $(AA) - A$ entangled state of form $a|2, -1\rangle + b|0, 1\rangle$ generated by braid action. Relative phase could be generated by braid operation acting on the entangled state of anyons of (AA) Cooper pair. Since the superposition of logical cubits corresponds to an entangled state $a|2, -1\rangle + b|0, 1\rangle$ for which coefficients are extended rational numbers, the number theoretic realization of the bound state property could pose severe conditions on possible relative phases.

3.5.2 Temperley-Lieb representations

The articles of Kaufmann [16] and Freedman [20, 13] provide enjoyable introduction to braid groups and to Tempeley-Lie representations. In the sequel Temperley-Lieb representations are discussed from TGD view point.

Temperley-Lieb representation for 3-braid group

In [16] it is explained how the so called Temperley-Lie algebra defined by 2×2-matrices I, U_1, U_2 satisfying the relations $U_1^2 = dU_1$, $U_2^2 = dU_2$, $U_1U_2U_1 = U_2$, $U_2U_1U_2 = U_1$ allows a unitary representation of Artin's braid group by unitary 2×2 matrices. The explicit representations of the matrices U_1 and U_2 (note that U_i/d acts as a projector) given by

$$\begin{aligned} U_1 &= \begin{pmatrix} d & 0 \\ 0 & 0 \end{pmatrix} , \\ U_2 &= \begin{pmatrix} \frac{1}{d} & \sqrt{1-\frac{1}{d^2}} \\ \sqrt{1-\frac{1}{d^2}} & d-\frac{1}{d} \end{pmatrix} . \end{aligned} \tag{3.5.1}$$

Note that the eigenvalues of U_i are d and 0. The representation of the elements s_1 and s_2 of the 3-braid group is given by

$$\begin{aligned} \Phi(s_1) &= AI + A^{-1}U_1 = \begin{pmatrix} -U^{-3} & 0 \\ 0 & U \end{pmatrix} , \\ \Phi(s_2) &= AI + A^{-1}U_2 = \begin{pmatrix} -\frac{U^3}{d} & \frac{U^{-1}}{\sqrt{1-(1/d)^2}} \\ \frac{U^{-1}}{\sqrt{1-(1/d)^2}} & \frac{U^{-5}}{d} \end{pmatrix} , \\ U &= exp(i\phi) . \end{aligned} \tag{3.5.2}$$

Here the condition $d = -A^2 - A^{-2}$ is satisfied. For $A = exp(i\phi)$, with $|\phi| \leq \pi/6$ or $|\pi - \phi| \leq \pi/6$, the representation is unitary. The constraint comes from the requirement $d > 1$. From the basic representation it follows that the eigenvalues of $\Phi(s_i)$ are $-exp(-3i\phi)$ and $exp(i\phi)$.

Tihs 3-braid representation is a special case of a more general Temperley-Lieb-Jones representation discussed in [20] using notations $A = \sqrt{-1}exp(-i2\pi/4r)$, $s = A^2$, and $q = A^4$. In this case all eigenvalues of all representation matrices are -1 and $q = exp(-i2\pi/r)$. This representation results by multiplying Temperley-Lieb representation above with an over-all phase factor $exp(4i\phi)$ and by the replacement $A = exp(i\phi) \to \sqrt{-1}A$.

Constraints on the parameters of Temperley-Lieb representation

The basic mathematical requirement is that besides entangling 2-gate there is minimum set of 1-gates generating infinite sub-group of $U(2)$. Further conditions come from the requirement that a braid representation is in question. In the proposal of [21, 20] the 1-gates are realized using Temperley-Lieb 3-braid representation. It is found that there are strong constraints to the representation and that relative phase gate generating the phase $exp(i\phi) = exp(i2\pi/5)$ is the simplest solution to the constraints.

The motivation comes from the findings made already by Witten in his pioneering work related to the topological quantum field theories and one can find a good representation about what is involve din [29] .

Topological quantum field theories can produce unitary modular functors when the $A = q^{1/4} = exp(i\phi)$ characterizing the quantum group multiplication is a root of unity so that the quantum enveloping algebra $U(Sl(2))_q$ defined as the quantum version of the enveloping algebra $U(Sl(2))$ is not homomorphic with $U(Sl(2))$ and theory does not trivialize. Besides this, q must satisfy some consistency conditions. First of all, $A^{4n} = 1$ must be satisfied for some value of n so that A is either a primitive l:th, $2l$:th of unity for l odd, or $4l$:th primitive root of unity.

This condition relates directly to the fact that the quantum integers $[n]_q = (A^{2n} - A^{-2n})/(A^2 - A^{-2})$ vanish for $n \geq l$ so that the representations for a highest weight n larger than l are not irreducible. This implies that the theory simplifies dramatically since these representations can be truncated away but can cause also additional difficulties in the definition of link invariants. Indeed, as Witten found in his original construction, the topological field theories are unitary for $U(Sl(2))_q$ only for $A = exp(ik\pi/2l)$, k not dividing $2l$, and $A = exp(i\pi/l)$, l odd (no multiples are allowed) [29] . $n = 2l = 10$, which is the physically favored choice, corresponds to the relative phase $4\phi = 2\pi/5$.

Golden Mean and quantum computation

Temperley-Lieb representation based on $q = exp(i2\pi/5)$ is highly preferred physically.

1. One might hope that the Yang-Baxter representation based on maximally entangling braid matrix R might work. $R^8 = 1$ constraint is however not consistent with Temperley-Lieb representations. The reason is that $\Phi^8(s_1) = 1$ gives $\phi = \pi/4 > \pi/6$ so that unitarity constraint is not satisfied. $\phi = exp(i2\pi/16)$ corresponding $r = 4$ and to the matrix $\Phi(s_2) = \hat{R} = exp(i2\pi/16) \times R$ allows to satisfy the unitarity constraint. This would look like a very natural looking selection since $\Phi(s_2)$ would act as a Hadamard gate and NMP would imply identical entanglement probabilities if a bound state results in a quantum jump. Unfortunately, s_1 and s_2 do not generate a dense subgroup of $U(2)$ in this case as shown in [20] .

2. $\phi = \pi/10$ corresponding to $r = 5$ and Golden Mean satisfies all constraints coming from quantum computation and knot theory. That is it spans a dense subgroup of $U(2)$, and allows the realization of modular functor defined by Witten-Chern-Simons $SU(2)$ action for $k = 3$, which is physically highly attractive since the condition

$$r = k + c_g(SU(2))$$

connecting r, k and the dual Coxeter number $c_g(SU(N)) = n$ in WCS theories is satisfied for $SU(2)$ in this case for $r = 5$ and $k = 3$.

$SU(2)$ would have interpretation as the left-handed electro-weak gauge group $SU(2)_L$ associated with classical electro-weak gauge fields. The symmetry breaking of $SU(2)_L$ down to a discrete

subgroup of $SU(2)_L$ yielding anyons would relate naturally to this. The conservation of the topologized Kähler charge would correlate with the fact that there is no symmetry breaking in the classical $U(1)$ sector. $k = 3$ Chern-Simons theory is also known to share the same universality class as simple 4-body Hamiltonian [21] (larger values of k would correspond to $k + 1$-body Hamiltonians).

3. Number theoretical vision about intentional systems suggests that the preferred relative phases are algebraic numbers or more generally numbers which belong to a finite-dimensional extension of p-adic numbers. The idea about p-adic cognitive evolution as a gradual generation of increasingly complex algebraic extensions of rationals allows to see the extension containing Golden Mean $\Phi = (1 + \sqrt{5})/2$ as one of the simplest extensions. The relative phase $exp(i4\phi) = exp(i2\pi/5)$ is expressible in an extension containing $\sqrt{\Phi}$ and Φ: one has $cos(4\phi) = (\Phi - 1)/2$ and $sin(4\phi) = \sqrt{5\Phi}/2$.

The general number theoretical ideas about cognition support the view that Golden Mean is in a very special role in the number theoretical world order. This would be due to the fact that $log(\Phi)/\pi$ is a rational number. This hypothesis would explain scaling hierarchies based on powers of Golden Mean. One could argue that the geometry of the braid should reflect directly the value of the $A = exp(i2\phi)$. The angle increment per single DNA nucleotide is $\phi/2 = 2\pi/10$ for DNA double strand (note that q would be $exp(i\pi/10)$, which raises the question whether DNA might be a topological quantum computer.

Bratteli diagram for $n = 5$ case, Fibonacci numbers, and microtubuli

Finite-dimensional von Neumann algebras can be conveniently characterized in terms of Bratteli diagrams [9]. For instance, the diagram a) of the figure 3.5.2 at the end of the chapter represents the inclusion $N \subset M$, where $N = M_2(C) \otimes C$, $M = M_6(C) \otimes M_3(C) \otimes C$. The diagram expresses the imbeddings of elements $A \otimes x$ of $M_2(C) \otimes C$ to $M_6(C)$ as a tensor product $A_1 \otimes A_2 \otimes x$

$$\begin{aligned} A_1 &= \begin{pmatrix} A & . & . \\ . & A & . \\ . & . & A \end{pmatrix} , \\ A_2 &= \begin{pmatrix} A & . \\ . & x \end{pmatrix} . \end{aligned} \tag{3.5.3}$$

Bratteli diagrams of infinite-dimensional von Neumann algebras are obtained as limiting cases of finite-dimensional ones.

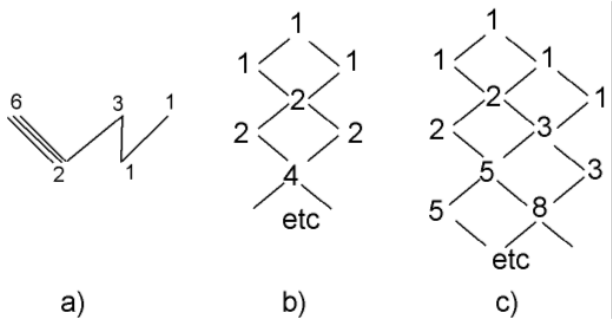

Figure 3.1: a) Illustration of Bratteli diagram. b) and c) give Bratteli diagrams for $n = 4$ and $n = 5$ Temperley Lieb algebras

2. Temperley Lieb algebras approximate II_1 factors

The hierarchy of inclusions of with $|M_{i+1} : M_i| = r$ defines a hierarchy of Temperley-Lieb algebras characterizable using Bratteli diagrams. The diagrams b) and c) of the figure 3.5.2 at the end of the chapter characterize the Bratteli diagrams for $n = 4$ and $n = 5$. For $n = 4$ the dimensions of algebras come in powers of 2 in accordance with the fact $r = 2$ is the dimension of the effective tensor factor of II_1.

For $n = 5$ and $B_m = \{1, e_1, ..., e_m\}$ the dimensions of the two tensor factors of the Temperley Lieb-representation are two subsequent Fibonacci numbers F_{m-1}, F_m ($F_{m+1} = F_m + F_{m-1}$, $F_1 = 1, F_2 = 1$) so that the dimension of the tensor product is $dim(B_m) = F_m F_{m-1}$. One has $dim(B_{m+1})/dim(B_m) = F_m/F_{m-2} \to \Phi^2 = 1 + \Phi$, the dimension of the effective tensor factor for the corresponding hierarchy of II_1 factors. Hence the two dimensional hierarchies "approximate" each other. In fact, this result holds completely generally.

The fact that r is approximated by an integer in braid representations is highly interesting from the point of view of TQC. For 3-braid representation the dimension of Temperley-Lieb representation is 2 for all values of n so that 3-braid representation defines single (topo)logical qubit as $(AA) - A - A$ realization indeed assumes. One could optimistically say that TGD based physics automatically realizes topological qubit in terms of 3-braid representation and the challenge is to understand the details of this realization.

2. Why Golden Mean should be favored?

The following argument suggests a physical reason for why just Golden Mean should be favored in the magnetic flux tube systems.

1. Arnold [4] has shown that if Lorentz 3-force satisfies the condition $F_B = q(\nabla \times B) \times B = q\nabla\Phi$, then the field lines of the magnetic field lie on $\Phi = constant$ tori. On the other hand, the vanishing of the Lorentz 4-forces for solutions of field equations representing asymptotic self-organized states, which are the "survivors" selected by dissipation, equates magnetic force with the negative of the electric force expressible as qE, $E = -\nabla\Phi + \partial_t A$, which is gradient if the vector potential does not depend on time. Since the vector potential depends on three CP_2 coordinates only for $D = 3$, this seems to be the case.

2. The celebrated Kolmogorov-Arnold-Moser (KAM) theorem is about the stability of systems, whose orbits are on invariant tori characterized by the frequencies associated with the n independent harmonic oscillator like degrees of freedom. The theorem states that the tori for which the frequency ratios are rational are highly unstable against perturbations: this is due to resonance effects. The more "irrational" the frequencies are, the higher the stability of the orbits is, and the most stable situation corresponds to frequencies whose ratio is Golden Mean. In quantum context the frequencies for wave motion on torus would correspond to multiples $\omega_i = n2\pi/L_i$, L_i the circumference of torus. This poor man's argument would suggest that the ratio of the circumferences of the most stable magnetic tori should be given by Golden Mean in the most stable situation: perhaps one might talk about Golden Tori!

3. Golden Mean and microtubuli

What makes this observation so interesting is that Fibonacci numbers appear repeatedly in the geometry of living matter. For instance, micro-tubuli, which are speculated to be systems performing quantum computation, represent in their structure the hierarchy Fibonacci numbers $5, 8, 13$, which brings in mind the tensor product representation $5 \otimes 8$ of B_5 (5 braid strands!) and leads to ask whether this Temperley-Lieb representation could be somehow realized using microtubular geometry.

According to the arguments of [21] the state of n anyons corresponds to 2^{n-1} topological degrees of freedom and code space corresponds to F_n-dimensional sub-space of this space. The two conformations of tubulin dimer define the standard candidate for qubit, and one could assume that the conformation correlates strongly with the underlying topological qubit. A sequence of 5 *resp.* 8 tubulin dimers would give 2^4 *resp.* 2^7-dimensional space with $F_5 = 5$- *resp.* $F_7 = 13$-dimensional code sub-space so that numbers come out nicely. The changes of tubulin dimer conformations would be induced by the braid groups B_4 and B_7. B_4 would be most naturally realized in terms of a unit of 5-dimers by regarding the 4 first tubulins as braided punctures and 5th tubulin as the passive puncture. B_7 would be realized in a similar manner using a unit of 8 tubulin dimers.

Flux tubes would connect the subsequent dimers along the helical 5-strand *resp.* 8-strand defined by the microtubule. Nearest neighbor swap for the flux tubes would induce the change of the tubulin conformation and induce also entanglement between neighboring conformations. A full 2π helical twist along microtubule would correspond to 13 basic steps and would define a natural TQC program module. In accordance with the interpretation of II_1 factor hierarchy, (magnetic or electric) flux tubes could be assumed to correspond to $r = 2$ II_1 factor and thus carry 2-dimensional representations of $n = 5$ or $n = 4$ 3-braid group. These qubits could be realized as topological qubits using $(AA) - A$ system.

Topological entanglement as space-time correlate of quantum entanglement

Quantum-classical correspondence encourages to think that bound state formation is represented at the space-time level as a formation of join along boundaries bonds connecting the boundaries of 3-space sheets. In particular, the formation of entangled bound states would correspond to a topological entanglement for the join along boundaries bonds forming braids. The light-likeness of the boundaries of the bonds gives a further support for this identification. During macro-temporal quantum coherence a sequence of quantum jumps binds effectively to single quantum jump and subjective time effectively ceases to run. The light-likeness for the boundaries of bonds means that geometric time stops and is thus natural space-time correlate for the subjective experience during macro-temporal quantum coherence.

Also the work with TQC lends support for a a deep connection between quantum entanglement and topological entanglement in the sense that the knot invariants constructed using entangling 2-gate R can detect linking. Temperley-Lieb representation for 3-braids however suggests that topological entanglement allows also single qubit representations for with quantum entanglement plays no role. One can however wonder whether the entanglement might enter into the picture in some natural manner in the quantum computation of Temperley-Lieb representation. The idea is simple: perhaps the physics of $(AA) - A - A$ system forces single qubit representation through the simple fact that the state space reduces in 4-batch to single qubit by topological constraints.

For TQC the logical qubits correspond to entangled states of anyon Cooper pair (AA) and second anyon A so that the quantum superposition of qubits corresponds to an entangled state in general. Several arguments suggest that logical qubits would provide Temperley-Lieb representation in a natural manner.

1. The number of braids inside 4-anyon batch (or 3-anyon batch in case that (AA) can decay temporarily during braid operation) 3 so that by the universality this system allows to compute the unitary Temperley-Lieb braid representation. The space of logical qubits equals to the entire state space since the number of qubits represented by topological ground state degeneracy is 1 instead of the expected three since $2n$ anyon system gives rise to 2^{n-1}-fold vacuum degeneracy. The degeneracy is same even when two of the anyons fuse to anyon Cooper pair. Thus it would seem that the 3-braid system in question automatically produces 1-qubit representation of 3-braid group.

2. The braiding matrices $\Phi(s_1)$ and $\Phi(s_2)$ are different and only $\Phi(s_2)$ mixes qubit values. This can be interpreted as the presence of two inherently different braid operations such that only the second braiding operation can generate entanglement of states serving as building blocks of logical qubits. The description of anyons as 2-dimensional wormholes led to precisely this picture. The braid group reduces to braid group for one half of anyons since anyon and its partner at the end of wormhole are head and feet of single dancer, and the anyon pair (AA) forming bound state can change partner during swap operation with anyon A and this generates quantum entanglement. The swap for anyons inside (AA) can generate only relative phase.

3. The vanishing of the topological charge in a pairwise manner is the symmetry which reduces the dimension of the representation space to 2^{n-1} as already found. For $n = 4$ only single topological qubit results. The conservation and vanishing of the net topological charge inside each batch gives a constraint, which is satisfied by the maximally entangling R-matrix R so that it could take care of braiding between different 4-batches and one would have different braid representation for 4-batches and braids consisting of them. Topological quantization justifies this picture physically. Only phase generating *physical* 1-gates are allowed since Hadamard

gate would break the conservation of topological charge whereas for *logical* 1-gates entanglement generating 2-gates can generate mixing without the breaking of the conservation of topological charges.

Summary

It deserves to summarize the key elements of the proposed model for which the localization (in the precise sense defined in [13]) made possible by topological field quantization and Z_4 valued topological charge are absolutely essential prerequisites.

1. $2n$-anyon system has 2^{n-1}-fold ground state degeneracy, which for $n = 2$ leaves only single logical qubit. In standard physics framework $(AA) - A - A$ is minimal option because the total homology charge of the system must vanish. In TGD $(AA) - A$ system is enough to represent 3-braid system if the braid operation between AA and A can be realized as an exchange of the dancing partner. This option makes sense because the anyons with opposite topological charges at the ends of wormhole threads can be negative energy anyons representing the final state of the braid operation. A pair of magnetic flux tubes is needed to realize single anyon-system containing braid.

2. Maximally entangling R-matrix realizes braid interactions between $(AA) - A$ systems realized as 3-braids inside larger braids and the space of logical qubits is equivalent with the space of realizable qubits. The topological charges are conserved separately for each $(AA) - A$ system. Also the more general realization based on n-braid representations of Temperley-Lieb algebra is formally possible but the different topological realization of braiding operations does not support this possibility.

3. Temperley-Lieb 3-braid representation for $(AA) - A - A$ system allows to realize also 1-gates as braid operations so that topology would allow to avoid the fine-tuning associated with 1-gates. Temperley-Lieb representation for $\phi = exp(i\pi/10)$ satisfies all basic constraints and provides representation of the modular functor expressible using $k = 3$ Witten-Chern-Simons action. Physically 1-gates are realizable using Φ_1 acting as phase gate for anyon pair inside (AA) and $\Phi(s_2)$ entangling (AA) and A by partner exchange. The existence of single qubit braid representations apparently conflicting with the identification of topological entanglement as a correlate of quantum entanglement has an explanation in terms of quantum computation under topological symmetries.

3.5.3 Zero energy topological quantum computations

As already described, TGD suggests a radical re-interpretation for matter antimatter asymmetry in long length scales. The asymmetry would be due to the fact that ground state for fermion system corresponds to infinite sea of negative energy fermions and positive energy anti-fermions so that fermions would have positive energies and anti-fermions negative energies.

The obvious implication is the possibility to interpret scattering between positive energy states as a creation of a zero energy state with outgoing particles represented as negative energy particles. The fact that the quantum states of 3-dimensional light-like boundaries of 3-surfaces represent evolutions of 2-dimensional quantum systems suggests a realization of topological quantum computations using physical boundary states consisting of positive energy anyons representing the initial state of anyon system and negative energy anyons representing the outcome of the braid operation.

The simplest scenario simply introduces negative energy charge conjugate of the $(AA) - A$ system so that no deviations from the proposed scenario are needed. Both calculation and its conjugate are performed. This picture is the only possible one if one assumes that given space-time sheet contains either positive or negative energy particles but not both and very natural if one assumes ordinary fermionic vacuum. The quantum computing system would could be generated without any energy costs and even intentionally by first generating the p-adic space-time sheets responsible for the magnetic flux tubes and anyons and then transformed to their real counterparts in quantum jump. This double degeneracy is analogous to that associated with DNA double strand and could be used for error correction purposes: if the calculation has been run correctly both anyon Cooper pairs and their charge conjugates should decay with the same probability.

Negative energies could have much deeper role in TQC. This option emerges naturally in the wormhole handle realization of TQC. The TGD realization of 1-gates in 3-braid Temperley-Lieb representation uses anyons of opposite topological charges at the opposite ends of threads connecting magnetic flux tube boundaries. Single 3-braid unit would correspond to positive energy electronic anyons at the first flux tube boundary and negative energy positronic anyons at the second flux tube boundary. The sequences of 1-gates represented as 3-braid operations would be coded by a sequence of 3-braids representing generators of 3-braid group along a pair of magnetic flux tubes. Of course, also n-braid operations could be coded in the similar manner in series. Hence TQC could be realized using only two magnetic flux tubes with n-braids connecting their boundaries in series.

Condensed matter physicist would probably argue that all this could be achieved by using electrons in strand and holes in the conjugate strand instead of negative energy positrons: this would require only established physics. One can however ask whether negative energy positrons could appear routinely in condensed matter physics. For instance, holes might in some circumstances be generated by a creation of an almost zero energy pair such that positron annihilates with a fermion below the Fermi surface. The signature for this would be a photon pair consisting of ordinary and phase conjugate photons.

The proposed interpretation of the S-matrix in the Universe having vanishing net quantum numbers encourages to think that the S-matrices of 2+1-dimensional field theories based on Witten-Chern-Simons action defined in the space of zero (net) energy states could define physical states for quantum TGD. Thus the 2+1-dimensional S-matrix could define quantum states of 4-dimensional theory having interpretation as states representing "self-reflective" level representing in itself the S-matrix of a lower-dimensional theory. The identification of the quantum state as S-matrix indeed makes sense for light-like surfaces which can be regarded as limiting cases of space-like 3-surfaces defining physical state and time-like surfaces defining a time evolution of the state of 2-dimensional system.

Time evolution would define also an evolution in topological degrees of freedom characterizing ground states. Quantum states associated with light-like (with respect to the induced metric of space-time sheet) 3-dimensional boundaries of say magnetic flux tubes would define quantum computations as modular functors. This conforms with quantum-classical correspondence since braids, the classical states, indeed define quantum computations.

The important implication would be that a configuration which looks static would code for the dynamic braiding. One could understand the quantum computation in this framework as signals propagating through the strands and being affected by the gate. Even at the limit when the signal propagates with light velocity along boundary of braid the situation looks static from outside. Time evolution as a state could be characterized as sequence of many-anyon states such that basic braid operations are realized as zero energy states with initial state realized using positive energy anyons and final state realized using negative energy energy anyons differing by the appropriate gate operation from the positive energy state.

In the case of n-braid system the state representing the S-matrix $S = S^1 S^2 .... S^n$ associated with a concatenation of n elementary braid operations would look like

$$\begin{aligned} |S\rangle &= P_{k_1} S^1_{k_1 k_2} P_{k_2} S^2_{k_2 k_3} P_{k_3} S^3_{k_3 k_4} \cdots \ , \\ P_k &= |k, <\rangle |k, >\rangle \ . \end{aligned} \tag{3.5.4}$$

Here S^k are S-matrices associated with gates representing simple braiding operations s_k for $n+1$ threads connecting the magnetic flux tubes. P_k represents a trivial transition $|k\rangle \to |k \to k\rangle$ as zero energy state $|k, > 0\rangle |k, <\rangle$. The states P_k represent matrix elements of the identification map from positive energy Hilbert space to its negative energy dual.

What would happen can be visualized in two alternative manners.

1. For this option the braid maps occur always from flux tube 1 to flux tube 2. A braiding transition from 1 to 2 is represented by S^{k_1}; a trivial transition from 2 to 1 is represented by P_k; a braiding transition from 1 to 2 is represented by S^{k_2}, etc... In this case flux tube 1 contains positive energy anyons and flux tube 2 the negative energy anyons.

2. An alternative representation is the one in which P_k represents transition along the strand so that S^k *resp.* S^{k+1} corresponds to braiding transition from strand 1 to 2 *resp.* 2 to 1. In this case both flux tubes contain both positive and negative energy anyons.

3.6 Appendix: A generalization of the notion of imbedding space

In the following the recent view about structure of imbedding space forced by the quantization of Planck constant is described. This view has developed much before the original version of this chapter was written.

The original idea was that the proposed modification of the imbedding space could explain naturally phenomena like quantum Hall effect involving fractionization of quantum numbers like spin and charge. This does not however seem to be the case. $G_a \times G_b$ implies just the opposite if these quantum numbers are assigned with the symmetries of the imbedding space. For instance, quantization unit for orbital angular momentum becomes n_a where Z_{n_a} is the maximal cyclic subgroup of G_a.

One can however imagine of obtaining fractionization at the level of imbedding space for space-time sheets, which are analogous to multi-sheeted Riemann surfaces (say Riemann surfaces associated with $z^{1/n}$ since the rotation by 2π understood as a homotopy of M^4 lifted to the space-time sheet is a non-closed curve. Continuity requirement indeed allows fractionization of the orbital quantum numbers and color in this kind of situation.

3.6.1 Both covering spaces and factor spaces are possible

The observation above stimulates the question whether it might be possible in some sense to replace H or its factors by their multiple coverings.

1. This is certainly not possible for M^4, CP_2, or H since their fundamental groups are trivial. On the other hand, the fixing of quantization axes implies a selection of the sub-space $H_4 = M^2 \times S^2 \subset M^4 \times CP_2$, where S^2 is a geodesic sphere of CP_2. $\hat{M}^4 = M^4 \backslash M^2$ and $\hat{CP}_2 = CP_2 \backslash S^2$ have fundamental group Z since the codimension of the excluded sub-manifold is equal to two and homotopically the situation is like that for a punctured plane. The exclusion of these sub-manifolds defined by the choice of quantization axes could naturally give rise to the desired situation.

2. Zero energy ontology forces to modify this picture somewhat. In zero energy ontology causal diamonds (CDs) defined as the intersections of future and past directed light-cones are loci for zero energy states containing positive and negative energy parts of state at the two light-cone boundaries. The location of CD in M^4 is arbitrary but p-adic length scale hypothesis suggests that the temporal distances between tips of CD come as powers of 2 using CP_2 size as unit. Thus M^4 is replaces by CD and $\hat{M}^4$ is replaced with $\hat{CD}$ defined in obvious manner.

3. H_4 represents a straight cosmic string inside CD. Quantum field theory phase corresponds to Jones inclusions with Jones index $\mathcal{M} : \mathcal{N} < 4$. Stringy phase would by previous arguments correspond to $\mathcal{M} : \mathcal{N} = 4$. Also these Jones inclusions are labeled by finite subgroups of $SO(3)$ and thus by Z_n identified as a maximal Abelian subgroup.

   One can argue that cosmic strings are not allowed in QFT phase. This would encourage the replacement $\hat{CD} \times \hat{CP}_2$ implying that surfaces in $CD \times S^2$ and $(M^2 \cap CD) \times CP_2$ are not allowed. In particular, cosmic strings and CP_2 type extremals with M^4 projection in M^2 and thus light-like geodesic without zitterwebegung essential for massivation are forbidden. This brings in mind instability of Higgs=0 phase.

4. The covering spaces in question would correspond to the Cartesian products $\hat{CD}_{n_a} \times \hat{CP}_{2n_b}$ of the covering spaces of $\hat{CD}$ and $\hat{CP}_2$ by Z_{n_a} and Z_{n_b} with fundamental group is $Z_{n_a} \times Z_{n_b}$. One can also consider extension by replacing $M^2 \cap CD$ and S^2 with its orbit under G_a (say tedrahedral, octahedral, or icosahedral group). The resulting space will be denoted by $\hat{CD}\hat{\times}G_a$ *resp.* $\hat{CP}_2\hat{\times}G_b$.

5. One expects the discrete subgroups of $SU(2)$ emerge naturally in this framework if one allows the action of these groups on the singular sub-manifolds $M^2 \cap CD$ or S^2. This would replace the singular manifold with a set of its rotated copies in the case that the subgroups have genuinely 3-dimensional action (the subgroups which corresponds to exceptional groups in the ADE correspondence). For instance, in the case of $M^2 \cap CD$ the quantization axes for angular momentum

would be replaced by the set of quantization axes going through the vertices of tedrahedron, octahedron, or icosahedron. This would bring non-commutative homotopy groups into the picture in a natural manner.

6. Also the orbifolds $\hat{CD}/G_a \times \hat{CP}_2/G_b$ can be allowed as also the spaces $\hat{CD}/G_a \times (\hat{CP}_2 \hat{\times} G_b)$ and $(\hat{CD} \hat{\times} G_a) \times \hat{CP}_2/G_b$. Hence the previous framework would generalize considerably by the allowance of both coset spaces and covering spaces.

There are several non-trivial questions related to the details of the gluing procedure and phase transition as motion of partonic 2-surface from one sector of the imbedding space to another one.

1. How the gluing of copies of imbedding space at $(M^2 \cap CD) \times CP_2$ takes place? It would seem that the covariant metric of M^4 factor proportional to $\hbar^2$ must be discontinuous at the singular manifold since only in this manner the idea about different scaling factor of M^4 metric can make sense. This is consistent with the identical vanishing of Chern-Simons action in $M^2 \times S^2$.

2. One might worry whether the phase transition changing Planck constant means an instantaneous change of the size of partonic 2-surface in CD degrees of freedom. This is not the case. Light-likeness in $(M^2 \cap CD) \times S^2$ makes sense only for surfaces $X^1 \times D^2 \subset (M^2 \cap CD) \times S^2$, where X^1 is light-like geodesic. The requirement that the partonic 2-surface X^2 moving from one sector of H to another one is light-like at $(M^2 \cap CD) \times S^2$ irrespective of the value of Planck constant requires that X^2 has single point of $(M^2 \cap CD)$ as M^2 projection. Hence no sudden change of the size X^2 occurs.

3. A natural question is whether the phase transition changing the value of Planck constant can occur purely classically or whether it is analogous to quantum tunneling. Classical non-vacuum extremals of Chern-Simons action have two-dimensional CP_2 projection to homologically non-trivial geodesic sphere S^2_I. The deformation of the entire S^2_I to homologically trivial geodesic sphere S^2_{II} is not possible so that only combinations of partonic 2-surfaces with vanishing total homology charge (Kähler magnetic charge) can in principle move from sector to another one, and this process involves fusion of these 2-surfaces such that CP_2 projection becomes single homologically trivial 2-surface. A piece of a non-trivial geodesic sphere S^2_I of CP_2 can be deformed to that of S^2_{II} using 2-dimensional homotopy flattening the piece of S^2 to curve. If this homotopy cannot be chosen to be light-like, the phase transitions changing Planck constant take place only via quantum tunnelling. Obviously the notions of light-like homotopies (cobordisms) and classical light-like homotopies (cobordisms) are very relevant for the understanding of phase transitions changing Planck constant.

3.6.2 Do factor spaces and coverings correspond to the two kinds of Jones inclusions?

What could be the interpretation of these two kinds of spaces?

1. Jones inclusions appear in two varieties corresponding to $\mathcal{M} : \mathcal{N} < 4$ and $\mathcal{M} : \mathcal{N} = 4$ and one can assign a hierarchy of subgroups of $SU(2)$ with both of them. In particular, their maximal Abelian subgroups Z_n label these inclusions. The interpretation of Z_n as invariance group is natural for $\mathcal{M} : \mathcal{N} < 4$ and it naturally corresponds to the coset spaces. For $\mathcal{M} : \mathcal{N} = 4$ the interpretation of Z_n has remained open. Obviously the interpretation of Z_n as the homology group defining covering would be natural.

2. $\mathcal{M} : \mathcal{N} = 4$ should correspond to the allowance of cosmic strings and other analogous objects. Does the introduction of the covering spaces bring in cosmic strings in some controlled manner? Formally the subgroup of $SU(2)$ defining the inclusion is $SU(2)$ would mean that states are $SU(2)$ singlets which is something non-physical. For covering spaces one would however obtain the degrees of freedom associated with the discrete fiber and the degrees of freedom in question would not disappear completely and would be characterized by the discrete subgroup of $SU(2)$.

   For anyons the non-trivial homotopy of plane brings in non-trivial connection with a flat curvature and the non-trivial dynamics of topological QFTs. Also now one might expect similar

non-trivial contribution to appear in the spinor connection of $\hat{CD}\hat{\times}G_a$ and $\hat{CP}_2\hat{\times}G_b$. In conformal field theory models non-trivial monodromy would correspond to the presence of punctures in plane.

3. For factor spaces the unit for quantum numbers like orbital angular momentum is multiplied by n_a *resp.* n_b and for coverings it is divided by this number. These two kind of spaces are in a well defined sense obtained by multiplying and dividing the factors of $\hat{H}$ by G_a *resp.* G_b and multiplication and division are expected to relate to Jones inclusions with $\mathcal{M} : \mathcal{N} < 4$ and $\mathcal{M} : \mathcal{N} = 4$, which both are labeled by a subset of discrete subgroups of SU(2).

4. The discrete subgroups of $SU(2)$ with fixed quantization axes possess a well defined multiplication with product defined as the group generated by forming all possible products of group elements as elements of $SU(2)$. This product is commutative and all elements are idempotent and thus analogous to projectors. Trivial group G_1, two-element group G_2 consisting of reflection and identity, the cyclic groups Z_p, p prime, and tedrahedral, octahedral, and icosahedral groups are the generators of this algebra.

By commutativity one can regard this algebra as an 11-dimensional module having natural numbers as coefficients ("rig"). The trivial group G_1, two-element group G_2¡ generated by reflection, and tedrahedral, octahedral, and icosahedral groups define 5 generating elements for this algebra. The products of groups other than trivial group define 10 units for this algebra so that there are 11 units altogether. The groups Z_p generate a structure analogous to natural numbers acting as analog of coefficients of this structure. Clearly, one has effectively 11-dimensional commutative algebra in 1-1 correspondence with the 11-dimensional "half-lattice" N^{11} (N denotes natural numbers). Leaving away reflections, one obtains N^7. The projector representation suggests a connection with Jones inclusions. An interesting question concerns the possible Jones inclusions assignable to the subgroups containing infinitely manner elements. Reader has of course already asked whether dimensions 11, 7 and their difference 4 might relate somehow to the mathematical structures of M-theory with 7 compactified dimensions. One could introduce generalized configuration space spinor fields in the configuration space labelled by sectors of H with given quantization axes. By introducing Fourier transform in N^{11} one would formally obtain an infinite-component field in 11-D space.

The question how do the Planck constants associated with factors and coverings relate is far from trivial and I have considered several options.

1. If one assumes that $\hbar^2(X)$, $X = M^4$, CP_2 corresponds to the scaling of the covariant metric tensor g_{ij} and performs an over-all scaling of metric allowed by Weyl invariance of Kähler action by dividing metric with $\hbar^2(CP_2)$, one obtains $r^2 \equiv \hbar^2/\hbar_0^2\hbar^2(M^4)/\hbar^2(CP_2)$. This puts M^4 and CP_2 in a very symmetric role and allows much more flexibility in the identification of symmetries associated with large Planck constant phases.

2. Algebraist would argue that Planck constant must define a homomorphism respecting multiplication and division (when possible) by G_i. This requires $r(X) = \hbar(X)\hbar_0 = n$ for covering and $r(X) = 1/n$ for factor space or vice versa. This gives two options.

3. Option I: $r(X) = n$ for covering and $r(X) = 1/n$ for factor space gives $r \equiv \hbar/\hbar_0 = r(M^4)/r(CP_2)$. This gives $r = n_a/n_b$ for $\hat{H}/G_a \times G_b$ option and $r = n_b/n_a$ for $\hat{H}\hat{times}(G_a \times G_b)$ option with obvious formulas for hybrid cases.

4. Option II: $r(X) = 1/n$ for covering and $r(X) = n$ for factor space gives $r = r(CP_2)/r(M^4)$. This gives $r = n_b/n_a$ for $\hat{H}/G_a \times G_b$ option and $r = n_a/n_b$ for $\hat{H}\hat{times}(G_a \times G_b)$ option with obvious formulas for the hybrid cases.

5. At quantum level the fractionization would come from the modification of fermionic anticommutation (bosonic commutation) relations involving $\hbar$ at the right hand side so that particle number becomes a multiple of $1/n$ or n. If one postulates that the total number states is invariant in the transition, the increase in the number of sheets is compensated by the increase of the fundamental phase space volume proportional to $\hbar$. This would give $r(X) \to r(X)/n$ for factor space and $r(X) \to nr(X)$ for the covering space to compensate the n-fold reduction/increase of states. This would favor Option II.

6. The second manner to distinguish between these two options is to apply the theory to concrete physical situations. Since G_a and G_b act as symmetries in CD and CP_2 degrees of freedom, one might of being able to distinguish between the two options if it is possible to distinguish between the action of G as symmetry of quantum states associated with covering and factor space. Also the quantization of the orbital spin quantum number at single particle level as multiples of n can be distinguished from that in multiples of $1/n$.

3.6.3 A simple model of fractional quantum Hall effect

The generalization of the imbedding space suggests that it could possible to understand fractional quantum Hall effect [1] at the level of basic quantum TGD. This section represents the first rough model of QHE constructed for a couple of years ago is discussed. Needless to emphasize, the model represents only the basic idea and involves ad hoc assumption about charge fractionization.

Recall that the formula for the quantized Hall conductance is given by

$$\begin{aligned} \sigma &= \nu \times \frac{e^2}{h} \ , \\ \nu &= \frac{n}{m} \ . \end{aligned} \tag{3.6.1}$$

Series of fractions in $\nu = 1/3, 2/5, 3/7, 4/9, 5/11, 6/13, 7/15...$, $2/3, 3/5, 4/7, 5/9, 6/11, 7/13...$, $5/3, 8/5, 11/7, 14/9...$ $1/5, 2/9, 3/13...$, $2/7, 3/11...$, $1/7....$ with odd denominator have been observed as are also $\nu = 1/2$ and $\nu = 5/2$ states with even denominator [1] .

The model of Laughlin [15] cannot explain all aspects of FQHE. The best existing model proposed originally by Jain is based on composite fermions resulting as bound states of electron and even number of magnetic flux quanta [13] . Electrons remain integer charged but due to the effective magnetic field electrons appear to have fractional charges. Composite fermion picture predicts all the observed fractions and also their relative intensities and the order in which they appear as the quality of sample improves.

The generalization of the notion of imbedding space suggests the possibility to interpret these states in terms of fractionized charge, spin, and electron number. There are four combinations of covering and factors spaces of CP_2 and three of them can lead to the increase of Planck constant. Besides this there are two options for the formula of Planck constant so that which the very meager theoretical background one can make only guesses. On the following just for fun consideration option I is considered although the conservation of number of states in the phase transition changing $\hbar$ favors option II.

1. The easiest manner to understand the observed fractions is by assuming that both M^4 and CP_2 correspond to covering spaces so that both spin and electric charge and fermion number are fractionized. This means that e in electronic charge density is replaced with fractional charge. Quantized magnetic flux is proportional to e and the question is whether also here fractional charge appears. Assume that this does not occur.

2. With this assumption the expression for the Planck constant becomes for Option II as $r = \hbar/\hbar_0 = n_a/n_b$ and charge and spin units are equal to $1/n_b$ and $1/n_a$ respectively. This gives $\nu = nn_a/n_b$. The values $m = 2, 3, 5, 7, ..$ are observed. Planck constant can have arbitrarily large values. There are general arguments stating that also spin is fractionized in FQHE.

3. The appearance of $\nu = 5/2$ has been observed [9] . The fractionized charge is $e/4$ in this case. Since $n_i > 3$ holds true if coverings are correlates for Jones inclusions, this requires to $n_b = 4$ and $n_a = 10$. n_b predicting a correct fractionization of charge. The alternative option would be $n_b = 2$ that also Z_2 would appear as the fundamental group of the covering space. Filling fraction $1/2$ corresponds in the composite fermion model and also experimentally to the limit of zero magnetic field [13] . $n_b = 2$ is however inconsistent with the observed fractionization of electric charge and with the vision inspired by Jones inclusions.

4. A possible problematic aspect of the TGD based model is the experimental absence of even values of n_b except $n_b = 2$ (Laughlin's model predicts only odd values of n). A possible explanation is

that by some symmetry condition possibly related to fermionic statistics (as in Laughlin model) n_a/n_b must reduce to a rational with an odd denominator for $n_b > 2$. In other words, one has $n_a \propto 2^r$, where 2^r the largest power of 2 divisor of n_b.

5. Large values of n_a emerge as B increases. This can be understood from flux quantization. One has $e \int BdS = n\hbar(M^4) = nn_a\hbar_0$. By using actual fractional charge $e_F = e/n_b$ in the flux factor would give $e_F \int BdS = n(n_a/n_b)\hbar_0 = n\hbar$. The interpretation is that each of the n_a sheets contributes one unit to the flux for e. Note that the value of magnetic field in given sheet is not affected so that the build-up of multiple covering seems to keep magnetic field strength below critical value.

6. The understanding of the thermal stability is not trivial. The original FQHE was observed in 80 mK temperature corresponding roughly to a thermal energy of $T \sim 10^{-5}$ eV. For graphene the effect is observed at room temperature. Cyclotron energy for electron is (from $f_e = 6 \times 10^5$ Hz at $B = .2$ Gauss) of order thermal energy at room temperature in a magnetic field varying in the range 1-10 Tesla. This raises the question why the original FQHE requires so low temperature. The magnetic energy of a flux tube of length L is by flux quantization roughly $e^2B^2S \sim E_c(e)m_eL$ ($\hbar_0 = c = 1$) and exceeds cyclotron roughly by a factor L/L_e, L_e electron Compton length so that thermal stability of magnetic flux quanta is not the explanation. A possible explanation is that since FQHE involves several values of Planck constant, it is quantum critical phenomenon and is characterized by a critical temperature. The differences of the energies associated with the phase with ordinary Planck constant and phases with different Planck constant would characterize the transition temperature.

As already noticed, it is possible to imagine several other options and the identification of charge unit is rather ad hoc. Therefore this model can be taken only as a warm-up exercise. In [54] Quantum Hall effect and charge fractionization are discussed in detail and one ends up with a rather detailed view about the delicacies of the Kähler structure of generalized imbedding space.

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Part II

PHYSICS INSPIRED MODELS FOR GENOME AND EVOLUTION OF GENETIC CODE

Chapter 4

Genes and Memes

4.1 Introduction

In TGD based model of consciousness genes and memes are in very similar position. The quantum self-organization process explains genetic code as an outcome of Darwinian selection basically carried out by dissipation, and also memes should be subject to similar selection. Cognitive codes would be for neuroscience what genetic code is for biology. Hence there are good motivations to guess what the precise form and realization of these codes might be if it really exists. In fact, p-adic length scale hierarchy suggests an entire fractal hierarchy of cognitive codes with quantized durations of the codeword and preferred numbers of bits per code word [79] . There exists however some preferred cognitive codes. A simple model for abstraction process leads to an entire hierarchy of genetic codes and one of them explains the basic numbers of the genetic code. A fascinating possibility is that the next level in the hierarchy yields memetic code and also this possibility will be studied in the sequel. Genetic and memetic codes represent particular examples associated with Mersenne primes $p = 127 = 2^7 - 1$ and $p = M_{127} = 2^{127} - 1$.

4.1.1 Combinatorial Hierarchy of codes

The basic numbers of genetic code are probably not accidental. This led for more than ten years ago to an attempt to construct a model for abstraction process reproducing the basic numbers of the genetic code.

Genetic code from a model for abstraction process

The simplest model for an abstraction process is based to a repeated formation of statements about statements starting from two basic statements representing the most primitive logical thoughts. If one drops at each step of construction the statement corresponding to empty set in the set theoretic realization of Boolean algebra, one obtains a hierarchy allowing to understand the basic numbers of genetic code.

The outcome is the so called Combinatorial Hierarchy [32] consisting of the Mersenne numbers $2, M(1) = 3, 7$,$127, 2^{127} - 1, ..$ constructed using the rule $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$. The explicitly listed ones are known to be primes. Combinatorial Hierarchy emerges from a model of abstraction process as sub-sequent transitions from level to meta level by forming Boolean statements about Boolean statements of level n and dropping one statement away. Combinatorial Hierarchy results also by constructing the sets of all subsets with empty set excluded starting from two element set. The set of statements at level n can be given a structure of Finite Field $G(M(n), 1)$ if $M(n)$ is prime. The multiplicative groups $Z_{M(n)-1}$ form a nested hierarchy and the coset spaces $Z_{k_n} \equiv Z_{M(n)-1}/Z_{M(n-1)-1}$ are cyclic groups ($k_n = (M(n) - 1)/(M(n-1) - 1)$). Hilbert's conjecture states that each Mersenne number in the Combinatorial Hierarchy is prime.

Combinatorial Hierarchy based model of genetic code explains the number of DNAs and amino-acids, and the representation of words of the genetic code as triplets of 4 different lower level codewords. Genetic code corresponds to $n = 3$ level of the hierarchy with 127 statements representable as 7-bit sequences with the sequence of seven '0':s dropped away. Only the 64 6-bit code words can be fully

realized and correspond to $(M(3)+1)/2 = 64$ DNA triplets. $k_3 = 126/6 = 21$ equals to the number of amino-acids plus stopping codon. There is a natural imbedding of subgroup Z_{21} identifiable as a representation of amino-acids to the group $Z_{126=6\times 21}$.

More abstractly, at level n the counterparts of DNA triplets correspond to the set $X_{N(DNA)} \subset Z_{M(n)-1}$ of $N(DNA) = (M(n)+1)/2$ statements consistent with a fixed atomic statement (64 for $n = 3$). Atomic statement corresponds to a fixed value, assumed to be one, of a fixed bit in a bit sequence representation and a subset consisting of single element in the set theoretic representation. These statements could be regarded as statements consistent with the axiom defined by the selection of the atomic statement. The counterparts of amino-acids and stopping codon correspond to k_n theorems of a formal system defined by n^{th} level of Combinatorial Hierarchy having a unique imbedding as the group $Z_{k_n} \subset Z_{M(n)-1}$. The DNAs coding for a given "amino-acid" correspond to the special cases of the theorem.

Mapping of DNA code words to amino-acids generalizes to the mapping $x \to x^{k_{n-1}}$ in $Z_{M(n)-1}$ mapping DNA type statements to amino-acid type statements. $(M(n)+1)/2$ DNAs can be imbedded to Z_{126} with several manners. Genetic code is fixed ones this imbedding is given. For $n = 3$ one obtains ordinary genetic code defined by the map $x \to x^6$ and imbedding of the DNAs to Z_{126}. The numbers of DNA:s coding single amino-acid can be reproduced by a symmetry breaking mechanism involving the finite groups $Z_{p_{n-1}}$ and Z_{k_n} and symmetry breaking is in a well defined sense minimal. The infinite hierarchy of possible genetic codes (at least if Hilbert's conjecture holds true) suggests the possibility of an infinite hierarchy of increasingly complex life forms.

If one allows only Mersenne primes, the model for the abstraction process predicts at least one further code, which I have used to call memetic code. It corresponds to the Mersenne prime $M_{127} = 2^{127} - 1$ and has 2^{126} code words and $(2^{126} - 1)/(2^6 - 1)$ "amino-acids". The secondary p-adic time scale $T(2, M_{127})$ is .1 seconds and defines a fundamental time scale in bio-systems.

There are reasons to expect that memetic code is an especially interesting higher level cognitive code and realized in terms of field patterns. In particular intronic portion of DNA could realize memetic codewords as sequences of 21 DNA triplets and memes would define the counterparts of computer programs at DNA level whereas genes would define the counterpart of computer hardware coded into lower level programs and built only when needed. Both memes and genes could express themselves in terms of field patterns.

Memes and genes should relate like computer software and hardware. In the case of language the rules producing a given linguistic expression can be seen as the software whereas words can be seen as the hardware built from phonemes. This leads to the idea that memetic codewords define the basic program modules producing linguistic expressions by activating genes which express themselves as words or word sequences. Phonemes could directly correspond to DNA triplets and define the basic building blocks of language having as such no meaning. If this view is correct, the development of spoken and written language would mean basically the emergence of a higher level of intentionality, which utilizes an already existing repertoire of memes already expressed in many other manners. This would in turn suggest that animals and even plants possess some kind of languages realized at cellular level, and that even inter-species communications using common memetic vocabulary.

Myth about Fall of Man as metaphor for codes

There are basically two genetic and memetic codes: 6-bit and almost-7-bit ($2^3 - 1$ code words represented consciously) genetic codes and 126- and almost-127 bit memetic codes. The myth about the Fall of Man provides a little bit tongue-in-cheek metaphor for the extension of 126-bit code to almost-127-bit code. God gave to Adam and Eve the moral code as a single moral law formulated as an atomic statement "Do anything but do not eat from the Tree of Good and Bad Knowledge". Adam and Eve of course did this and probably as many fractally scaled versions.

The first Fall occurred probably already at the molecular level and meant the replacement of 6-bit genetic code with almost-7-bit code: $63 = 9 \times 7$ sins beside 64 good deeds appeared (there are 9 classes of sins containing one sin for every day of the week, one of them containing the seven deadly ones!). Imagination and intentions realized as deeds emerged and Adam and Eve became moral agents. For the memetic code the replacement of 126-bit memetic code led to almost 127-bit code and the repertoire of good and bad deeds was now much more impressive: 2^{126} good deeds and $2^{126} - 1$ sins (the basic classification sins to 7 basic types makes senses still!). One can of course wonder what was this un-doable sin with strong Gödelian flavor. A code word with only zeros cannot give rise to a

conscious experience. Hence the un-doable sin could be such that the sinner cannot experience its consequences in this life, that is suicide.

Genetic code and thinking at DNA level

TGD predicts entire infinite hierarchy of selves starting from elementary particle level so that consciousness should be present also at DNA and protein level. The notion of self indeed allows to understand protein folding, which is rather mysterious phenomenon in standard physics framework.

The physical model of the genetic code constructed in [41] , when interpreted in terms of the model for an abstraction process, suggests the interpretation of the genetic code as mapping the fundamental 64 truths to 20 basic conscious experiences, perhaps the protein level emotional experience about truthness: it must be emphasized that our experiences are probably not in question. Amino-acid P could correspond to the emotionally experienced truth '$G_1(P)$ or $G_2(P)$.. or $G_n(P)$ is true', where G_i code for protein P. 3 stopping sign codewords cannot be experienced emotionally as truths not non-truths (holy trinity at protein level!).

In the model for introns discussed in the chapter [41] cognitive neutrino play an essential role in the genetic program of eukaryotes and suggests that Boolean mind appears already at molecular level and could correspond to the logical statements represented by genes. This Boolean mind does not correspond to our conscious logical thinking.

Does memetic code emerge at the next level of abstraction process?

The natural question is whether a counterpart of the genetic code could make sense for memes. Combinatorial Hierarchy model for abstraction process that memetic code should correspond to the level M_{127} of the hierarchy. This leads to a precise realization of the memetic code in terms of binary sequences. The secondary p-adic time scale associated with M_{127} is .1 seconds, which seems to define the duration for the immediate subjective memory. If this time scale corresponds to a sequence consisting 127 bits, the duration of single bit is 1/1270 seconds, which happens to be very near to definite p-adic time scale but is somewhat shorter than the typical duration of nerve pulse. This suggests that nerve pulse patterns as such cannot realize the full memetic code. The time scale associated with $k = 252 = 2 \times 6 \times 21$ is .05 seconds and one half of the duration of 127-bit memetic codon. $k = 252$ allows the representations of both 6- and 7-bit genetic codes and of the 126-bit memetic code.

An attractive hypothesis is that the temporal sequences for the Z^0 magnetization directions for a block cognitive antineutrinos at cell membrane space-time sheet provide a representation of the almost 127-bit memetic codeword. The conscious experience results when the Z^0 magnetization directions flip back to the direction of external Z^0 magnetic field in spin flipping cyclotron transition. $M_{127} = 2^{127}-1$ different conscious experiences results since nothing happens if all cognitive antineutrinos are in the same direction as external Z^0 magnetic field. Z^0 magnetization direction could be altered by the Z^0 magnetic pulse associated with the Z^0 ME inducing cell membrane oscillations of nerve pulse pattern.

This raises obvious questions. Does genome have a memetic counterpart; what would be the function of the memone; what would be the memetic counterparts of the transcription and translation processes for genes? The natural guess is that memes are the basic building blocks of cognition and language. Perhaps also memes are coded by DNA, most naturally by introns, whose portion from the genome increases with the evolutionary level of organism and is 99 per cent for Homo Sapiens. The sequences of 21 DNA triplets would naturally realize 126-bit memetic codons 2^{126} memetic codons at DNA level. The prediction is that the intronic portions of the genome should consist of basic units containing 21 DNA triplets. This would also mean that the language conscious-to-us is only a tip of an iceberg. The intronic part of the DNA would be expressed in terms of MEs and involve communications between cell membrane and nucleus. The dynamics of this realization would be fast and nucleus would play the role of cellular brain.

4.1.2 The product model for the evolution of genetic code

It became as a surprise to me personally that the genetic code has an exact A-G permutation symmetry and an almost exact T-C permutation symmetry with respect to the third nucleotide. Seen with the eyes of a theoretical physicist knowing the enormous importance of spontaneous symmetry breaking in

physics, these simple symmetries point the way to the understanding of the basic mechanism behind the evolution of the genetic code.

This inspired a simple model for our genetic code allowing to see the genetic code as a product of much simpler doublet and singlet codes with a small symmetry breaking due to the interaction between singlets and doublets. This model, even admittedly rather formal, might have deep implications for the theories how the life at the molecular level has involved. The physical realization of this model will be also discussed briefly. A detailed discussion can be found in [29] .

4.1.3 General ideas about codes and languages

By quantum-classical correspondence space-time sheets provide a symbolic representation for the contents of consciousness. Therefore one can say that everything in principle represents and the task is to understand how these symbolic representations are generated, how codes are established, and how these symbolic representations generated the desired mental images. This obviously means a profound departure from the basic belief system of standard biology.

Computer languages form a hierarchy such that highest level languages are very flexible approaching gradually to the spoken language whereas lowest level languages are very precise and rigid. The notion of self hierarchy suggests that our spoken language is only a top of an iceberg and that below it is a hierarchy of languages ending down to the cellular level and DNA is one particular example about "computer language" realized in terms of p-adic cognitive codes, in particular genetic and memetic codes. In an attempt to understand whether and how memetic and other p-adic cognitive codes might relate to the spoken and written language one must have some general ideas codes and language.

The hierarchy of cognitive codes

p-Adic length scale hypothesis suggests an entire hierarchy of cognitive codes and languages. The primes $p \simeq 2^k$, k integer seems to be interesting physically, and prime values of k seem to be especially interesting. The codes would be characterized by the duration of the codeword given by n-ary p-adic time scale $T_p(n) = p^{(n-1)/2}T_p$, $T_p = 2^{k/2-127}T(2,127)$, $T(2,127) = .1$ seconds. The most general assumption is that number k_1 of bits of the codeword for given integer k_1 corresponds to some factor of k, the largest factor maximizing the information content. Codes could be represented either as temporal sequences of bits represented as pulses of maximal duration $T_p(n)/k_1$ or as superpositions of k_1 harmonics of $f_1 = 1/T_p(n)$, where Fourier components having intensity above/below critical value would represent bit 1/0. These representations will be referred to as pulse and frequency representations. Frequency representations would be realized in terms of topological light rays ("massless extremals", MEs) representing topologically quantized transverse radiation and pulse representations in terms of scalar wave pulses not possible in Maxwell's electrodynamics [25] . This representational dichotomy reflects particle-wave duality and talking left brain and singing right brain dichotomy.

Memetic and genetic codes represent special examples of cognitive codes. One must distinguish between two representations: the representations involving 6 bits or almost 7 bits and 126 bits or almost 127 bits. 'Almost' means that only $2^k - 1$ bit sequences rather than all 2^k bit sequences are realized as conscious bits if bits are realized as phase transitions.

Codes are always involved with classical communications involving transformation of mental images to a symbolic representation by some code. At our level of the hierarchy this symbolic representation could be speech, written language, picture, body language... This would suggest that also p-adic cognitive codes are involved with conscious communications. If these codes are realized in living systems, the bit sequences with the predicted durations and bit contents should induce biological effects serving as correlates for the conscious understanding of the message generated by the codewords at some level of the hierarchy.

TGD based view about living matter relies on the notion of field body or magnetic body associated with any system and having size much larger than the material body. Also these bodies form a fractal hierarchy. The communications from material body to field body could be based on cognitive codes. Given p-adic frequency corresponds f_p to a p-adic length scale $L_p = c/f_p$ characterizing the size of the magnetic body involved and for EEG frequencies the size scale of Earth is natural unit. For instance, p-adic cognitive codes realized in terms of field patterns would be involved with the communication of long term declarative memories from the geometric past.

What language is?

The attempt to understand the possible role of memetic code, a rough vision about what language is, allows to eliminate several ideas which look promising at first.

1. Language involves generation of symbolic representation of a mental image by a more or less rigid code. An example of a very flexible code is code based on associations. The symbolic representation of mental image should induce in the receiver the original mental image as faithfully as possible. This requires that a lot of common context. In particular, the neurologies and biologies of the sender and receiver must resemble each other sufficiently. In the case of high level languages like ordinary language even this is not enough and only simplest verbal signals and body language are understood universally. The cognitive codes associated with say cell level communications might make possible communications between cells of even different species remaining however unconscious to us.

2. The p-adic vision about evolution of cognitive skills like spoken language is that they evolve from long time and length scales to shorter ones. First a rough sketch about the motor action is created and gradually more and more details are added. This applies also at the level of the evolution of language itself. Simple signals expressing and generating emotions evolve gradually to spoken language which evolves to written language which in turn evolves to computer languages.

3. Learning of language requires learning of the conventions assigning to a given symbol a mental image. Sharing of mental images which represent more primitive "telepathic" communication makes possible this process. The observation that even plants and cells can react to our emotions and that this reaction does not depend much on distance [14] , suggest that the sharing of mental images is in question. This allows to consider the possibility of inter-species linguistic communications using field patterns.

4. The understanding of language requires transformation of symbolic representation to conscious experience and here the notion of conscious bit ("cbit" [48]) realized as a phase transition or as an absence of phase transition suggests itself. Phase transition could correspond to magnetization or formation of electret state and living matter could generate these representations in various length scales.

5. In TGD Universe intentions are realized as actions by a process, which proceeds from the magnetic body downwards along the hierarchy much like a desire of a boss of some institution to the lower levels of hierarchy. At each level intention or intentions are transformed to desires communicated to the lower levels of hierarchy. Intentions have p-adic space-time sheets as space-time correlates and are transformed to real ones representing the desire.

The most plausible realization of this process is in terms of time mirror mechanism. The space-time sheets in question would correspond to negative energy topological light rays representing the propagation of signals to the geometric past and induce processes. The process would continue down to the level of neurons and even DNA level and generate the desired action as a reaction to the resulting complex of desires. The beauty of the mechanism is that the communication to the geometric past makes it instantaneous.

Spoken and written language would rely on the same process and could propagate down to the level of genome and select the memes to be expressed. The expression of these memes as field patterns would then be a process propagating upwards in the hierarchy and finally generating speech or written word. When I decide to say something say the words "time mirror", this intention is transformed to a desire communicated to the geometric past to the lower level of the self hierarchy, and that at this level this desire generates further desires communicated to the lower levels. Ultimately this process ends down to the level of cells and even cell nuclei and DNA and induces response which propagates to the higher levels as neural and other activities inducing muscular activities in speech organs and generates the words "time mirror".

The signal to the geometric past involves negative energy photons and topological light rays. The working hypothesis has been that the signal to the geometric past is only a space-time correlate for sharing of the desire to generate the action, and does not involve any code. If this is the case then only the response propagating to the geometric future would be classical signal based on some code.

One must however keep mind open to the possibility that also communications to the geometric past involve code.

Conscious bits and cognitive representations

The symbols representing message must be transformed to standardized mental images. The simplest possibility is that the mental images are coded to patterns of conscious bits or cbits. The general model for sensory and other qualia suggests that conscious bits should be realized as quantum jumps sequences associated with phase transitions. In this manner same quantum number increment is occurs for many particle for single quantum jump and for sufficiently long sequence of quantum jumps. Bit 1 would correspond to the occurrence of phase transition and bit 0 to the non-occurrence of the phase transition. For a code of k bits this has important implication: the codeword containing only zeros does not generate any conscious experience so that the number of experienced code words is $2^k - 1$. This could explain why Mersenne primes seem to be define especially important p-adic time scales.

Living matter is populated by dynamical electrets so that phase transitions between ordinary and electret states at various length scales are expected to be of special importance. Also magnetization of super phases at magnetic flux tubes of say Earth's magnetic field is expected to be one mechanism producing basic qualia serving as as bits.

Computer metaphor at DNA level

Software and hardware are essential elements of the computer and at DNA level this could mean that genes code for hardware which is not stable as in case of ordinary computers. This means that computer hardware is replaced by the possibility to generate it and genes carry the information needed for this. Introns would in turn represent the software, the programs and therefore also the linguistic aspect of DNA. An interesting possibility is that introns realize memes as sequences of 21 DNA triplets. This picture allows and even suggests that even DNA level might be involved with the generation of spoken words and define the deep structure of language.

4.2 Combinatorial Hierarchy and Genetic Code

It is already found that Combinatorial Hierarchy emerges as a unique hierarchy of mappings of Boolean thoughts to association sequences, which could perhaps correspond to nerve pulse patterns, or more probably, to temporal field patterns. In the following the connection of Combinatorial Hierarchy with genetic code is demonstrated.

4.2.1 Combinatorial Hierarchy as a model for abstraction process

One could view the development of intelligence as a process, which takes place as sub-sequent transitions from hierarchy level to a higher hierarchy level, meta-level. First there are statements about concrete things, say numbers. Then come the statements about statements (say theorems about theorems of number theory): "If theorem A is true then theorem B is true". Then come the statements about statements about...

What is remarkable is that the so called Combinatorial Hierarchy [32] (which emerged first in particle physics context) results from this kind of gradual abstraction process consider Z_2 valued functions. The value 1 might correspond to "true" and 0 to "not true".
i) Assume that lowest level corresponds to 2 statements.
ii) Go to the meta level and consider statements about statements (theorems about theorems in mathematics). Therefore one must consider Z_2 valued Boolean functions in Z_2 corresponding to statements of type 'P is true' and 'P is not true' : there are altogether 4 of them. Drop the statement represented by $(0, 0)$.
iii) Again one goes to meta level and considers statements about statements about statements that is functions from 3-element set to Z_2: 7 elements altogether, when one throws away the statement represented by sequence of zero bits.
iv) Continuing this process one clearly gets Combinatorial Hierarchy.

The somewhat mysterious feature is the dropping of one statement. If the construction corresponds to the construction assigning creation of the cognitive fermion pair with the splitting of a wormhole

contact connecting two space-time sheets, then the requirement that the two space-time sheets form a connected structure drops exactly one configuration (no wormhole contacts connecting the two space-time sheets) from consideration. Second interpretation would be in terms of conscious bit. If conscious bit '1' is represented as a phase transition of some kind then the sequence of '0's is not representable as a conscious bits so that only $2^k - 1$ code words are representable for k bit code and the only $k - 1$ bits are fully representable which suggests that only 2^{k-1} bits represent information and remaining bits could play the same role as parity bits.

There is second construction which is purely set theoretical and gives a natural explanation for the dropping of one statement. Consider subsets of the set $(0, 1)$. There are 3 of them if the physically non-realizable empty set is excluded. Consider next the subsets of the 3-element set: there are $2^3 - 1 = 7$ of these sets if empty set is excluded. By continuing the process one finds that the numbers of the Combinatorial Hierarchy result. This suggests that the physical non-realizability of $(0, 0, ...)$ Boolean statement is basic reason for dropping it from consideration.

The numbers of the Combinatorial Hierarchy have some properties, which suggest that they are very closely related to Genetic Code.

1. The numbers $p = 3 = M_2, 7 = M_3, 127 = M_7, M_{127}$ are Mersenne primes. It is possible that all the Mersenne numbers $M(n + 1) = M_{M(n)}$ of the sequence are primes. This implies that the statements can be given the algebraic structure of Finite Field $G(p, 1)$. Therefore the set of the Boolean statements has also interpretation as a simplified model for arithmetics and the arithmetic abilities of the intelligent system grow gradually in transitions from level to meta level. As a consequence the basic conjecture

$$M(n+1) \quad = \quad M_{M(n)} = 2^{M(n)} - 1 \text{ prime } n = 1, 2, ... \ , \tag{4.2.1}$$

   roughly means that there is no upper bound for the arithmetic abilities of intelligent system!

2. The statements at the level p are of two types: 'P is true' and 'P is not true' and there are clearly $N(p) = (p + 1)/2$ mutually consistent statements at level p. These numbers come as $2, 4, 64, 2^{126}, ..$ for $p = 3, 7, 127, ...$ What is remarkable is that $N(7) = 4$ is the number of different DNA:s and $N(127)$ is the number of different DNA sequences. This suggests that DNA:s represent physically consistent with a given atomic statement at level p.

3. The finite field $G(p, 1)$ has the cyclic group Z_{p-1} as the multiplicative group of nonzero elements. The dimensions of these groups read as $1, 2, 6 = 2 \cdot 3, 126 = 6 \cdot 21, ...$ for Combinatorial Hierarchy. The multiplicative group of the previous level can be regarded as a subgroup of the next level multiplicative group for the lowest members of the Combinatorial Hierarchy at least: $Z_{p_n-1} \subset Z_{p_{n+1}-1}$. The reason is that $p_{n+1} - 1$ is divisible by $p_n - 1$ for the lowest Mersenne primes. In fact divisibility holds true also for $M_{127} - 1$ and $M_7 - 1$. Divisibility condition gives

$$2^{126} - 1 \quad = \quad 63n \ . \tag{4.2.2}$$

   The condition is satisfied!: $63 = 3^2 \cdot 7$ divides $2^{126} - 1$, whose prime factorization [13] is given by

$$\begin{aligned} 2^{126} - 1 \quad &= \quad 3^3 \cdot 7^2 \cdot 19 \cdot 43 \cdot 73 \cdot 127 \cdot X \ , \\ X \quad &= \quad 337 \cdot 5419 \cdot 92737 \cdot 649657 \cdot 77158673929 \ . \end{aligned} \tag{4.2.3}$$

Actually the divisibility follows quite generally from the following little theorem:
Theorem: $M(n) - 1$ divides $M(n + 1) - 1$ always and $M(n)$ divides $M(n + 1) - 1$ if $M(n)$ is prime.
The divisibility of $M(M(n)) - 1$ by prime $M(n)$ follows as a particular case $a = 2, p = M(n)$ of Fermat's theorem stating that $a^{p-1} = 1 \ mod \ p$ holds true for any natural number a and any prime

p. The divisibility of $M(M(n))-1$ by $M(n)-1$ is equivalent with the divisibility of $2^{M(n)-1}-1$ with $2^{M(n-1)-1}-1$. This property holds true for the lowest Mersenne numbers of the Combinatorial Hierarchy and can be proven to hold true generally by induction using the following lemma [8] :
Lemma: The greatest common multiplier (x,y) for integers $x=2^a-1$ and $y=2^b-1$ satisfies $(2^a-1,2^b-1)=2^{(a,b)}-1$. The proof of the lemma is based on the observation that the polynomial x^n-1 ($x=2$ now) factorizes into a product of factors (x_i^n-1), where n_i is factor of n. For the polynomials x^a-1 and x^b-1 the largest common multiplier is therefore $x^{(a,b)}-1$.
For $a=M(n)-1$ and $b=M(M(n+1))-1$ lemma together with the induction assumption gives $(a,b)=2^{(M(n)-1,M(n-1)-1)}-1=2^{M(n-1)-1}-1$: the result means that $2^{M(n-1)-1}-1=M(n)-1$ divides $2^{M(n)-1}-1=M(n+1)-1$. The prime number property of Mersenne numbers is not needed in the proof.

As a consequence one has an infinite hierarchy of coset spaces $Z_{p_{n+1}-1}/Z_{p_n-1}=Z_{k_n}$, which are also cyclic groups. The first members of this hierarchy are $Z_{k_1)}=Z_2,Z_3,Z_{21},....$ Also the groups Z_{k_n} satisfy the condition $Z_{k_n}\subset Z_{k_{n+1}}$ for the lowest values of k with k_1 excluded and an interesting possibility is that k_n divides k_{n+1} quite generally for some number theoretic reason. What is remarkable is that $k_2=3$ is the number of DNA:s in DNA triplets and $k_3=21$ is the number of amino-acids plus stopping sign coded by DNA:s. This observation suggests that amino-acids correspond to the subset of the statements of $G(p_n,1)$ imbeddable as subgroup Z_{k_n} to Z_{p_n-1} for $p_n=127$. A little consideration shows that the map $x\to x^{k_{n-1}}$ gives a unique imbedding for the amino-acid type statements to Z_{p_n-1}.

n	1	2	3	4
$M(n)$	3	7	127	$2^{127}-1$
$N(DNA,n)=(M(n)+1)/2$	2	4	64	2^{126}
$N(amino,n)=(M(n)-1)/(M(n-1)-1)$	2	3	21	$(2^{126}-1)/63$

Table 1. The lowest Mersenne numbers of Combinatorial Hierarhcy (known to be primes), the numbers of 'DNA' k_{n-1}-plets and the numbers of 'amino-acids' for these levels.

These observations suggest a general model for Genetic Code. The 64 DNA sequences give a physical representation for the statements compatible with a given atomic statement at $p=127$ level of the Combinatorial Hierarchy. The choice of these mutually compatible statements as a subset of $G(127,1)$ is by no means unique and is determined by the evolution. The 21 amino-acids (stopping sign is regarded formally as 'amino-acid') at $p=127$ level correspond to the unique statements representable in the form $y=x^6$ in Z_{126} and form cyclic group Z_{21}. Genetic code can be regarded as the mapping $x\to x^6$ mapping all DNA type statements to amino acid type statements. The interpretation of the amino-acid type statements is as general axioms and DNA type statements are regarded as special cases of these axioms. Amino-acid sequences in turn are regarded as theorems derivable from axioms by constructing amino-acid sequences: the direction of the sequence is unique by the chirality of the amino-acid molecules.

The formation of theorems in formal system indeed corresponds to the formation of symbol sequences by some rules (now the rules are extremely simple, perhaps too simple!). The representability of DNA:s as triplets of 4 basic units has explanation: actually a more general the formula $N(DNA,n)=(p_n+1)/2=((p_{n-1}+1)/2)^{k_{n-1}}=N(DNA,n-1)^{N(amino,n-1)}$ holds true for all levels of the Combinatorial Hierarchy. In particular, for $p=127$ one has $64=4^3$. Actually an infinite hierarchy of Genetic Codes suggests itself: for the n:th member of the Hierarchy there are k_n axioms and if k_n divides k_{n+1} the axioms of level n are imbeddable as a subgroup $Z_{k_n}$to the group $Z_{k_{n+1}}$ of axioms at level $n+1$ and the counterpart of Gödel's Incompleteness Theorem holds true.

4.2.2 Interpretation of genetic code

Finite Field Computer picture leads to the interpretation of genetic code as a map from the set of well defined truth values $X_{64}\subset G(127,1)$ (DNA:s) to the set $Z_{126}/Z_6=Z_{21}\subset G(127,1)$ (amino-acids).

1. The interpretation of the previous observation is that amino-acids and 'stopping sign' correspond to the elements x of the coset space $Y=Z_{126}/Z_6=Z_{21}$ obtained by identifying two elements a and b of Z_{126} are identified if $a^6=b^6$ holds true. The realization of Z_{21} as a subset of $G_{127,1}$ is obtained as the set of non-vanishing sixth powers of $G(127,1)$ elements

$$z \in Z_{21} <=> z = x^6, \quad 0 \neq x \in G(127,1) \quad . \tag{4.2.4}$$

Since a coset space is in question $d = 126/21 = 6$ elements of Z_{126} are mapped to a given element of Z_{21} in the map $x \to x^6$.

2. According to the proposed model of intelligent system DNA triplets correspond to a subset X_{64} of 64 well determined truth values of $p = 127$ logic but at this stage there is no first principle telling which subset corresponds to truth values. Let us however assume that X_{64} corresponds to subset of Z_{126} so that zero element is excluded from X_{64}.

3. With these identifications genetic code correspond to the mapping $x \to x^6$ from the set X_{64} of well defined truth values to Z_{21}

$$x \in X_{64} \quad \to \quad x^6 \in Z_{21} \quad . \tag{4.2.5}$$

The number of DNA triplets d coding same amino acid is just the number of elements of X_{64} mapped to same element of Y and this gives strong constraints for the identification of X_{64} as subset of $G(127,1)$. Clearly, genetic code is to a high degree equivalent with the identification of 64-element DNA triplets as subset of Z_{126}. The identification of X_{64} as subset of Z_{126} cannot however be determined uniquely since the group Z_6 acts as the symmetry group of the code permuting the 6 elements of Z_{21} mapped to same element of Z_{126} and leading to a code with same degeneracies d.

An important prediction is that at most six DNA triplets can correspond to same amino acid. As the following table shows the condition is satisfied: there are three amino acids for which DNA degeneracy d is 6. This means that it is indeed possible to realize genetic code in the proposed manner.

d	6	4	3	2	1
N	3	5	2	9	2

Table 1. The number of amino acids N associated with a given degeneracy d telling the number of DNA triplets mapped to the amino acid in genetic code. The degeneracies are always smaller than 7 as predicted by the proposed explanation of the Genetic Code.

One can consider first simple guesses for the identification of X_{64} as a subset of $G(127,1)$. The identification as even elements $y = 2k$, $k = 0, 63$ is not possible since zero cannot belong to X_{64}: same applies to the identification as odd elements. The identification as the elements expressible as squares $y = x^2$ is excluded for the same reason. One could include the 64^{th} DNA by identifying it as an arbitrary element of Z_{126}. All these identifications yield almost completely symmetric genetic code: $d = 3$ for all 21 amino acids except one for with one has $d = 4$ so that something more complicated is needed.

4.2.3 Genetic Code as a result of geometric symmetry breaking

One could try to understand the pattern of degeneracies as a symmetry breaking pattern, but not in terms of group representations as is done usually but in terms of group orbits. For single DNA multiplet associated with given amino-acid the natural symmetry group is Z_6 or some of its subgroups and DNA multiplet of given amino-acid can be regarded as a union of orbits for the subgroup in question. The subgroups of $Z_{126}/Z_6 = Z_3 Z_7$ in turn can transform the DNA multiplets with same degeneracy to each other and amino-acids with same degeneracy can be regarded as a union of orbits of Z_7, Z_3 or Z_1. This symmetry pattern seems to work!

1. Consider first the group Z_6 acting inside DNA multiplets associated with given amino-acid. The definition of Z_{21} implies that the DNA:as associated with $d = 6$ amino-acids must be identified as six-element orbits of Z_6 symmetry. $d = 3$, $d = 2$, $d = 1$ amino acids correspond to the

breaking of Z_6 to Z_3,Z_2 and to Z_1 respectively. $d = 4$ amino-acids are however problematic since Z_6 does not have 4-element subgroup. One can interpret $d = 4$ DNA:s either as a union of two Z_2 orbits or as a union of Z_3 and Z_1 orbits: Z_1 orbit corresponds most naturally to the mirror image of one Z_3 point, when the points of Z_{126} are represented as points of unit circle. This interpretation seems to be more appropriate.

2. Consider next the group Z_{21} acting on amino-acids. The 3 $d = 6$ amino-acids could be identified as an orbit of $Z_3 \subset Z_{21}$. If one regards the 5 $d = 4$ multiplets as unions of Z_3 and Z_1 orbits one can obtain altogether $2 + 5$ $Z_3 \subset Z_6$ orbits, which could be regarded as Z_7 orbit. What remains is $5 + 2 = 7$ Z_1 orbits, which could be regarded as Z_7 orbit. Therefore it seems that amino-acids can be ordered nicely into the orbits of Z_3 and Z_7. It turns however that exact symmetry is broken and some orbits are slightly deformed or even broken to pieces.

There are good reasons for symmetry breaking.

1. Besides symmetry also redundancy of the genetic code is desirable: this means that the number of the amino-acids with small degeneracy should be as small as possible. Z_6 (or some subgroup) symmetry and redundancy are competing factors since average degeneracy is always same and symmetry tends to increase the redundancy associated with some amino acids. Therefore redundancy requirement might be one underlying reason for symmetry breaking.

2. It turns out that also the competition between symmetries Z_3 and Z_7 in Z_{27} forces either Z_7 or Z_3 symmetry breaking already before the 'actual' symmetry breaking.

3. The third reason for the symmetry breaking is the constraint that the numbers of DNA triplets and amino-acids are constrained to 64 and 21 respectively. For, instance 63 DNA:s allows representation as a union 9 Z_6 orbits having $Z_3 \subset Z_{21}$ as symmetry group but for 64 DNA:s there is necessarily one Z_1 orbit present.

It would be nice if one could understand the genetic code as a small perturbation of some code with both high symmetry and high redundancy. One could even assume that the number of amino-acids before the symmetry breaking is smaller than 21 so that symmetry breaking is necessary to obtain 21 amino-acids. A geometric picture of the situation is obtained by regarding the points of Z_{126} as points $\Phi = n2\pi/126$ of a unit circle endowed with standard metric so that it becomes possible to define what 'small' symmetry breaking means.

4.2.4 Symmetry breaking scenarios

The genetic code can be reproduced as the following symmetry breaking pattern.

1. Unbroken symmetry corresponds to the following situation. There are $6 = 3+3$ amino-acids with maximal degeneracy $d = 6$ and 7 amino-acids with degeneracy $d = 4$: altogether $13 < 21$ so that symmetry breaking is necessary. $d = 6$ multiplets correspond to 6 Z_6 orbits $\Phi = n2\pi/6 + k\Delta(i)$, with $\Delta(i) = k_i 2\pi/126 < 2\pi/6$. Single $d = 4$ multiplet corresponds to Z_3 orbit plus single point, which is diametrically opposite to one of the points at Z_3 orbit. More explicitly: basic $(3, 1)$ multiplet corresponds to the Z_3 orbit $\Phi_3(k) = 6\Delta + k2\pi/3$, $k = 0, 1, 2$ plus the point $\Phi_1 = 6\Delta + \pi$. By acting on this orbit with rotations $\Delta_1(i) = k_i 2\pi/126$, $i = 0, ..., 6$, $\Delta_1(i) < 2\pi/6$ one obtains 7 $d = 4$ multiplets. Obviously one must have $\Delta(i) \neq \Delta_1(j)$ for each i, j pair in order to avoid overlapping. The actual imbedding of Z_6 multiplets is not relevant for the degeneracies of the genetic code and will be discussed later.

2. The first symmetry breaking is $Z_6 \to Z_2$ and occurs for 3 $d = 6$ amino-acids and leads from 3 Z_6 orbits to 9 Z_2 orbits so that 9 $d = 2$ amino-acids result. Breaking can be understood geometrically as follows. Single $d = 6$ multiplet is obtained by Z_2 action (reflection) from Z_3 orbit, say $\Phi(k) = k2\pi/3$. What happens is that two points on Z_3 orbit that for Z^3 orbit the points $\Phi(k)$ with $k = 1$ and 4 are rotated slightly with different rotation angles

$$\begin{aligned}
\Phi(1) &\rightarrow \Phi(1)+\delta_1 \ , \\
\Phi(4) \rightarrow \Phi(4)+\delta_1 \ , & \\
\Phi(5) &\rightarrow \Phi(5)-\delta_2 \ , \\
\Phi(6) &\rightarrow \Phi(6)-\delta_2 \ , \\
\delta_i &= \frac{k_i 2\pi}{126} \ , \\
1 < k_i &< 6 \ . \qquad (4.2.6)
\end{aligned}$$

Here δ_i must be chosen so that the deformed points do not coincide with already 'occupied' points. Minimal symmetry breaking is obtained with $k_1 = 1 = k_2$ but would lead to overlapping. One must also have $k_1 \neq k_2$ ($k_1 = k_2$ would imply additional reflection symmetry). The symmetry breaking leads to $9 + 7 = 16$ amino acids with degeneracies $d \geq 2$.

3. The second symmetry breaking leads from 7 $d = 4$ multiplets to 5 $d = 4$ multiplets, 2 $d = 3$ multiplets and 2 $d = 1$ multiplets. What happens is that 2 basic $d = 4$ multiplets consisting of Z_3 orbit and mirror image of one of Z_3 points is deformed $d = 3$ plus $d = 1$ multiplet: this is achieved if mirror image point is slighly shifted. The deformation is obtained by performing for the basic multiplet $(\Phi_3(k) = k2\pi/3, \Phi_1 = \pi)$ the deformation

$$\Phi_1 = \pi \quad \rightarrow \quad \pi \pm \delta_3 \ . \qquad (4.2.7)$$

$\delta_3 = k_3 2\pi/126$, $1 < k_3 < 6$ followed by appropriate rotation carrying broken multiplet to its own position. $k_3 = 1$ is not allowed since it would lead to overlapping and $k_3 = 2$ leads to the smallest possible symmetry breaking.

One can try to find unique imbedding of X_{64} (and also try to understand the uniqueness of the genetic code) by requiring that amino-acids form orbits of Z_{21} or its subgroups. Z_3 and Z_7 are competing symmetries and not consistent with each other: the reason is that Z_3 orbits and Z_7 orbits in same basic angular range of length $2\pi/6$ necessarily overlap since between two points of Z_3 orbit there are always just 6 points so that Z_7 orbit cannot be put between two points on Z_3 orbit. Therefore one must choose between either enhanced Z_3 or Z_7 symmetry for the imbedding of X_{64}.

Consider first Z_3 symmetric situation.

1. $6 = 3 + 3$ Z_6 orbits decompose naturally into two orbits of Z_3. The first Z_3 orbit corresponds to $\Phi(k, m) = 6m \cdot 2\pi/126 + k2\pi/6$, $m = 0, 1, 2$ and second Z_3 orbit is obtained from this orbit by a rotation $\Delta\Phi = 2\pi/126$. When Z_6 orbits break down to 9 Z_2 orbits the Z_2 orbits can form 3 separate orbits of Z_3.

2. The graphical experimentation with various possibilities shows that one must split Z_7 orbit to three pieces $7 = 1 + 2 + 2 + 2$ so that the 2:s form Z_3 orbit. Therefore complete breaking of Z_7 symmetry makes possible additional Z_3 symmetry. This means that one $d = 4$ orbits arrange into 2 Z_3 orbits and one Z_1 orbit before symmetry breaking. After the symmetry breaking the 2 $d = 3$ multiplets and $d = 3$:s belonging to 5 $d = 4 : s$ form still Z_3 orbits but two $d = 1$:s are thrown out of corresponding Z_3 orbits.

3. An example of an imbedding satisfying these constraints is given by the following formulas

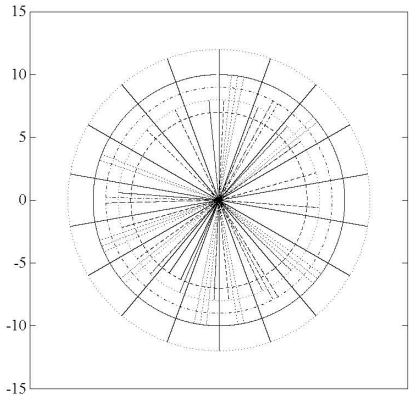
d	N(d)	$\Phi/\Delta = n \ mod \ 126$, $\Delta = 2\pi/126$
6	3	$n = A(i) + B(k)$,$A(i) = 21i$, $B(k) = 7k$, $i \in I$, $k \in K$
		$I = \{0, 1, .., 5\}$, $K = \{0, 1, 2\}$
2	9	$n = (A(i) + B(k) + 1 + \delta_1(i))$, $i \in I$, $k \in K$
		$\delta_1(0) = \delta_1(3) = 0$, $\delta_1(1) = \delta_1(4) = -3$, $\delta_1(2) = \delta_1(5) = 4$
4	5	$n = i + 42k$, $n = i + 63$, $i = 2, 10, 11, 17, 18$, $k \in K$
3	2	$n = i + 42k$,$i = 3, 4$, $k \in K$
1	2	$n = i + 63 + \delta_2(i)$,$i = 3, 4$, $\delta_2(3) = -1$, $\delta_2(4) = 1$

Table 2. Explicit form for the Z_3 symmetric imbedding of X_{64} consistent with Genetic Code. The index k appearing in the formulas labels points on Z_3 orbit. The imbedding is illustrated in figure 4.2.4.

Consider next Z_7 type scenario. 7 $d = 4$:s can be put into single Z_7 orbit. $d = 6$ representations cannot however form neither Z_7 full orbits nor full Z_3 orbits in this case. After the symmetry breaking the 2 $d = 3$ multiplets and $d = 3$:s belonging to 5 $d = 4 : s$ form still Z_7 orbits but two $d = 1$:s are thrown out of corresponding Z_7 orbits. There exists no full Z_7 orbit consisting of amino-acids with same d after symmetry breaking so that in this sense Z_7 sceneario possesses much less symmetry than Z_3 scenario. An explicit example is given by the following formulas

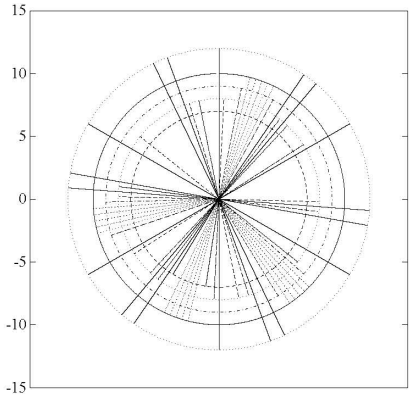
d	N(d)	$\Phi/\Delta = n \ mod \ 126$, $\Delta = 2\pi/126$
6	3	$n = A(i) + B(k)$, $A(i) = 21i$, $B(k) = 7k + \delta_1(k)$,$i \in I$,$k \in K$
		$I = \{0, .., 5\}$, $K = \{0, 1, 2\}$, $\delta_1(1) = 5$, $\delta_1(0) = delta_1(2) = 0$
2	9	$n = A(i) + \delta_2(i) + 1 + B(k)$,$i \in I$, $k \in K$
		$\delta_2(1) = \delta_2(4) = -2$, $\delta_2(2) = \delta - 2(5) = 2$,
4	5	$n = 3 + i + 42k$, $n = i + 63$, $i = 2, ..., 6$, $k \in K$
3	2	$n = 3 + i + 42k$,$i = 1, 7$, $k \in K$
1	2	$n = i + 63 + \delta_3(i)$,$i = 1 \ or \ 7$, $\delta_3(1) = -1$, $\delta_3(7) = 1$

Table 3. Explicit form for the Z_7 type imbedding of X_{64} consistent with Genetic Code. The imbedding is illustrated in figure 4.2.4.



1

Figure 4.1: The imbedding $X_{64} \subset Z_{126}$ reproducing Genetic Code and possessing Z_3 type symmetry. The lengths of radial lines are $6 + d$, where $d = 1, 2, 3, 4, 6$ is the number of DNA:s associated with amino-acid. The angular distance between points on Z_3 (Z_7) orbits is to 20 (2.85) degrees.



1

Figure 4.2: Z_7 type imbedding $X_{64} \subset Z_{126}$ reproducing Genetic Code. Symmetry breaking is much larger for this imbedding although visually the imbedding looks perhaps more symmetric than Z_3 type imbedding.

4.2.5 In what sense the physical genetic code is unique?

The proposed symmetry breaking scenario is certainly not the only one. A constraint on symmetry breaking patterns comes from the requirement that all amino acids are coded. In terms of orbit multiplicities $g(k)$ (number of amino acids with same number of DNA:s) one has two conditions

$$\begin{aligned} \sum_{k=1,2,3,4,6} g(k) &= 21 \ , \\ \sum_{k=1,2,3,4,6} g(k)k = 64 \ . \end{aligned} \tag{4.2.8}$$

$k = 4$ case corresponds to two Z_3 and Z_1 orbits associated with single amino acid. This gives

$$\begin{aligned} g(1) &= -22 + g(3) + 2g(4) + 4g(6) \ , \\ g(2) &= 43 - 2g(3) - 3g(4) - 5g(6) \ . \end{aligned} \tag{4.2.9}$$

This means that all possible genetic codes are labeled by the three integers $g(3), g(4)$ and $g(6)$. The conditions imply

$$\begin{aligned} g(3) + 2g(4) + 4g(6) &\geq 22 \ , \\ 2g(3) + 3g(4) + 5g(6) &\leq 43 \ . \end{aligned} \tag{4.2.10}$$

These conditions restrict the possible symmetry breaking scenarios. In particular, $g(6) \leq 8$ must hold true so that maximal symmetry corresponds to the codes with $(g(3), g(4), g(6))$ equal to $(1, 0, 8)$ or $(0, 1, 8)$.

In the proposed symmetry breaking scenario the number of DNA:s is automatically fixed to 64 and the only requirement is that deformation of X_{64} is such that the number of amino-acids is not smaller than 21. If one assumes that the only symmetry breakings are of form $6 \to 3 \cdot 2$ and $4 \to 3 + 1$ and denotes the numbers of broken $d = 6$ and $d = 4$ multiplets with k_6 and k_4 respectively the condition for 21 amino acids reads as $(6-k_6)+3k_6+(7-k_4)+2k_4 = 21$, which gives $k_6 = 4-k_4/2$, $k_4 = 0, 2, 4, 6$. k_4 gives the number of $d = 1$ amino-acids and $k_4/2 + 2$ gives the number of the unbroken 6 orbits: these numbers clearly measure redundancy and symmetry. The numbers of amino-acids with various degeneracies are given by

$$\begin{aligned} N(d=1) = N(3) &= k_4 \ , \\ N(2) &= 3(4 - k_4/2) \ , \\ N(4) &= 7 - k_4 \ , \\ N(6) &= 2 + k_4 \ . \end{aligned} \tag{4.2.11}$$

The following table summarizes the 4 genetic codes possible under these assumptions

$N(d=1)$	$N(d=2)$	$N(d=3)$	$N(d=4)$	$N(d=6)$
0	12	0	7	2
2	**9**	**2**	**5**	**3**
4	6	4	3	4
6	3	6	3	5

Table 4.: The 4 possible genetic codes assuming unbroken initial Z_3 symmetry with numbers of amimo acids with same degeneracy.

The physically realized genetic code (second row) is clearly a compromise between symmetry and redundancy. By the previous construction the physically realized code is characterized by additional symmetry: namely the group $Z_3 \subset Z_{21}$ transforming both 3 $d = 6$ amino-acids and 3 triplets of $d = 2$ amino acids to each other. For all other Z_3 type alternatives this symmetry is broken. Therefore the physical genetic code corresponds in a well defined sense to minimal symmetry breaking.

4.2.6 Hierarchy of Genetic Codes?

Genetic Code generalizes to an entire hierarchy of genetic codes at formal level, at least.

1. The spaces $X_4 \subset X_{64} \subset X_{(M_{127}+1)/2} = X_{2^{126}} \subset ....$ an be regarded as a hierarchy of 'DNA triplets'.
2. The preceding results suggest that the multiplicative groups associated with the Combinatorial Hierarchy form also a hierarchy: $Z_2 \subset Z_6 \subset Z_{126} \subset Z_{M_{127}-1} \subset .....$ This is true if the dimensions divide each other: $2|6|126|M_{127}-1|.....$ 126 indeed divides $M_{127}-1 = 2(2^{126}-1)$ and the number of 'amino-acids' at the third level is $(2^{126}-1)/63$! The result holds generally from Fermat's theorem ($2^{p-1} = 1 \; mod \; p$) if the Mersenne numbers of the Combinatorial Hierarchy are primes.
3. If Combinatorial Hierarchy consists of primes the coset spaces $Z_6/Z_2 = Z_3 \subset Z_{126}/Z_6 = Z_{21} \subset Z_{M_{127}-1}/Z_{126} \subset ....$ exist and form a hierarchy of 'amino-acids'.
   The redundancy of the genetic code could be interpreted as resulting from a hierarchy of discrete gauge symmetries: Z_{M_n-1} acts as gauge symmetry in the space $Z_{M_{M_n}-1}$.

There is still further apparent numerical co-incidence. For the first 3 levels the numbers of 'amino-acids' are

$$\begin{aligned} a_0 &= 2 \; , \\ a_1 &= 3 \end{aligned} \tag{4.2.12}$$

per,

$$\begin{aligned} a_2 &= 21 \; , \\ a_3 &= ((M_{127}-1)/2)/((M_7+1)/2)) = (2^{126}-1)/63 \; . \end{aligned} \tag{4.2.13}$$

The numbers of 'DNA'-n-plets (well defined truth values) are

$$\begin{aligned} d_0 &= 2 \; , \\ d_1 &= 4 = 2^2 = d_0^{a_0} \; , \\ d_2 &= 64 = 4^3 = d_1^{a_1} \; , \\ d_3 &= 2^{126} = 64^{21} = d_2^{a_2} \; . \end{aligned} \tag{4.2.14}$$

The formulas imply that one can construct the physical DNA-triplets at level 2 as $d_2 = d_1^{a_1} = 4^3$ triplets of DNA molecules. At level 3 one can construct $d_3 = d_2^{a_2} = 63^{21} = 2^{126}$ 'DNA' 21-plets of 64 different DNA-triplets. More generally, DNA-plets at given level n correspond to a_{n-1}-plets of DNA formed from the DNA-plets of the previous level since the identity

$$d_n = \frac{(M_n+1)}{2} = d_{n-1}^{a_{n-1}} = 2^{a_{n-1}a_{n-2}a_{n-3}...a_0} \; . \tag{4.2.15}$$

holds true in general since the groups Z_{M_n-1} forms a hierarchy of nested subgroups.

The result means that the concrete physical representation of truth values of M_n logic as 'DNA' sequences is an internal property of the Combinatorial Hierarchy. The immediate prediction is that sequences of 21 DNA-triplets should code for $a_3 = (2^{126}-1)/63$ generalized amino-acids consisting of sequences of 21 amino-acids acids: these units could be regarded as some kind of 'pre-genes'. The number of amino-acid sequences consisting of 21 amino-acids (of order 2^{91} is much smaller than the number of generalized amino-acids (of order 2^{120}), which means that the ordinary amino acids cannot provide an optimal realization of DNA sequences: many generalized amino-acids have no DNA sequence as their representative. DNA sequences are known to contain passive sections, introns, which do not code DNA. An interesting question is whether these sections could represent M_{127} level sequences: if so the number of DNA triplets in these sections should be a multiple of 21.

If the lowest level of the Hierarchy is present DNA:s should be representable as doublets formed from two different $p = 3$ 'pre-DNA':s and these should code for 3 different 'pre-amino-acids'. This kind of structure is not realized in Nature so that the $p = 7$ level of DNA:s is in this sense irreducible.

4.2.7 The structure of the negation map

The negation map mapping statement to its negation is highly non-unique unless it possesses symmetries and it is interesting to find what one can conclude about the structure of this map by symmetry arguments.

1. For each amino-acid type general statement there are six special cases of the statement. The fact that only 64 statements are actually consistent with a given atomic statement means that some special cases associated with different amino-acids correspond to statement and its negation whereas two points at given Z_6 orbit cannot correspond to a statement and its negation.

2. 62 negations of 64 DNA type statements belong to Z_{126}. One lacking negation corresponds to the zero element of $G(127,1)$ and the second one corresponds to the excluded statement in the construction of the Combinatorial Hierarchy. One can associate to each amino-acid definite number of negations as the number of elements in the complement of DNA type statements on the Z_6 orbit defined by amino-acid (at Z_6 orbit all statements must be consistent with a fixed atomic statement). These numbers are $d_1 = 0$ for 3 $d = 6$ amino-acids , $d_1 = 2$ for 5 $d = 3 + 1$ amino-acids, $d_1 = 4$ for 9 $d = 2$ amino-acids and $d_1 = 5$ for the 2 $d = 1$ amino-acids so that negations 'code' only 18 amino-acids so that duality symmetry between statements and their negations is not possible.

3. Negation must map statements at given orbit to a different orbit. It is however natural to require that points on same orbit, say A, are mapped on same orbit, say B, if possible and that the angles and ordering of points belonging to same orbit are preserved in negation map. More generally, the ordering of points on circle should be preserved.

4. For 2 $d = 3$ amino-acids, call them a and b, the Z^3 orbit a (b) is mapped to the complement of Z^3 orbit b (a). The map is unique apart from Z^3 rotation.

5. For 9 $d = 2$ amino-acids Z^2 orbits (pairs of diametrically opposite points) form 3 Z^3 orbits and Z^3 rotation plus a rotation inside Z^6 orbit gives good candidate for negation map. As a consequence 9 Z_2 orbits in the complement remains 'free' and form 3 Z_3 orbits, call them G_i.

6. It is natural map $d = 6$ orbits to these free 9 Z_2 orbits in Z_3 symmetric manner, which means that the content of single Z_6 orbit i is mapped into 3 $d = 2$ orbits in G_i. Diametrically opposite point pair on Z_6 orbit is mapped to a similar point pair in G_i. The map is unique if one requires that Z_6 element on the initial orbit goes to same Z_6 element on the final orbit and this in turn makes the map of 9 Z_2 orbits unique apart from reflection.

7. The 5 $d = 3+1$ amino-acids form unions of diametrically opposite point pair A_i plus point pair B_i,$i = 1, ..., 5$ separated by angle of 120 degrees. Point pairs B_i can be mapped to the mirror image $\bar{B}_j$ of B_j, $j \neq i$: one can require that cyclic ordering of pairs B_i is preserved in map to remove part of the non-uniqueness. $2 + 2$ pairs A_i can be mapped to the $2 + 2$ pairs C_i in the complements of 2 $d = 1$ orbits containing 5 points each (2 diametrically opposite pairs C_i plus single point). The remaining pair, say A_{i_0}, can be mapped to zero element of $G(127,1)$ and to the 'dropped out' statement.

8. Denoting the mirror images of 2 $d = 1$ statements a and b by $\bar{a}$ and $\bar{b}$ the negation map for them reads as $(a, b) \to (\bar{b}, \bar{a})$.

4.2.8 Combinatorial Hierarchy as a hierarchy of formal systems

Usually [19] formal system is understood as a system of symbols, axioms interpreted as allowed basic strings of symbols and rules for constructing new sequences from the symbols. In [19] the exciting analogies between the symbol sequences of formal systems and DNA and amino acids sequences and Genetic Code were emphasized and it indeed seems that more than analogy is in question. The model for the Genetic Code suggests an interpretation of Combinatorial Hierarchy as a hierarchy of formal systems with DNA type statements identifiable as a maximal set of mutually consistent statements and amino-acid type statements as basic axiom type truths. Genetic code results from the

necessary but non-unique selection of these statements consistent with a fixed atomic statement and the selection of these statements could be a result of fight for survival at the level of amino-acids. The rule for forming statements in this system is simple: just form DNA sequences with building blocks consisting of a_{n-1}(number of 'amino-acids' at level $n-1$) DNA-sequences of previous level. Theorems are obtained by coding these statements to amino-acid sequences.

Consider first DNA type statements.

1. It was already suggested that the elements of Finite Fields in the Combinatorial Hierarchy correspond to a hierarchy of statements about statements about .... and therefore a sequence of formal systems formed from basic formal system by successive construction of meta level statements.

2. Finite Field provides a language to construct all possible statements. As already found, the $(p+1)/2$ (p is Mersenne prime in the Combinatorial Hierarchy) statements correspond to maximal set of statements consistent with a fixed atomic statement of this formal system. This is indeed a possible interpretation. Combinatorial Hierarchy was constructed by starting from a set containing just two statements 1 and 0. In the first $p = 3$ level one forms 4 statements about these two statements and drops the one representable as $(0, 0)$. There are however 2 contradictory statements of type P and *not* P in this set so that only $2 = (p+1)/2$ statements are consistent with a given atomic statement in the real world. At the level p one has $p = M_n$ statements about lower level statements and by construction $(p-1)/2$ statements P have also their negation in the set of all possible statements so that $(p+1)/2$ consistent statements with a fixed atomic statement are possible. Thus the conclusion is that 64 DNA triplets represent the maximum number of mutually consistent statements at level $p = M_7 = 127$ of a formal system possibly having a hierarchy of meta levels.

Consider next the interpretation for the set $Z_{k_n} = Z_{p_n-1}/Z_{p_{n-1}-1}$, $k_n = (p_n - 1)/(p_{n-1} + 1)$ of amino-acid type statements.

1. In any formal system there are two kind of meta statements that is statements $P(Q_1, ..Q_n)$ about statements. The first class corresponds to theorems $P(Q_1, ...Q_n)$ without any reference to the particular value of statements Q_i: a simple example is general theorem stating the conditions under which an orthogonal triangle with two integer sides is Pythagorean triangle: $m^2 + n^2 = l^2$ with m, n, l integers. Second class corresponds to the theorems with $(Q_1, ..., Q_n)$ possessing definite values: a simple example is previous theorem for triangle having sides $2, 1$ and 3: $2^2 + 1^2 = 3^2$. The set of 'amino-acid' type statements does not depend on the choice of the choice fo the $(p+1)/2$ statements consistent with a given atomic statement and this suggests the interpretation 'amino-acid' type statements as general axiom like truths without any reference to the values of the argument of the statement.

   What is special in the proposed hierarchy of formal systems that the substitution operation corresponds to the multiplication of Z_k element with the element $Z_{p_{n-1}-1}$. The introduction of mutual consistency by selecting $(p+1)/2$ special statements implies that the number of DNA:s per amino-acid corresponds to the number of special cases associated with a given 'axiom' depends on the 'axiom'. There is still upper bound for special cases given by $p_{n-1} - 1$.

2. In a good formal system the choice of DNA type statements should be such that there is at least one statement per each truth. The most important truths (as far as survival is considered) should correspond to full $Z_{p_{n-1}-1}$ orbits.

Gödel's Incompleteness Theorem was one of the basic themes in the book of Hofstadter [19] . Theorem states that in any sufficiently complicated formal system (,that is, practically interesting) there are truths, which are not provable. The Incompleteness Theorem seems to have its analog in bio-systems. As already observed at the level M_{127} DNA sequences consisting of 21 triplets correspond to true statements, which can be regarded as special cases of general truths, whose number is $(2^{126-1})/63 \sim 2^{120}$. Amino-acid sequences consisting of 21 amino-acids give a natural realization for a subset of these truths and the genetic code map is induced from the Genetic Code at the basic level $p = 127$. The number of the truths given by these sequences is of order $20^{21} \sim 2^{91}$ (taking into account the reduction caused by the stopping sign) and much smaller than all possible truths. The

interpretation is that the number of possible theorems obtained by forming amino-acid sequences is much smaller than the number of truths. One could always add 'axioms' by realizing the remaining truths in some new manner but since the number of levels in the Combinatorial Hierarchy is infinite (assuming that the Mersenne numbers in question are primes) there are always unprovable truths in the system. One can obviously classify the formal systems according to which level is the basic irreducible level inducing genetic code at higher levels.

$p = 7$ ($n = 2$) and $p = 3$ ($n = 1$) level as the defining, irreducible level are also in principle possible.

1. At level $p = 7$ 4 doublets of level $p = 3$ 'DNA' code 2 'pre-amino-acids' plus stopping sign and at the next level this coding induces $2^3 = 8 < 21$ different 'amino-acids' since stopping sign does not appear in theorems. If stopping sign would correspond to actual amino-acid there would be $3^3 = 27 > 21$ theorems so that the number of theorems would be larger than the number of truths!

2. At level $p = 3$ 2 'DNA':s of code one amino-acid plus stopping sign so that genetic code is one-to-one.
   An interesting possibility is that $p = 3$ and $p = 7$ levels might have been defining, irreducible levels for bio-systems at some early stage of evolution. These formal systems can be regarded as a subsystem of the full DNA-amino-acid system. RNA-triplets of form UXY, $X, Y \in \{A, C\}$ give indeed realization for $p = 7$ system: UAA codes stopping sign,UAC codes cys and UCA and UCC code ser (using the standard short hand notation for RNA:s and amino-acids [19]). The sequences formed from these DNA:s and corresponding amino-acids indeed realize $p = 7$ formal system as subsystem of $p = 127$ system. $p = 3$ formal system can be realized as UAA coding stopping sign and UAC coding cys. An interesting possibility is that this DNA-amino-acid subsystem has formed first in the biochemical evolution. For both $p = 3$ and $p = 7$ degenerate genetic codes one has $G + C/A + U = 1/2$. $G + C/A + U$ content varies in the range $(.7, 1.5)$ for insects and in the range $(1.17, 1.56)$ in the case of fish and for younger evolutionary forms A+U content is known to increase [207] .

3. The transition to '$p = M_{127}$ life' would require the addition of a rather large number of new 'amino-acids' to the set of all possible amino-acid sequences consisting of 21 amino-acids whereas DNA triplets could be simply replaced with sequences of 21 DNA triplets. In the transition to $p = 127$ life tRNA triplets binding single amino-acid would be replaced by sequences of 21 tRNA triplets binding besides amino-acid sequences suitably modified amino-acid sequences in order to achieve maximal number of 'amino-acids' at level $p = 127$. Also the modification of the translation system (in ribosomes) is required so that the 'reading head' recognizes a sequence of 21 mRNA-triplets instead of single mRNA triplet. An interesting question is whether biochemistry might allow this kind of extension.

4.2.9 Summary

The simple model of abstraction has rather interesting connections with genetic code.

1. Combinatorial Hierarchy results as hierarchy of abstraction levels for statements or thoughts. Lowest level A_2 corresponds to the two possible values of Boolean variable and thoughts of the level A_{n+1} correspond to statements about statements of level n that is Boolean maps $A_n \to A_2$. If the statement corresponding to sequence of zero bits is excluded the dimensions form a series of Mersenne numbers $3, 7, 127, M_{127}, ...$ Combinatorial Hierarchy is obtained also by considering the set of subsets with empty set excluded. The hypothesis that there is no upper bound for intelligence is equivalent with the hypothesis that these numbers are primes and that the numbers $p_n - 1$ in the sequence have the property that $p_n - 1$ divides $p_{n+1} - 1$. This implies that one obtains a hierarchy of Finite Fields $G(p_n, 1)$ and their multiplicative groups Z_{p_n-1} as well as coset groups $Z_{p_n-1}/Z_{p_{n-1}-1} = Z_{k_n}$, $k_n = (p_n - 1)/(p_{n-1} - 1)$.

2. There are $(p_n + 1)/2$ statements consistent with a given atomic statement at level n and the numbers come as $2, 4, 64, ...$ These statements are referred to as 'DNA' type statements for obvious reasons. The dimensions k_n comes as $2, 3, 21, ...$ The hypothesis is that amino-acid type statements correspond to the statements of $Z_{k_n} \subset Z_{p_n-1}$ and can be regarded as general theorems whereas DNA type statements correspond to special cases of these theorems and are

mapped to general theorems the mapping $x \to x^{p_{n-1}-1}$ at level n. At level n the genetic code corresponds to the non-unique choice of the $(p_n+1)/2$ DNA type statements consistent with a given atomic statement in Z_{p_n-1}.

3. Biologically Genetic Code is determined by the competition between amino-acids: each amino-acid tries to maximize the number of DNA:s coding it (amino-acids are like politicians who are representatives of one truth and DNA:s are in the role of voters). The tendency favors $Z_{p_{n-1}-1}$ (Z_6) symmetry. The physically realized code can be understood as resulting from the symmetry breaking caused by the competition between the groups $Z_{p_{n-1}-1}$ (Z_6) acting on DNA:s associated with single amino-acid and factor groups of Z_{k_n} ($Z_{21} = Z_3 Z_7$) transforming amino-acids to each other. Instead of finite dimensional representations of Lie groups the orbits of the cyclic groups Z_n are basic objects in the symmetry breaking mechanism.

4. At level n basic objects are k_{n-1}-plets of DNA:s of level $n-1$ and sequences of same DNA units can in principle appear at all levels of the hierarchy. At the next $k = M_{127}$ level 'DNA':s could therefore be regarded as sequences of 21 DNA triplets.

5. A hierarchy of increasingly complicated formal systems is predicted if one accepts the hypothesis. For the formal system of order n n:th level of the Combinatorial Hierarchy is the defining level in the sense that the number of 'amino-acids' is maximal and equal k_n. Formal systems of order $n_1 < n$ are imbeddable into the formal system of order n. The formation of amino-acid sequences corresponds to the formation of theorems. For a formal system of order n amino-acid sequences realize only a small subset of all possible k_{n_1} truths at higher levels $n_1 > n$ of the Combinatorial Hierarchy in accordance with Gödel's theorem. One can also classify all possible bio-systems according to the value of n for the corresponding formal system. The Earthly life corresponds to $n = 3$ formal system and 'life of order 4' would require the addition of rather large number of new 'amino-acids' to the set of all possible amino-acid sequences consisting of 21 amino-acids whereas DNA triplets could be simply replaced with sequences of 21 DNA triplets. The realization of '$n = 4$ life' requires that tRNA triplets binding single amino-acid are replaced by sequences of 21 tRNA triplets binding besides amino-acid sequences suitably modified amino-acid sequences in order to achieve maximal number of 'amino-acids' at level $n = 4$. Also the modification of the reading system (in ribosomes) is required so that the 'reading head' recognizes a sequence of 21 mRNA triplets instead of single mRNA triplet.

6. An open problem relates to the precise role of DNA and proteins. The model of Boolean thoughts represented in terms of the cognitive fermion pairs leads to the correspondence between fermions and mind like space-time sheets and gives Combinatorial Hierarchy a special status. What comes in mind is that DNA provides a hardware representations of thoughts analogous to a computer memory. DNA molecules would be conscious selves representing 3 basic symbols in the mind of higher level self formed by DNA triplet. DNA sequences would be selves, experiencing DNA triplets as their sub-selves. Individual DNA molecules would represent sub-sub-selves so that DNA sequence would experience only the average of the experiences of individual DNA molecules.

7. It deserves to be noticed that I Ching claims that there are 64 fundamental mental states: could it be that these mental states correspond to all possible DNA triplet selves? It this interpretation is correct then Buddhist meditators would have achieved bio-feedback at DNA level! Genetic Code itself could be interpreted as a mapping of DNA selves to protein selves: this could be perhaps regarded as kind of mimicry or conscious abstraction process. Protein selves would represent theorem like abstractions of conscious thoughts represented by DNA selves.

8. It is known that cell numbers of different cell types in nervous, muscular, adipose, gonadic and homopoietic organs concentrate themselves around powers of two – 2^n, where n in the range $20-40$ [182] : this can be understood if they result in n regularly occurring cell divisions. It might however be that the explanation of the regularity involves something much deeper. For instance, the cell types represent various n-bit sequences.

4.3 Genes, memes, and universal language

In TGD framework the notion of magnetic body plays a key role in the understanding of bio-systems and communications between magnetic and material body could be based on memetic code words. Magnetic body is the fundamental intentional agent is in the same relation to the material body as memetic code to the genetic code and computer software to the hardware or the manual to the electronic instrument. Hence there is a strong temptation to believe that memetic codewords represented as field patterns of duration .1 seconds is associated with the communications between magnetic body and brain.

For instance, the fact that 10 Hz is basic hippocampal frequency suggests that declarative memories could be based on time mirror mechanism with negative energy signal from the magnetic body of the geometric future reflected from the brain of the geometric past as a positive energy signal back to the magnetic body of the geometric future. Classical communications could utilize memetic code using pulse or frequency coding. These field patterns could also define shared mental images. For instance, sequences of the memes represented as field patterns could activate intronic memes, which in turn would activate genes.

4.3.1 Genes-memes, biology-culture, hardware-software?

The reports of the Public Consortium about human genome in Nature, Feb 15, 2001 [122] and of Celera Genomics in Science of Feb 16th, 2001, [157] demonstrated that the amount of human genome differs relatively little from those of lower organisms: we have only about 30,000 genes, little more than twice the number 13,601 of genes for fruit fly. This paradoxical finding strongly supports the view that our genome is not solely responsible for what we are and that the intronic portion of DNA (only about 1 per cent codes of human DNA codes or amino-acid sequences), is not "junk DNA", but contains important biological information and expresses it non-chemically.

In TGD Universe introns would express memes as the classical field patterns associated with MEs ("topological light rays") responsible for the basic expressions of language understood in an extremely general sense. This language includes body language and even cellular signalling, and could quite well make possible (not necessarily conscious) interspecies communications based on the memes and genes expressed by both communicating species and forming a common portion of grammar and vocabulary. All eukaryotes (cells with nuclei), even bacteria, would possess part of the memes of this universal language. The memetic code word is predicted to consist of a sequence of 21 DNA triplets and carries 126 bits of information instead of 6 bits of genetic code. Of course, also genes could be expressed in terms of MEs and could define a lower level language possessed also by prokaryotes.

The actual role of DNA could be understood using a computer analogy. Memes represent the program modules written using the programming language defined by the memetic code and realized in terms of the field patterns associated with MEs. Genes represent the lower level programs coding for the necessary hardware. System builds only the hardware needed, that is cell expresses only a small fraction of the genome. For neurons this fraction is known to be highest. DNA engineering requires besides the addition of the new programs (memes, introns) also the insertion of the necessary hardware (new genes). Memes and corresponding genes should have very intimate relationship. In this conceptual framework the standard view is wrong since it identifies the build-up of a new hardware as the sole activity at the DNA level. This would be like identifying the addition of a net card to a computer as the fundamental activity related with computers.

4.3.2 Pulse and frequency representations of the genetic and memetic code words

The most general form of p-adic length scale hypothesis implies that each p-adic prime $p \simeq 2^k$, k integer, defines a hierarchy of physically favored p-adic time scales given by $T_p(n) = p^{(n-1)/2}T_p \equiv T(n,k)$, $T_p = \sqrt{p}T_{CP_2}$, where T_{CP_2} is the so called CP_2 time scale about 10^4 Planck times. The most general assumption assigns to any prime $p \simeq 2^k$, k integer, a hierarchy of cognitive codes with codeword having a duration equal to n-ary p-adic time scale $T_p(n)$ such that the number of bits is factor k_1 of k.

Code words could be realized either as k_1 first harmonics of the fundamental frequency $f_p(n) = 1/T_p(n)$ or as temporal sequences of k_1 bits of duration $\tau = T_p(n)/k_1$ represented as pulses of max-

imal duration τ. These representations will be referred to as frequency and pulse representations respectively. EEG represents a good candidate for frequency representation.

1. Pulse representations, scalar wave pulses, and transformation of intentions to actions

Pulse representations could be realized in terms of scalar wave pulses predicted by TGD and claimed to exist already by Tesla [25] . Scalar wave pulses can be visualized as capacitors moving with light velocity and carrying longitudinal essentially constant electric field. If charged particles of matter end up temporarily to the space-time sheets of the scalar wave pulse, they are accelerated without dissipation and generate negative energy "acceleration radiation" rather than brehmstrahlung at harmonics of the frequency determined by the duration of the scalar wave pulse. Under obvious conditions on the duration of the scalar wave pulse the negative energy radiation can be amplified to positive energy radiation by time mirror mechanism.

Quite generally, the generation of scalar wave pulses seems to provide a basic mechanism generating negative energy radiation (phase conjugate radiation) and nerve pulses are probably accompanied by scalar wave pulses. The transformation of the p-adic counterpart of the space-time sheet of the scalar wave pulse to a real one, a kind of switch-on process, could provide a generic realization of intention besides a direct generation of the p-adic counterpart of the negative energy topological light ray. The hierarchy of magnetic bodies could use this process as a generic manner to realize cascades of intentions proceeding from magnetic body down to the level of DNA.

Denoting by $f(\omega)$ the Fourier transform of single pulse in the interval $T(n,k)$, one can write the Fourier transform of the pulse sequence as

$$F(\omega_n) = \sum_k \delta_k exp(ik\tau_b\omega_n) f(\omega_n) \quad , \quad \omega_n = \frac{n2\pi}{T(n,k)} \quad ,$$

where τ_b is the duration of the bit and δ_k is equal to 1 or 0 depending on whether k^{th} bit corresponds to a pulse or not. The duration of the pulse can be anything in the range $(0, \tau_b)$. If $f_b = 1/\tau_b$ corresponds to a frequency of some oscillation a resonant coupling occurs. Magnetic transition frequencies and the frequencies corresponding to the increments of zero point kinetic energies are especially interesting as far as the transformation of the pulse representation to a conscious experience or controlled action is considered. For instance, pulses could correspond to magnetic pulses used in the transcranial magnetic stimulation and known to induce altered states of consciousness [39] .

2. Genetic and memetic codes as cognitive codes associated with spoken and written language

Genetic and memetic codes are the most obvious candidates for the codes associated with spoken and written language. Genetic code would correspond to $k = 2^7 - 1 = 127$ and one must distinguish between 6-bit(64 DNA triplets) and almost-7-bit representations. These codewords can be realized dynamically as temporal field patterns. For genetic code primes $p \simeq 2^k$, $k = 6 \times n$ define candidates for the duration of the genetic code word if all factors of k are assumed to define a possible number of bits of the code word. The time scales come as powers of 8 so that they cover the entire range of biologically relevant time scales and genetic code could appear as fractally scaled versions unlike memetic code. What is interesting is that the possible durations of code word range down to about 11 CP_2 times. Therefore one cannot exclude the possibility that the biological realization of the genetic code is only a particular example of its realizations and that genetic code makes possible communications even between living and so called non-living matter.

Representations of the genetic code

$k = 2 \times 126 = 2 \times 6 \times 21 = 252$ allows the representation of both 126-bit memetic codeword, 6-bit genetic codeword, and 7-bit code word. For pulse representation corresponding to $k = 252 + 6n$ the genetic codon the duration of the code word and bit are $\tau = 2^{-3n} \times 50$ ms and $\tau_b = 2^{-3n} \times 8.3$ ms respectively. The realization using nerve pulse patterns certainly possible for $n \geq 0$, $n = 1$ would $\tau_b = 1.04$ ms which seems to be somewhat too short. Frequency representation would be realized using the 6 first harmonics of the fundamental frequency $f_1 = 2^{3n} \times 20$ Hz. In the following only 6-bit representations are discussed.

1. Representations of 6-bit code in the range of audible frequencies

20 Hz corresponds to the lowest end of audible frequencies ($20 - 2 \times 10^4$ Hz). Audible range allows 3 representations of the genetic code corresponding to the fundamental frequencies f_1 equal to

20 Hz, 160 Hz and 1280 Hz. 1 kHz frequency is between the frequency ranges associated with the latter two representations. Above (below) 1 kHz the wavelengths of incoming sound waves are shorter (longer) than head size so that the mechanisms determining the direction of the sound source are different above and below this frequency. Speech might correspond naturally to pulse representations whereas music could correspond to frequency representations. Also nerve pulse-EEG dichotomy could correspond to talking-singing dichotomy (left brain speaks and right brain sings).

2. EEG and nerve pulse representations of 6-bit code

1. Cortical EEG frequency range favors the realization using $f_1 = 2.5$ Hz: all harmonics in the range 2.5-15 Hz are important EEG resonance frequencies. For 20 Hz representation 120 Hz would represent the highest harmonic and it is questionable whether cortical EEG contains it with a sufficient intensity. Cerebellar EEG however allows much higher frequencies than cortical EEG.

2. The cyclotron frequency of Si^{++} ion is 21.4 Hz so that it could define a frequency representation of the genetic code in Earth's magnetic field, at least if its value is subject to a homeostatic control.

3. Ca^{++} has cyclotron frequency of 15 Hz in Earth's magnetic field with value $B_E = .5$ Gauss. A pulse representation of the genetic code with $\tau_B \simeq 66.7$ ms ($f_b = 15$ Hz) would excite harmonics of Ca_{++} cyclotron frequency and thus couple the representation to the Bose-Einstein condensate of Ca_{++} ions. Nerve pulses could realize this representation. Blackman [17] has found that the harmonics of $f_b = 15$ Hz frequency have effects in living matter, and Ca^{++} waves are known to play an exceptional role in biology [31] (for TGD based model see [37] . Hence the Bose-Einstein condensate of Ca^{++} ions might provide a fundamental pulse representation of the genetic code.

4. The presence of fractally scaled-up versions of the Earth's magnetic field the sheets of the many-sheeted DNA would allow also scaled versions of Ca^{++} representation with durations $\tau = 8^{-n} \times .05$ ms of the code word. Depending on whether magnetic flux quanta are tubes or sheets the p-adic primes of space-time sheets of magnetic flux tubes comes as $k = 169 - 3n$ or $k = 169 - 6n$. For sheets one would have $k = (169 = 13^2, 163, 157, 151)$: all these prime define important p-adic length scales relevant to DNA in the range 10 nm-5 μm and three of these primes define Gaussian Mersennes. Sheet option is favored by the explanation of the findings of Peter Gariaev about radio emission induced by irradiation of DNA by laser light [149] . All these representations except $k = 169$ are realizable also using audible frequencies, which suggests a direct connection between the sheets of the many-sheeted DNA and the representations of the genetic code at audible frequencies.

Representations of the memetic code

For the memetic code one must distinguish between almost-127-bit representations and 126-bit representations. In both cases there is a very limited number of representations, which suggests that the emergence of memetic code might relate to the emergence of explosive cultural evolution. The first representations corresponds to the time scales $T(126)$ and $T(127)$: the latter defines the Compton time of electron. Next representations corresponds to the time scale of about .05 seconds and .1 seconds respectively.

1. 126-bit representations

1. 126-bit memetic code word can be represented using the same representation as for the genetic code, namely $k = 2 \times 126 = 252$ with $\tau = .05$ ms and $\tau_b = .4$ ms and $f = 20$ Hz and $f_b = 2520$ Hz. Audible frequencies could realize both representations and music experience might involve both frequency and pulse representation of 126-bit memetic code corresponding to the left brain (rhytm) and right brain (melody) aspects of music.

2. 126-bit representation using nerve pulses as such is not possible. The analog of the intronic representation of the memetic code using sequences of 21 DNA triplets could be however possible. $k = 252$ allows 21-bit representation for which bit is replaced by 6-bit with duration $\tau_6 = 50/21 =$

2.38 ms, which corresponds to a typical duration of nerve pulse. Each of the 21 nerve pulses should generate a genetic codon of duration $\tau = 50/64 = .78$ ms presumably communicated to the neuronal nucleus and/or vice versa. 6-bit fine structure could be perhaps expressed at the microtubular level as has been originally proposed by Koruga [176] , [36] . One would have $\tau_b/\tau_6 = 21/64$, the ratio of the number of amino-adics (stopping sign counted as effective amino-acid) to the number of DNA codewords. τ_b/τ_6 represents a reduction of information: this loss of information is not due to the degeneracy of the code but due to the fact that only one third of the total duration of the bit of 21-bit code is used to represent information.

One could imagine that the 6 bits represented as negative energy topological light rays activate the corresponding DNA triplet by coupling 3 switches on so that supra-current can flow through it. Sequence of 21 pulses would switch a unique memetic codon and sequences of these pulses in turn would switch on meme forming by definition a closed supra current circuit with return current flowing along conjugate strand. Switches could correspond to join along boundaries bonds connecting atomic space-time sheet to some larger space-time sheet, where the supra-current can flow. Each pair of bits would switch on one nucleotide of the triplet. This would occur in correct order if the three nucleotides are ordered by pulse length associated with bit (which can indeed vary) and 4 different bit pairs switch on A, T, C, and G. Bit could be represented by the polarization direction associated with the negative energy topological light ray.

The generation of nerve pulses using 64 bit sequence to code additional information at microtubular level could be based on frequency representation. Pairs of em MEs with opposite polarizations could represent a bit pair corresponding to a single nucleotide. These waves would induce microtubular excitation representing the DNA triplet.

2. 127-bit representations

For 127-bit representation the duration of the memetic codeword would be $T(2, M_{127}) = .1$ seconds. This time scale might be identified as the minimal duration of cortical mental images, and the so called features introduced by Walter Freeman [6] could define a pulse representation of memetic code words of almost-127 bits. $\tau_b = .8$ ms is definitely too short a time scale to be realized by the neuronal dynamics alone. Frequency representation is realized utilizing 127 first harmonics of $f_1 = 10$ Hz, which defines the average frequency of alpha band and is fundamental hippocampal frequency. $f_b = 1270$ Hz could define the frequency responsible for synchronous neuronal firing known to be about 1 kHz. Note that the code word containing only f_1 would not generate any conscious experience (10 Hz is not audible frequency) so that the highest bit is not quite fully represented.

1. One can imagine at least two electromagnetic realizations (for the spectrum of magnetic transition frequencies see [59]).
   i) Living matter contains both Co and Fe ions and the harmonics of Co_{++} and Fe_{++} cyclotron frequencies are 10 Hz for the nominal value $B_E = .5$ of the Earth's magnetic field. Thus pulse both pulse representations and frequency representations of memetic code coupling to these magnetic transitions are in principle possible.
   ii) For $B = 127/90 \times B_E$, $B_E = .5$ Gauss, both the third harmonic of proton cyclotron frequency and electron's spin-flip-cyclotron transition frequencies are 1270 Hz so that the bits of the memetic codon would couple to the Bose-Einstein condensate of the Cooper pairs of electrons and protons in the pulse representation.

2. Also classical Z^0 fields make possible realizations of the memetic code (for the spectrum of Z^0 magnetic transition frequencies see [59]).

   (a) Z^0 cyclotron frequencies of nuclei are proportional to $(A - Z)/A$ and around 10 Hz if one assumes the earlier hypothesis that Earth's Z^0 magnetic field corresponds to the space-time sheet $k = 173$ [56] . The value $(A - Z)/A = 1/2$ characterizing surprisingly many biologically important ions (C, N, O, S and Si [29]) is ideal in this respect. Thus it would seem that Z^0 cyclotron transitions might provide a rich repertoire of frequency representations of the memetic code. Note that neutron could define a cyclotron representation of the genetic code with 20 Hz fundamental frequency.

   (b) The temporal field patterns associated Z^0 topological light rays provide one possible pulse representation of the memetic code [59] .

(c) Temporal sequences for the changes Z^0 magnetization directions for a block of cognitive antineutrinos at cell membrane space-time sheet provide a conscious pulse representation of the memetic codeword [56] . Conscious experience would result, when the Z^0 magnetization directions flip back to the direction of external Z^0 magnetic field in spin flipping cyclotron transition. $M_{127} = 2^{127} - 1$ different conscious experiences results since nothing happens if all cognitive antineutrinos are in the direction of the external Z^0 magnetic field. Z^0 magnetization direction could be altered by the Z^0 magnetic pulse associated with the Z^0 ME inducing cell membrane oscillations of nerve pulse pattern.

4.3.3 Mapping of the memetic code to microtubular code

The importance of microtubuli for long term memory is evident [13, 36] . Microtubule decomposes into a sequence of cylinders containing 13×13 tubulins such that the helical twist is 2π along each of the 13 helical strands consisting of 13 tubulins. Therefore the code with $k = 13^2 = 169$ bits with bit realized as a tubulin conformation is a natural microtubular cognitive code [48] .

$k = 169$ defines the p-adic time scale associated with the Earth's magnetic field and next to the p-adic length scales $k = 151, 157, 163, 167$ associated with DNA so that microtubular level would naturally correspond to the level next to DNA in evolution, and have therefore some sort of self-reflective character. Microtubular representation of long term memories would certainly be consistent with this self-reflective character. This suggests that 169-bit microtubular code words represent the log file of neuron as a temporal list of activated 126-bit memetic code words with remaining bits representing parity bits making possible error correction at both microtubular and DNA level.

In the following some arguments for why microtubular code words should represent memetic code words are developed, and a mechanism for how to achieve this is proposed. Needless to say, this is only one possible scenario and it is easy to imagine variants of this scenario.

Microtubuli and long term memory

In spin glass phase tubulin conformations are spatially uncorrelated but temporally stable (the the excellent articles of Dimitri Nanopoulos [13, 36] provides a model for microtubule as spin glass). Therefore microtubuli in spin glass phase are ideal for the representation of memories coded to bits represented by tubulin conformations [48] , [36] . The two tubulin conformations have different electric dipole moments and conscious bits would result as "spin-flips" when the microtubule is in a strong longitudinal electric field forcing tubulins to the same conformational state. Essentially ferro-electric polarization is in question. The fundamental quale would be the change of the tubulin conformation. The patterns for the changes of tubulin conformations would generate mental images, and could also give rise to conscious memories by sharing of mental images. They could also give rise to signals communicated classically to the geometric future where they could induce reverse transition generating copies of the microtubular code words.

Time mirror mechanism for the realization of intentions proceeding as a process initiated from the magnetic body allows to consider two possible options for the role of the microtubuli. The options are not of course mutually exclusive.

1. Microtubuli as log files and communication lines

For this option intentional action does not involve microtubuli and they would be specialized to represent memories and serve as communication lines. The intentional action from higher than microtubular level would affect intronic DNAs directly, and patterns of tubulin conformations would provide a log file listing the memetic codons activated during the history of the neuron. Since the hierarchy of the magnetic bodies must have been there for all the time, one an indeed argue that neuronal microtubules have emerged later and do not participate in the intentional actions at intermediate level. Intentional action and the memory about it would be decoupled from each other completely.

Microtubuli allow besides ferro-electric and spin glass phase also phase which is optimal for signal transfer. The proposed realization of memetic code words as sequences of 21 nerve pulses with each pulse accompanied by genetic codon would suggest that microtubuli also mediate propagation of memetic codon, which can represent the desire to activate corresponding memetic codon in the post-synaptic neuron. Here the error correcting code $K_2(13, 64, 5)$ originally proposed by Koruga [176, 36] could be involved.

2. Why microtubuli cannot serve as intentional agents?

One must also consider the option for which microtubuli would represent the last step before DNA level in the hierarchy of desires propagating downwards in the self hierarchy. One can however represent heavy criticism against this alternative.

1. One can wonder whether the microtubular memes are generated intentionally or in a random manner in a phase transition leading to spin glass phase with basically un-predictable meme sequence. In the latter case, intentional action would be reduced to a selection to activate or not to activate the existing memes.

2. In this case it would be possible to have long term memories about events that never occurred, which seems strange. Random generation of the memes would also be in conflict with the notion that there are at least 42 parity bits making possible error correction. Thus it would seem that microtubular codewords can be activated only from the DNA level. In the case that microtubuli act as signal pathways this would indeed be the case.

3. Not all memetic code word sequences representable at microtubular level need to have counterpart at DNA level. This would lead to a situations in which meme could not be expressed at all.

These arguments favor the view that microtubuli are passive historians making possible self-reflection by providing a log file about activated memetic codons and possibly serve also as communication lines allowing the propagation of memetic codons between neuronal nuclei as sequences of 21 nerve pulses accompanied by genetic codon each. Only this option will be discussed in the sequel.

3. How to generate and read microtubular code words?

The coding of the intronic memetic code word to a microtubular code word would involve switching-on mechanism in spin glass phase of the microtubule for which initial state consists of '0':s. The tubulins corresponding to bit '1' would make transition to the conformation representing bit '1'. The activation of intronic meme should automatically generate the positive energy photons at frequency corresponding to the energy difference between two conformations of tubulin. Intronic memes should have kind of hardwired connection to a fixed ordered sequence of microtubular code words. Note that in TGD framework there is no need to static microtubular memory since memories can be communicated from geometric past. Therefore memory capacity would be unlimited in this sense.

The conscious reading of the microtubular code word using strong enough longitudinal electric field would generate positive energy photons, which could be communicated to the geometric future and generate declarative memory mental images. Also a direct sharing of mental images yielding episodal memories is possible.

Representation of the memetic code words as microtubular code words

The challenge is to understand how 126-bit genetic code word or (possibly 127-bit codeword) is mapped to 169-bit microtubular codeword. There are several hints how this mapping could be realized.

1. Number theoretical decomposition of the microtubular code word to memetic code word and 43 parity bits

It is possible to represent microtubular 169-bit codewords as $13 \times 13 = 169$ square lattice of bits.

1. One can write the number of microtubular bits as

$$169 = 126 + 43 = 3 \times 42 + 42 + 1 \ ,$$

and there is a temptation to assume that the first 126 bits correspond to the memetic codon and 42+1 bits represent parity bits making possible error detection. From the geometric representation it is clear that the bit in the middle of the 13×13 square is an excellent candidate for '1' in $42 + 1$.

2. 126-bit memetic code word allows a natural identification of the parity bits. The $126 = 3 \times 42$ decomposition allows also 42-bit code word, whose bits are obtained by decomposing 126-bit code word to a sequence of 42 3-bits, and defining each bit B of 42-bit as some Boolean function $B = f(b_1, b_2, b_3)$, say as a product $B = b_1 b_2 b_3$ of the bits of the corresponding 3-bit by representing bits as 1 and -1: the result is -1 (bit '0') if the number of bits '0' is odd and 1 otherwise. The comparison of codewords with a reference codeword assumed to be the correct one would allow to locate errors leading to internal inconsistency of the code word. The comparison of 42-bit codeword with the original one would allow to locate single bit changes of the memetic code word with a resolution of 3-bits.

3. A possible interpretation of the 43^{th} bit results from the requirement that each memetic code word gives rise to a conscious experience. This is guaranteed if the bit in the middle of the square is always '1' so that in the phase transition it changes the direction always and conscious experience results even when all the remaining bits are '0':s: the interpretation in this case would be as a mental image representing "nothing happened". An alternative possibility is that this bit represents parity bit. For instance, the product of all memetic bits or of all 42 parity bits. This bit could also be '1' only if there are no erratic bits. This bit could also represent 127^{th} bit of the 127-bit memetic code word.

2. How intronic DNA could represent parity bits?

If microtubule represents passively the information communicated to it, intronic memes should be accompanied by 42-bit parity code words. The minimal portion of DNA helix containing an integer number of DNA triplets consists of 10 triplets and corresponds to a length of $L(151) = 10$ nm (cell membrane thickness). 20 triplets would correspond to 2 full 2π twists. This encourages to consider the possibility that memetic codons correspond to 3 2π twists (length of 30 nm) along DNA so that memetic code words are followed by by a sequence of 9 DNA triplets serving some control function.

These 9 DNA triplets represent 54 bits. 7 of these codons could represent the 42 parity bits of the memetic codon preceding it. The remaining two genetic codons (12 bits) should represent further control information. The factorization $Z_{126} = Z_2 \times Z_3^{a)} \times Z_3^{b)} \times Z_7$ allows to identify two coset groups $Z_{126}/Z_{21} = Z_6$ as $Z_6^{a)} = Z_2 \times Z_3^{a)}$ and $Z_6^{b)} = Z_2 \times Z_3^{b)}$ corresponding to the identifications $Z_{21}^{a)} = Z_3^{a)} \times Z_7$ and $Z_{21}^{b)} = Z_3^{b)} \times Z_7$. This would mean the possibility to define two non-equivalent 6-bit parity code words as products $B = b_1 \times ....b_{21}$ of 21 memetic bits corresponding to the two sub-groups Z_{21}. The two DNA triplets could represent these parity 6-bits. Needless to say, these prediction are very strong and immediately testable by studying the intronic DNA.

3. The helical structure of the microtubule and the representation of the memetic code word and of parity bits

The tubulins representing parity bits should differ physically from those representing memetic bits. Time mirror mechanism suggests that the energy difference between two tubulin conformations differs considerably from that for the memetic tubulins. A weaker symmetry breaking induced by the helical electric field should order the bits of helical genetic code words and also order the 7 genetic code words to a sequence of vertical pairs running from left to right. Genetic code words should correspond to connected regions, most naturally helical stripes. Also the memetic code word and parity bits should correspond to a connected regions. There should be a clear signature telling where the microtubular code word ends.

The breaking of the rotational and translational symmetries is necessary and the helical structure of microtubuli could induce it. Denote by a the vertical distance between tubulins and by $\Delta\phi = 2\pi/13$ the angular distance between two tubulins along horizontal circle.

1. Genetic codons would be arranged to the helical stripes rotating making full 2π around the vertical section section of the microtubule defined by 13×13 tubulins. The 10 helices span a helical region spanning the angle range $\Delta\phi = 10 \times 2\pi/13$. Each helix would represent 2 memetic codons whereas the 13^{th} tubulins at $z/a = 13$ would represent parity bit. This would give 20 genetic codons. The 21^{th} genetic codon would correspond to the 6 lowest tubulins of the 11^{th} helical stripe. Therefore the pairs of 2 sub-sequent genetic code words would correspond to helices beginning at

$$(\tfrac{z}{a} = 1, \phi = k \times \Delta\phi) \ , \quad (\tfrac{z}{a} = 7, \phi = k \times \Delta\phi + \pi) \ ,$$

$$\Delta\phi = \tfrac{2\pi}{13} \ , \qquad k \in \{1, 2, ..5\} \cup \{9, 10, ..13\} \ .$$

The 21^{th} code word would correspond to $z = na$, $n = 1, ..., 6$, $k = 11$. The region representing parity bits would be connected and consist of vertical part and the 13^{th} horizontal stripe. It turns out that this guess is probably quite not correct: it seems that the first pair of helices representing genetic codons starts at $(z/a = 2, k = 2)$ so that the the horizontal line at $z/a = 13$ contains 12 tubulins (2 genetic code words).

2. Perhaps the simplest mechanism guaranteing the desired symmetry breaking is based on a static helical electric field, which is non-rotational and thus representable as a gradient of a scalar potential V. Electric field could be constant in the memetic section of the microtubule since tubulins are charged and Coulombic interaction energy would grow linearly with the azimutal angle ϕ and longitudinal coordinate z along the helical strands. In this case the potential would be of form

$$V(z, \phi) = k_1 \times \frac{z}{a} + k_2 \times \frac{\phi}{2\pi}$$

in the region populated by the genetic code words.

The value of the potential should fall rapidly down at $z = 13 \times a$ defining the upper edge of the microtubular codon and the vertical stripes defining the parity bits. The strong gradient of the electric field in the parity bit region could give rise to a strong dipole interaction and change the energy difference between microtubular conformations dramatically both at $z/a = 13$ and inside the
i) lower helical stripe S_{low} having having height of 6 units and width of 2 units starting at $(z/a = 1, \phi = k \times \Delta\phi)$, $k = 12, 13$ and
ii) upper helical stripe S_{up} having height of 6 units and width of 3 units and starting at $(z/a = 7, \phi = k \times \Delta\phi) + \pi)$, $k = 11, 12, 13$.
This behavior of electric field dictated by its non-rotational character would differentiate between memetic and parity bits.

3. Genetic codons are ordered to a sequence of pairs of codons if the value of the potential increases with constant steps along the helical stripe, and also in the transition from the top of k^{th} helical stripe to the bottom of $(k+1)^{th}$ helical stripe. This gives

$$k_1 = -\frac{k_2}{13} \ ,$$

which fixes the potential apart from overall scaling:

$$V(z, \phi) = V_0 \times (\tfrac{z}{a} - 13 \times \tfrac{\phi}{2\pi}) \ ,$$

giving

$$V(z = n \times a, \ \ \phi = s \times \tfrac{2\pi}{13}) = V_0 \times (n - 13 \times s) \ .$$

The length of a single tubulin in the vertical direction is $a \simeq 8$ nm and the outer radius of microtubule is $R \simeq 12.5$ nm [13] . This gives $\Delta z / R\Delta\phi \simeq 1.32$ whereas $\Delta V_z / \Delta V_\phi = -1$ rather than $-1/1.32$ required by the orthogonality with respect to the helical strands. Thus the electric field can be regarded as a superposition of a field orthogonal to helical strands with a weaker field parallel to the z-axis.

4. The requirement that the 5+5+1 (5+5) microtubular codons are represented at the lower (upper) half of codon can be satisfied if the the value of the potential becomes in some sense too large at the point $(z/a = 7, \phi/2\pi = 11/13)$ and that this forces V to rapidly raise up from the minimum value

$$V_{min} = -137V_0 \ .$$

The maximum of the potential at $(n = 1, s = 1)$ given by

$$V_{max} = -12V_0 \ .$$

$(n = 1, s = 1)$ bit is non-memetic bit and shifted by one unit upwards from the horizontal $n = 13$ row of 13 bits: this distinguishes it as a natural candidate for the 43^{th} bit. With this identification the first helical stripe containing two genetic codons would start at $(n = 2, s = 2)$ and $n = 13$ horizontal line would contain only 12 points corresponding to two genetic codons. Vertical stripes of parity bits would contain 5 genetic codons represented as helical stripes. Thus all genetic codons would correspond to helical or horizontal stripes. Horizontal and helical genetic codons should differ somehow but the origin of difference remains unclear.

Symmetries of the genetic code and the error detection

The ratio of the number of the number of parity bits to memetic bits is $R = 42/126 = 1/3$ and almost equals to the ratio 21/64 of the number of genetic code words to the number amino-acids. If parity bits represent directly the "memetic amino-acids" the action of all memetic code words with given 42 parity bits is identical and the comparison of parity bits would be enough to check that everything is in good shape at the level of the memetic expression. Obviously, this option is trivial.

If the memetic code is directly induced by the genetic code, the ratio R would be $R = log_2(21)/6 \simeq .73$. For both options the number of the "memetic amino-acids" would be considerably smaller than $(2^{126}-1)/63$ suggested by the direct generalization from the case of the genetic code, and corresponding to $R \simeq 20/21$.

If the memetic code is induced by the genetic code which is same for both chemical and field pattern expressions, intronic memetic codons possess the A-G symmetry and almost exact T-C symmetry of the genetic code in the sense that memetic code words related by these symmetries would activate the same genes. This would allow to improve further the error detection.

1. A-G and almost T-C symmetries imply that the last 2 bits of 6-bit defining genetic code word in good approximation reduce to single bit, say the last bit. Therefore the second parity bits could be taken to be the product b_4b_5. This improves considerably the effectiveness of error detection at the level of expression.

2. Also the first bit of the genetic code word is less significant since the genetic code table contains many 4-sub columns (codons of form XYZ, with Y fixed) for which all 4 amino-acids are same and quite a many 2-sub-columns (codons of form XYZ, X= A,G or X= T,C) are identical. Therefore a relatively safe choice is to take the first parity bit for the genetic codon to be the product b_2b_3. This choice would localize with a reasonable reliability the errors with 2-bit accuracy at the level of expression.

Could error correction mechanism be used to detect mutations of memes?

The first question to be answered concerns the purpose of the error correction process. Is error correction used

1. to remove the internal inconsistencies of the memetic code words at intronic level due to mutations or,

2. to stabilize long term memories represented at microtubular level?

Only the first option would be needed if the refreshment of the memetic code words by activated intronic DNA occurs all the subjective time in the geometric past. Both types of error correction could rely on the following mechanism.

The comparison of the microtubular code word with that of the geometric past by time mirror mechanism, assumed to yield resonant interaction if the compared code words are identical, could reveal the emergence of those mutations at DNA level which alter some parity bits and memetic bits

in such a manner that the parity bit pattern ceases to be consistent with the memetic bit pattern. There would be simply no internally consistent microtubular code words in the geometric past identical with this pattern. Large number of temporal copies of the codeword in geometric past would make the mechanism reliable.

The internally inconsistent change of the microtubular codeword and even a change in general could be detected by this mechanism. In absence of resonance a process trying to fix up the meme at DNA level by trial and error could be initiated and could yield an internally consistent or even original meme. Note that this comparison mechanism would be conscious and even the correction mechanism might be conscious intentional process.

To sum up, the model for the mapping of memetic code to microtubular code is dictated by the general ideas about realization of intentions and p-adic cognitive codes. When combined with general number theoretical arguments and physical considerations the model becomes highly unique. The prediction for the intronic representation of the memetic codon is readily testable, and also the prediction for the microtubular electric field is in principle testable.

4.3.4 Genes, memes, and language

The idea about intronic memes as computer programs running in the hardware coded by genes together with quantitative facts lead to a view about how memes and genes could relate to language. It must be emphasized that the idea about correspondence between genes and language is not new. The article [111] gives a nice summary about various findings supporting the view that language and DNA are closely related.

Zipf's law

One of the basic resemblances between genes and language is Zipf's law relating the rank r of the event with its frequency f of occurrence [47] . The rank of a given event is defined by ordering the events in sequence using as a criterion the frequency of occurrence: the event occurring most often has rank 1, etc.. Zipf's law states $f = C/r^a$, where a is a constant near one, and C is a constant depending on the size of the sample. In linguistics the event could correspond to the occurrence of a given word or character, and in genetics to the occurrence of a given DNA triplet.

Zipf's law holds also for many systems regarded as non-living, such as masses of stars in a constellation of stars. Interestingly, the sum of the frequencies for an infinite number of events is proportional to Riemann Zeta function $\zeta(a) = \sum_n 1/n^a$ at point $a \simeq 1$, which can be regarded as a product of thermal partition functions associated with primes regarded as bosons: $\zeta(a) = \prod_p 1/(1-p^a)$, $log(p)$ plays here the role of energy and a to the role of inverse temperature. Interestingly, the line $a = 1$ defines a critical line such that $\zeta(a)$ converges for $Re(a) > 1$. $a = 1$ corresponds to the temperature at which Bose-Einstein condensation occurs and the system becomes macroscopic quantum system. Thus Zipf's law might relate to p-adicity and macro-temporal quantum coherence in some deep manner.

There is also evidence in favor of a typological relationship between the words of human speech and DNA "words" (see the references in [111]). The word formation appears to obey laws similar to those of formal genetics so that one can speak of dominant and recessive features, mutations, etc.. In [111] graphical representations character sequences defined by written texts and nucleotide (A,T,C,G) sequences are studied (amino-acid sequences of long proteins would be more appropriate for comparison with character sequences). The fractal dimensions of the resulting planar fractals are in the range $0 < D < 1$. A random sequence of characters corresponds to $D = 0$ and repetition of single character to $D = 1$, whereas written texts correspond to $D = .7 - .8$.

Could the phonemes of language be expressions of DNA triplets?

The previous construction of representations of genetic and memetic codes, in particular the facts that the frequency $f \sim 10$ Hz represents the fundamental frequency associated with speech organs and that 20 Hz frequency represents the lower limit for audible frequencies and the rate of mRNA-amino-acid translation, suggest that memetic code might be involved with speech and speed recognition. Since the duration of a phoneme in speech is $\sim .05 - .1$ seconds, one must seriously consider the possibility that phonemes might somehow relate to genetic or memetic codewords.

The number of phonemes of native origin in Finnish language the same as the number of characters and equals to 21, the number of amino-acids plus stopping codon counted as an effective amino-acid. In English language the number of phonemes it is not so easy to estimate the number of phonemes since written language differs so much from spoken but the number is not too far from 21. In Russian the number of different characters is 32, half of the number of DNA codons. Certainly one cannot expect precise correspondence between the numbers of phonemes/letters and amino-acids and it might well be that DNA→phoneme coding differs from the DNA→amino-acid coding.

These findings together with the observation force to consider the possibility that phonemes might play a role similar to that of amino-acids, and be interpreted as resulting in the translation of DNA triplets to field patterns to neural activity to the motor activity of speech organs. Words in turn would represent analogs of protein sequences coded by sequences of DNA triplets. The fact that memetic code represents statements about statements would suggest that memes represented by introns correspond to higher level structures of language, kind of main computer program producing meaningful expressions of language while running. Words represented by genes could be the hardware of language or lower level language and DNA triplets would represent the basic material of the hardware expressed as phonemes. This would of course require expression of genes and memes in terms of field patterns inducing the generation of nerve pulse patterns.

Consonants carry more information than vowels (early form or written language used symbols only for consonants). This picture is consistent with the fact that the property of being consonant is determined by the very brief time interval in the beginning of the pulse sequence defining the phoneme so that the occurrence of high frequencies make it consonant. There are 8 (7) vowels in Finnish (English) language, which suggests that the first 3 bits of the generic codeword in the frequency representation and representing lowest frequencies are responsible for the basic vowels and the remaining 3 bits corresponding to the higher frequencies add to the beginning of the phoneme something making it consonant.

The frequencies for the occurrence of various phonemes should be the same as for the occurrence of the DNA triplets coding them. The simplest working hypothesis that the DNA-phoneme code is same as DNA-amino-acid code does not work in case of say Russian language (32 characters) but deserves a testing in the case of Finnish language. Of course, one could consider the possibility of context dependent coding of phonemes: also ordinary genetic code can be context dependent in some situations (the same codon codes for stopping sign or amino-acid depending on context). The prediction would be that the frequencies for the occurrence of phonemes would equal to those of amino-acids.

It is not possible to assign a definite duration to the intronic representation of the memetic codeword. Speech is indeed extremely flexible: the rate of speech can vary, vowels can be represented multiply, etc.. This variation would be made possible by flexibility at the DNA level or at level higher than this (magnetic body would control introns). If speech represents genetic code, 50 ms would however be a good guess for the minimal duration of phoneme and 20 Hz for the lower end of consciously experienced frequencies (as it indeed is). Rather remarkably, the rate for the translation of mRNA triplets to amino-acids is 20 nucleotides per second so that one codon corresponds to the duration of the genetic codon in $k = 252$ representation of the genetic code.

On the other hand, the memetic code words generated while listening speech or reading text could correspond to the mental images representing the meaning of a word, and could quite well have a duration of .1 seconds whereas the minimal duration of phoneme would be about 50 milliseconds. If time mirror mechanism is involved time is not problem: the understanding of speech would occur at the level of DNA in the geometric past. Same applies also to the production of speech: the desire to produce an expression of language would generate DNA activity in the geometric past.

The overall conclusion is that memes and genes of DNA would define language independent universal grammar introduced by [20] [20] . Languages would differ from each other only in the different association of phonemes to the DNA triplets. Also languages based on electromagnetic realization and not directly conscious to us are possible and even probable.

How memes could control genes in the production of language?

Language is not expected to be the only function controlled by memes. Memes could be responsible for a high level control of genes also in their ordinary activities. Memes would represent a higher level control structure utilizing the existing program like structures defined by genes activating genes. In

case of language the fundamental expression would be in terms of field patterns inducing nerve pulse patterns inducing in turn speech motor activities.

Computer metaphor suggests that memetic programs correspond to sequences of memetic codewords with each memetic codeword defining a main program as a sequence of sub-program calls. Production of speech would mean activating these programs from magnetic body by time mirror mechanism. Genetic program calls would be realized as addresses pointing to genes defining the subprograms: 2^{126} different addresses is much more than needed to point to any desired gene. Also genes could use this addressing to point to other genes. The pointed gene could generate field pattern giving rise to a word or sequence of words or it could point to another gene. In this manner meme could generate entire sequence of words by inducing a sequence of subprogram calls (computer language LISP suggests a possible model for what occurs). Genes have a hierarchical structure, and one expects that higher levels of this hierarchy could fix the parameters determining the rate of speech, durations of phonemes, accents, emotional content, etc....

Pointing could be achieved by electromagnetic field patterns utilizing time mirror mechanism so that address would be expressed by negative energy topological light rays (phase conjugate laser waves). Pointing could be based on avoidance of starvation. Negative energy photons at the frequency serving as the name of the pointed system would induce the dropping of charged particles to a larger space-time sheet. The pointed system would lose energy and would generate negative energy topological light rays at characteristic frequencies to compensate the lost energy. If the frequency is higher, the pointed system would point to a lower level in the hierarchy of sub-programs. One cannot of course exclude the possibility that pointed gene points back to the pointing gene or meme. This could give rise to recursive self-referential program structures. At the lowest level of hierarchy there would be gene which act as a population inverted many-sheeted laser generating a cascade of positive energy photons at various frequencies and in this manner yielding the desired response.

4.3.5 Does memetic code make possible communications between different species?

The observations of Cleve Backster [14] give scientific support for the view that plants react to human emotions. The TGD based interpretation would be as sharing as mental images. One can however ask whether sharing of mental images might make possible the development of more evolved communications involving signalling by codes. For instance, people in hypnosis report that they can share the experiences of plants and shamans claim that they can experience what it is to be an animal and communicate with plants. According to what the shamans of the South America tell, their refined medical knowledge is told to them by plants [37] . In principle common intronic memes could make possible this kind of communications even between different species: these communications would not of course be conscious to us under normal circumstances.

Interspecies communications by sharing of mental images

Sharing of mental images does not require neither target nor receiver to be able to communicate symbolically. Therefore the target and receiver could be any living system: animal, plant, even bacterium. In TGD Universe one cannot exclude even "non-living" systems as targets and even sharers of mental images. The remote viewing of non-living targets is indeed possible and in this case either mental images of target or some system perceiving target are shared. Since emotions represent holistic summaries about contents of consciousness, they are good candidates for universal mental images and the sharing of emotions could occur even between different species.

Support for the extreme generality of the sharing of the mental images as a basic mechanism of remote viewing comes the fascinating experimental discoveries made by Cleve Backster [10, 14] . These findings have led Backster to introduce the notion of primary perception, which seems to have a natural identification as sharing of mental images.

1. Plants, eggs, and even bacteria are able to have primary perceptions. Backster tells in the interview that even yoghurt got wild when he took a chicken out of refrigerator and began pulling off strips of meat. Plants respond elecrically to strong negative emotions and to the violence or death suffered by other living organisms. That primary perception correlates with the strength of emotions conforms with the view that entropy gradients with respect to subjective time, which are indeed identifiable as emotions, measure the strength of perception.

2. Distance does not seem to matter much. Sperm separated by a large distance from its donor reacted when the donor inhaled amyl nitrate. White cells were found to remotely react to the emotions of their donors. Same was found to apply to plants and their owners.

3. Plants and even bacteria seem to have a defence mechanism resembling shock. If bacteria share the mental images of suffering organisms by receiving negative energy MEs sent by them, the shock could be interpreted as resulting from the depletion of positive energy resources (all excited states of population inverted many-sheeted lasers decay to the ground state) or be a mechanism preventing this depletion.

An interesting question is whether humans have lost this ability or is this reaction usually unconscious at our level of self hierarchy and whether human skin could exhibit galvanic skin response to say death of other life-forms.

Interspecies classical communications using common memes and genes

The assumption that even classical communications between different species are possible is much stronger hypothesis than the assumption that mere sharing of mental images occurs. The general model for interspecies communications using symbolic representations for the communicated information rather than mere sharing of mental images relies on the pan-psychic view about life and consciousness ("Everything is consciousness and consciousness can be only lost"). Also the hypothesis that speech and written language are only one particular realization of language involving at fundamental level memes controlling genes expressing themselves in one of the many possible manners, supports this view.

1. General model

1. If the intronic portion of the DNA corresponds to memone defining basic linguistic repertoire expressed using genes defining the vocabulary. Even plants could possess language possibly realized using MEs ("topological light rays"). Introns could control genes in terms of electromagnetic MEs and genes could could express themselves by MEs. Genes would define the words of the language. One could say that interspecies communications reduce actually to intercellular communications between cells of different species.

2. Successful communication requires that the languages of communicators have common portion in their vocabularies. Cells possessing common expressed memes defining basic expressions and genes defining the vocabulary could communicate with each other. Meme level communications would be possible between any two eukariotes (organisms having cell nucleus): bacteria, plants, fungi, animals. Also communications between plants and humans would be possible.

3. Communications could occur by sharing of DNA level mental images induced by activated memes: negative energy MEs would make possible the needed quantum entanglement. Communications could occur also classically. The simplest form of classical communication would involve the coding of the meme to the field pattern of em or Z^0 ME to a name of meme using memetic code in turn activating the same meme in the receiving organism. Memes could express themselves by controlling genes in turn generating various types of expressions for the meme This could in principle allow even translation of memes to speech in altered states of consciousness in which back projection to ears would transform the internal speech to sounds.

4. The general model for sensory representations and motor actions based on time mirror mechanism involves both quantum and classical communications. There is a great temptation to assume that the same model applies also in the case of inter-species communications. Both the psychokinetic aspect corresponding to the remote motor action aspect, and the remote sensing aspect corresponding to the remote sensory perception would be present and would be essentially geometric time reversals of each other. Psychokinetic aspect of course represents more than mere communications.

5. Unless the code is universal so that the classical signal induces directly a standard mental image, most plausibly emotion, irrespective of species, a code assigning symbols to mental images must

be established by sharing of mental images. There are good justifications to argue that the establishment of a code requires sufficiently intelligent communicators. On the other hand, even if the signals from say plant do not have any "meaning" for a human receiver, they could generate effects analogous to synesthesia.

6. Organisms living in symbiosis (say some insects and flowers) could have common memes and genes allowing them to communicate. Common memes and genes would be the analogs of common genes causing the coloring of the flower and insect to be similar. This kind of communication could also explain the refined medicine of South American shamans. Shamans tell that plants have taught this medicine to them. In the book "The cosmic Serpent" [37] , Jeremy Narby proposes that shamans communicate directly with the DNA of the plant and that bio-photons might be essential for these communications.

2. Are "skin senses" in preferred role in inter-species communications

The general model of sensory organs [31] provides further pieces to the model. The basic hypothesis is that sensory organs are the seats of primary qualia and that the experiencing self corresponds to the magnetic body of size much larger than the material body. The feedback via brain to the sensory organs is assumed to make possible the active processing of the sensory input to sensory percept.

The model introduced also a division of sense to "brain" and "skin" senses motivated by the following observation. During the development of vertebrate embryo three basic types of cells are formed: ectoderm giving rise to skin and central nervous system, endoterm giving rise to many internal organs, and mesoderm giving rise to muscles, skeleton, connective tissue,... What is remarkable is that the ectoderm giving rise to brain, spinal cord, eye,.. suffers an inversion during the formation of the neural tube. The wall of the neural tube is inverted so that inside becomes outside and vice versa. This explains the strange finding that the eyes of vertebrates are inversion of the eyes of invertebrates and apparently look very awkward from engineering view point.

This leads to the distinction between "brain senses" and "skin senses".

1. For "brain senses" (vision, olfaction) the back projection by the telepathic sharing of mental images from brain to sensory organs allows to build sensory percept as a caricature.

2. For "skin senses" (with hearing included) the entanglement of the sensory organ with brain is replaced with the entanglement with external world, and can thus give rise to remote sensing based on the sharing of mental images using time mirror mechanism. This remote viewing need not be conscious-to-us except in special situations, say during hypnosis.

If this distinction is sensible, skin senses would be in a special role as far interspecies communications are considered.

A model for insect-plant communications

Callahan has made very important discoveries related to the olfaction of insects and insect-plant interaction. Callahan's work [117, 105] demonstrates that the insect olfaction is based on infrared light generated by the odorant molecules interacting with the antennae of the insects. This might be true for our olfaction too. Callahan has also shown plants communicate with insects by generating infrared light [105] . This finding conforms with the findings of Albrecht-Buehler [108] showing that all cells contain microtubular structures acting as receiving antennae for infrared light. Furthermore, plants suffering from de-nutrition are found more easily by insects than healthy plants.

These findings encourage to consider the following mechanism for insect-plant communications. This mechanism could apply also to the plant-human interactions.

1. Insects generate infrared MEs propagating like massless particles inside low frequency negative energy MEs acting as bridges quantum entangling the plant and the insect. Both classical communications by positive energy IR MEs and quantum communications by negative energy IR MEs are in principle possible.

2. In the case that plant suffers from de-nutrition, it can gain metabolic energy by sending negative energy MEs received by insect. This gives for plant metabolic energy and at the same time

generates the quantum entanglement bridge making it possible for the insect to find the plant. The same mechanism explains also the episodal memory feats of synesthetes: due to the overactivity of subcortical parts of brain the neurons of the left cortex suffer starvation and generate negative energy MEs providing them metabolic energy and simultaneously entangling them with the geometric past so that episodal memories result. Also the life review of NDE experiences could be a by-product of the neuronal starvation.

Are human-plant communications possible?

Concerning the ideas about human plant-communications, I am grateful for Peter Hageman [1] for inspiring discussions. Hageman claims to be able to express "plant language" by "dancing" in meditative state, and has made detailed maps of motor expressions of plant mental images and proposed a detailed taxonomy about plant language, and also developed refined ideas such as the notion of dialect. It is easy to debunk Hageman's views since the interpretations necessarily involve a lot of subjective elements. One could imagine a scientific testing of Hageman's claims by checking whether the vocabulary defined by the bodily expressions is invariant of a given plant. Similar testing is used in the case of motor synesthesia.

The common portions of the memone and genome of plant and human would in principle make possible this communication. Thus the memes and genes, which plant can communicate to humans are those which are expressed also by some cells of the human body. Since plants do not have a central nervous system, it seems that the communicable memes and genes should correspond to rather primitive expressions common to us and animals. Obviously, the memes and genes responsible for the body language is a good first guess in this respect. Note however that genes could define lower level language and could also be communicated in this manner.

This body language representation brings in mind motor synesthesia in which sensory input from some sensory modality is expressed as motor activity. The memes and genes expressible by body language could of course be expressed also by using ordinary language. The universality of the memetic and genetic codes is indeed consistent even with the transformation of communications to linguistic expressions.

4.3.6 Intronic portions of genome code for RNA: for what purpose?

The last issue of [121] contains an article about the discovery that only roughly one half of DNA expresses itself as aminoacid sequences. A detailed summary of the results has been published in Nature [45] . The Encyclopedia of DNA Elements (ENCODE) project has quantified RNA transcription patterns and found that while the "standard" RNA copy of a gene gets translated into a protein as expected, for each copy of a gene cells also make RNA copies of many other sections of DNA. In particular, intron portions ("junk DNA", the portion of which increases as one climbs up in evolutionary hierarchy) are transcribed to RNA in large amounts. What is also interesting that the RNA fragments correspond to pieces from several genes which raises the question whether there is some fundamental unit smaller than gene.

None of the extra RNA fragments gets translated into proteins, so the race is on to discover just what their function is. TGD proposal is that the RNA gets braided and performs a lot of topological quantum computation [81] . Topologically quantum computing RNA fits nicely with replicating number theoretic braids associated with light-like orbits of partonic 2-surfaces and with their spatial "printed text" representations as linked and knotted partonic 2-surfaces giving braids as a special case. An interesting question is how printing and reading could take place. Is it something comparable to what occurs when we read consciously? Is the biological portion of our conscious life identifiable with this reading process accompanied by copying by cell replication and as secondary printing using aminoacid sequences?

This picture conforms with TGD view about pre-biotic evolution. Plasmoids [183] , which are known to share many basic characteristics assigned with life, came first: high temperatures are not a problem in TGD Universe since given frequency corresponds to energy above thermal energy for large enough value of $\hbar$ [27] . Plasmoids were followed by RNA, and DNA and aminoacid sequences emerged only after the fusion of 1- and 2-letter codes fusing to the recent 3-letter code. The cross like structure of tRNA molecules carries clear signatures supporting this vision. RNA would be still responsible for roughly half of intracellular life and perhaps for the core of "intelligent life".

I have also proposed that this expression uses memetic code which would correspond to Mersenne $M_{127} = 2^{127} - 1$ with 2^{126} codons whereas ordinary genetic code would correspond to $M_7 = 2^7 - 1$ with 2^6 codons. Memetic codons in DNA representations would consist of sequences of 21 ordinary codons. Also representations in terms of field patterns with duration of .1 seconds (secondary p-adic time scale associated with M_{127} defining a fundamental bio-rhythm) can be considered.

A hypothesis worth of killing would be that the DNA coding for RNA has memetic codons scattered around genome as basic units. It is interesting to see whether the structure of DNA could give any hints that memetic codon appears as a basic unit.

1. In a "relaxed" double-helical segment of DNA, the two strands twist [93] around the helical axis once every 10.4 base pairs of sequence. 21 genetic codons correspond 63 base pairs whereas 6 full twists would correspond to 62.4 base pairs.

2. Nucleosomes [70] are fundamental repeating units in eukaryotic chromatin [21] possessing what is known as 10 nm beads-on-string structure. They repeat roughly every 200 base pairs: integer number of genetic codons would suggest 201 base pairs. 3 memetic codons makes 189 base pairs. Could this mean that only a fraction $p \sim 12/201$, which happens to be of same order of magnitude as the portion of introns in human genome, consists of ordinary codons? Inside nucleosomes the distance between neighboring contacts between histone and DNA is about 10 nm, the p-adic length scale L(151) associated with the Gaussian Mersenne $(1+i)^{151} - 1$ characterizing also cell membrane thickness and the size of nucleosomes. This length corresponds to 10 codons so that there would be two contacts per single memetic codon in a reasonable approximation. In the example of Wikipedia [70] nucleosome corresponds to about 146=126+20 base pairs: 147 base pairs would make 2 memetic codons and 7 genetic codons. The remaining 54 base pairs between histone units + 3 ordinary codons from histone unit would make single memetic codon. That only single memetic codon is between histone units and part of the memetic codon overlaps with histone containing unit conforms with the finding that chromatin accessibility and histone modification patterns are highly predictive of both the presence and activity of transcription start sites. This would leave 4 genetic codons and 201 base pairs could decompose as memetic codon+2 genetic codons+memetic codon+2 genetic codons. The simplest possibility is however that memetic codons are between histone units and histone units consist of genetic codons. Note that memetic codons could be transcribed without the straightening of histone unit occurring during the transcription leading to protein coding.

4.4 Corals and men

The comparison of the human genome with that of invertebrates during great genome project yielded some surprises [122, 157] . In particular, it was found that human genome possesses 223 genes which are lacking from the genome of the model invertebrates. Even more, a considerable fraction of these genes seems to be lacking even from the genome of other vertebrates and should have thus appeared relatively recently to the human genome. This led to the TGD inspired proposal that human genome has been subject to genetic engineering relatively lately with an even more crazy sounding proposal that intelligent intra-terrestrial life forms are responsible for this engineering (see [20, 21]). Needless to say, this hypothesis is absolute non-sense unless one takes completely seriously the notion of many-sheeted space-time and related ideas.

Towards the end of year 2003 a new sensational result was published [198] . The genome of certain coral, Cnidarian Acropora millepora, was compared with the genomes of fly (Drosophila melanogaster), nematode worm (Caenorhabditis elegans) and human genome. For simplicity, I shall refer to these animals as corals, flies, and worms in the sequel.

Before going to results, it deserves to mention that the phylum Cnidaria [24] is a major group of invertebrates that includes the sea anemones, corals, jellyfishes, hydroids. Radial symmetry is characteristic for these animals whereas more advance animals have bilateral symmetry. All cnidarians are carnivors. The name cnidaria comes from 'cnida', stinging capsules used to deliver toxin, to stick to a prey, or to entangle with an object. Cnidarians are believed to branch from the evolutionary tree much before flies, worms and vertebrates, and the expectation was that its genome should give information about the genome of the common predecessor of metazoans ("animals"). Obviously, coral

genome should possess genome having much stronger resemblance to fly and worm genomes than that of vertebrates.

The astonishing result was that the genome of coral resembles human genome to a surprisingly high degree but much less the genomes of the fly D. melanogaster and nematode worm C. elegans. The conclusion of the authors is that the genes usually regarded as vertebrate inventions have been possessed by the believed-to-exist common predecessor of all animals, and that invertebrates have lost most of the genes common to human and coral during their evolution.

These strange conclusions are based on the existing wisdom about the evolution of animals and about the role of genome, and thus also challenge this wisdom.

1. The mutation rate of flies and nematode worms is high but it is not known whether genes can disappear. One can of course criticize the conclusion. Is the loss of genes, kind of "de-evolution", really a good survival strategy? Could it be that the gene loss hypothesis is dictated by some hidden assumptions? One can imagine several assumptions of this kind.

   (a) It makes sense to speak about continuously growing evolutionary tree from which corals branch before the emergence of the flat worms believed to be common predecessors of vertebrates, flies, worms, and other invertebrate phyla.

   (b) There are no of interventions from outside to the genetic evolution (genetic engineering by some more advanced life forms).

   (c) There is no horizontal gene transfer between corals and vertebrates (say fishes) living belonging to the ecosystems containing corals.

2. Corals possess relatively few tissue types. Coral is in fact the the most primitive animal possessing neurons. The neurons are organized into a homogenous neural net like structure. Therefore the presence of genes of vertebrates with highly developed nervous systems in the coral genome looks paradoxical. Could genes have some unknown functions besides those related to the coding of "hardware"?

4.4.1 Why corals and vertebrates should have common genes?

The fact that corals and higher vertebrates have a lot of common genes, must have some sensible explanation. If flies and worms have never possessed genes common to vertebrates and corals, there must be something common to corals and vertebrates but not to higher vertebrates and flies, worms, perhaps all other invertebrates than corals.

1. Corals (polyps) are simple multi-cellulars consisting of two cell layers, epidermis and gastrodermis. The non-tissue layer between them is called the mesoglea. Corals are in a complex interaction with an ecosystem involving also vertebrates. Interestingly, corals are the only animals living in symbiosis with plants (dino-flagellates, which are simple mono-cellulars) providing them metabolic energy produced in photosynthesis. Social life requires communications and language of some kind, and this might explain why corals possess so complex genome.

2. Corals form large populations, coral reefs. One could regard coral reef as a super-organism, with corals taking the role of the cell in ordinary organisms. Some corals could even define super-neurons of the super-neural system of this super-organism. This could resolve the paradox caused by the simplicity of the nervous system of the coral itself viz. the complexity of the coral genome: complexity would reside in the connections and communications of the super-neural system.

3. Rather remarkably, both vertebrates and corals possess skeletons having calcium as a basic building brick. Coral skeleton consists of calcium carbonate $CaCO_3$ or limestone (calcium carbonate plus sediment). Usually the basic function of skeleton is thought to be that of a mere supporter but it might have also other functions as following arguments suggest.

The function in question could be that of antenna.

1. Ca_{++} waves are known to play key role in the functioning of the nervous system [31] . The finding, which led to the notion of magnetic body crucial for the functioning of living systems in TGD Universe, was that irradiation of living matter at the harmonics of Ca_{++} cyclotron frequency in Earth's magnetic field has effects in living matter [17] and that these effects can be best understood if living cells are macroscopic quantum systems.

2. What makes Ca_{++} (and Mg_{++}) ions so special that they are bosons and can therefore form super-conducting Bose-Einstein condensates at the magnetic flux tubes of (say) Earth's magnetic field. The dropping of Ca_{++} ions from smaller space-time sheets to the magnetic flux tubes generates cyclotron radiation at the harmonics of the cyclotron frequency, and this mechanism is crucial for the generation of EEG.

3. The fact that EEG is associated with vertebrate neural systems and corals representing the simplest life forms having neurons, suggests that communications could be on Ca_{++} cyclotron radiation and be between neural systems of corals and vertebrates living around it. The calcium containing skeletons possessed by both vertebrates and corals could serve as antennae allowing to generate field patterns representing the communicated signals strong enough to make possible communications with say fishes.

These observations can be combined with the earlier vision about the role of genome.

1. TGD based view for genetic code predicts that genes are not expressed only chemically but also in terms of field patterns representing one particular expression of the universal language defined by genes and memes, the latter being represented by the intronic portions of the genome. The hypothesis is that common memes and genes make possible even inter-species communications. Thus DNA would not characterized so much species than communications in the ecosystem in which the species.

2. The proposed electromagnetic realization of the language defined by DNA and utilizing genetic code is as transitions at the harmonics of cyclotron frequency of Ca_{++} ions. The time $\tau_c = 1/f_c$ defined by cyclotron frequency $f_c = 15$ Hz of Ca_{++} ion in the magnetic field of $B_e = .5$ Gauss, defines the duration of the code word consisting of 6 bits. Bit '1' can be realized as a pulse of duration about $\tau_c/6$. Second realization if the codeword is as superpositions 6 lowest harmonics of cyclotron frequency generated when Ca_{++} ions drop to larger space-time sheets (bit '1' corresponds to harmonic with Fourier amplitude above critical intensity).

The combination of these ideas leads to the following vision about why corals and vertebrates possess common genes.

1. Linguistic communications based on electromagnetic field patterns are crucial for the functioning of the complex ecosystem formed by corals and various species belonging to it. In particular, fishes are vertebrates so that it would be advantageous for the coral to possess a considerable fraction of vertebrate genome responsible for the universal language.

2. The basic difference between humans and corals is due to the intronic portion of the genome, which dominates human genome and defines higher level linguistic structure based on menetic codewords with duration of .1 seconds and having 126 (or 127) bits. One could test whether fishes and other vertebrates living in the coral environment share identical genes with the coral.

4.4.2 Did corals and vertebrates receive their common genes via horizontal transfer?

One can imagine several alternative models for how corals and vertebrates received their common genes. These "language genes" could have been "invented" by either corals or vertebrates and transferred horizontally from corals to vertebrates or vice versa. The most general view is that the system inventing the "language genes" was the entire system coral + vertebrates (possessing magnetic body), and the transfer of genes occurred in both directions.

Many-sheeted space-time allows to consider the possibility that the genes were transferred along magnetic flux tubes connecting the many-sheeted DNAs of corals and vertebrates involved (recall that

many-sheeted DNA involves hierarchy of magnetic flux tubes with magnetic field strengths scaled by powers of two). The large sized magnetic body of the coral might have played essential role in this transfer. If one sees the magnetic body associated with corals and associated life-forms as a single conscious organism, this hypothesis looks natural.

Horizontal transfer of genes from vertebrates to corals?

Perhaps the simplest hypothesis is that the genes of vertebrates not possessed by invertebrates like flies and worms, appeared in the genome of corals, only after they were needed, that is during the co-existence with vertebrates as parts of same ecosystem.

The simplest possibility is a horizontal gene transfer from vertebrates to corals, so that vertebrate genes could be seen as genuine vertebrate inventions as usually believed. Since corals possess calcium backbone, it is indeed sensible to transfer "language genes" to corals. The transfer of "language genes" could have occurred also to other organisms but, by the absence of Ca containing skeleton, the transferred "language genes" would have been useless for them. The genes coding for the calcium containing skeleton of coral must have been present from the beginning, and for this option must be independent of "language genes".

Horizontal transfer of genes from corals to vertebrates?

The horizontal transfer of genes could have also occurred from corals to vertebrates so that vertebrate genes could be seen as coral inventions. This makes sense if the common genes were primarily involved with the communications between corals and vertebrates so that the co-evolution of vertebrates and corals was basically evolution of communications using genetic code. Also the vertebrate genes responsible for coding Ca_{++} based structures like bones should have counterparts in the genome of the coral. If corals possessed neurons from the beginning, the genes allowing to differentiate the cell to a neuron could have been transferred, not only to vertebrates but also to the invertebrates with nervous system, and corals could have functioned as a kind of organizing centers of evolution.

4.4.3 What happened in Cambrain explosion?

The most science fictive hypothesis is that the vertebrate genes were possessed by corals from the beginning. Ironically, this is the hypothesis forced also by the standard view about evolutionary tree. Since these genes had no function at the time when even flat forms preceding flies, worms, and vertebrates were still absent, the only reasonable conclusion seems to be that some advanced life forms intervened the terrestrial evolution somehow.

There are two basic options.

1. "Language" genes could have appeared to the genome of coral by some kind of genetic engineering. Since corals are the simplest organisms possessing neurons, also the genes responsible for the differentiation of cells to neurons could have emerged during this intervention.

2. Corals themselves could have been these extra- or intra-terrestrial life forms possessing these genes.

Corals would have served as kind of gene banks and "language" genes would have been transferred horizontally to the genomes of vertebrates during the evolution of the ecological co-existence with vertebrates such as fishes. "Neuronal genes" would have been transferred also to other phyla than future vertebrates.

Obviously, this intervention could have have induced profound changes, entirely new phyla could have emerged as a result of these genetic modifications by horizontal gene transfer. Although this scenario sounds un-necessarily science-fictive, it deserves a serious consideration since, as will be found, it could allow to resolve the puzzles related to the Cambrian explosion.

This option can be tested by looking whether corals possess genes possessed by higher vertebrates like humans but not by any of the vertebrates, which have possibly been members of same ecosystem with corals. One could also try to test the hypothesis that coral has possessed "language genes" already at Cambrian period. This could be the case, if "language genes" and genes coding for Ca^{++} body of coral belong to the same gene cluster.

Did Cambrian explosion involve the intervention of intra- or extraterrestrial life forms?

According to the fossil records, multicellular fauna emerged suddenly in the so called Cambrian explosion [161] . Already Darwin realized that the absence of fossils from pre-Cambrian era posed serious challenges for the idea about gradual evolution in which evolutionary tree develops gradually new branches. The problems are following.

1. Why did the Cambrian explosion occur so late? This problem is discussed in the chapter [29] .

2. Why no fossils of the pre-Cambrian predecessors of the Cambrian fauna have been found? The obvious explanation is that the faunas of pre-Cambrian era did not contain hard parts and thus yielded no fossils. During last decades two pre-Cambrian faunas have been however found. Edicaria are multi-cellulars with a pan-cake like shape whereas Tommotian fauna consists of simple cup and cap like multi-cellulars [161] . Contrary to what one might expect, there is however no continuous evolution of these faunas to the Cambrian fauna and it seems that Cambrian explosion suddenly generated the predecessors of the recent day fauna.

3. The third problem which Darwin could not yet face emerged much later. The Burgess Shale fauna found 1909 by Charles Doolittle Wallcott challenged even the very notion of the evolutionary tree (for an excellent popular discussion of implications of Burgess Shale fauna see the book "Wonderful Life" of Stephen Jay Gould [161]). It was found that several phyla of animal kingdom (kingdoms consist of phyla), which do not exist today, emerged in Cambrian explosion and then disappeared. The usual view about evolution is that it creates complexity from simplicity rather than vice versa. Obviously, just the opposite occurred in Cambrian explosion. Even more remarkably, not a single phylum has appeared to the fauna after the Cambrian explosion.

All these problems would have a nice resolution if Cambrian explosion were due to the intervention of intra- or extra-terrestrial life forms. Suppose that life evolved in intra-terrestrial conditions, in the safe womb of Mother Gaia, one might say. In this frame of mind Cambrian explosion could be seen as a moment when Mother Gaia gave birth to new phyla preceding the recent day fauna. After the moment of birth these children of Mother Gaia had to survive by their own in the harsh Cambrian environment and many of them did not. This would elegantly explain why Cambrian explosion was followed by a strong extinction of phyla.

The metaphor about mother Gaia giving birth to life forms could have at least two meanings.

1. The most concrete meaning is as the emergence of these life-forms from intra-terrestrial conditions to the surface of Earth: many-sheeted space-time might make this Jules Verne like travel possible. Corals might have been these intra-terrestrial life-forms realizing genetic code in terms of field patterns using calcium containing skeletons as antennae, and being the first animals possessing primitive nervous system and ability to realize genetic code electro-magnetically in EEG frequency range. After this the horizontal transfer of intra-terrestrial genes would have stimulated the evolution of vertebrates from more primitive life forms and have generated various phyla.

   Although corals are simple life forms, coral populations are not, and they could be seen as super-organisms with cells being replaced by double cell layers, corals. If this interpretation is accepted, coral populations represent "alien" life forms at a higher level in the evolutionary hierarchy. This interpretation would make natural the identification of corals as organizing centers of evolution. The radial geometry of corals would nicely symbolize their role as evolutionary organization centers.

2. A less concrete realization of the metaphor would be as intra-terrestrial genetic engineering involving the insertion of packets of introns and genes (software plus necessary hardware) to the DNAs of already existing life forms. Of course, option

3. could be seen as are representing a special manner to perform this genetic engineering by utilizing a life form possessing the genes possessed also by the highest vertebrates and radiating them horizontally.

Variants about the genetic engineering theme

The idea about genetic engineering performed by intra- and/or extraterrestrials could have been realized in several manners.

1. The first vertebrates got their vertebrate genes from intra- or extraterrestrials, and these genes were horizontally transferred to corals living in symbiosis with them. This genetic intervention should have occurred after the Cambrian explosion if it turns out that the nearest predecessors of vertebrates do not possess the common genes.

2. The transfer of genes was from corals to vertebrates and corals received their vertebrate genes in Cambrian explosion from some highly advanced life form, or corals themselves were this advanced life form. During the gradually evolving co-existence with simpler life forms these genes were gradually horizontally transferred to the predecessors of recent day vertebrates.

3. Corals and the predecessors of the vertebrates living in symbiosis with them got their common vertebrate genes simultaneously from outside. Note however that they could have been inventions made by the entire ecosystem in question.

4.4.4 What ontogeny recapitulates phylogeny principle means at the level of DNA?

The idea about corals as a gene bank could resolve some other mysteries related to the genome.

1. The revised view about the evolution of organisms possessing nervous systems would not rely so much on mutations but already existing and possibly conserved gene and meme banks inherited from corals. Only a fraction of these genes would be in use and evolutionary pressures would determine which portion of these memes/genes is activated. Mutations might only have a secondary and mostly harmful role in the evolution.

2. Introns are the basic candidate for the gene reservoir. This conforms with the idea that introns code for memes since it is plausible that the activation of memetic programs becomes possible only when genes coding for the needed hardware are activated.

The quite recent finding [44] that the removal of massive portions of the conserved part of the genome has no apparent effect on the organism's functioning supports the idea about genetic repertoire. It is usually believed that conserved regions of genome have some function. Many of these conserved regions are in the "junk" portion of DNA and do not code for proteins. They could however still have some function and in some cases the conserved regions indeed seem to affect the expression of the nearby genes. To identify the function of the highly conserved intronic regions the team of Edward Rubin at the Lawrence Berkeley National Laboratory deleted two huge regions of intronic DNA from mice containing nearly 1000 highly conserved sequences shared by human and mice. One of the chunks was 1.6 million DNA bases long, the other one was over .8 million bases long. The unexpected result was that the genetically modified mice were virtually indistinguishable from normal mice in every characteristic they measured, including growth, metabolic functions, lifespan and overall development.

The result could be understood if the intronic portion of both mice and men derives from a very early period of evolution, perhaps the evolution leading to corals (where-ever it occurred). These conserved genes would have developed to their stable forms during the evolution leading to corals and represent a repertoire of functions waiting for their activation. One could understand the instantaneous popping up of highly developed biological functions, which is often used as a counter argument against the view that the evolution is made possible by random mutations. The interpretation also conforms with the idea that at least part of introns code for memes. In the case of mouse memone would not be yet of much use since speech organs and culture are lacking. The comparison of the introns of man and apes to see whether memes having some function related to language are active in humans but not in apes could serve as a test of this prediction.

Ontogeny recapitulates phylogeny principle would be realized as a gradual shift of the activated portion of the memone and genome during the development of the embryo. Also the memes and genes still waiting circumstances allowing for their expression would be present in the DNA. It might be

possible to create artificially earlier evolutionary forms of a given organism and evolution might be studied in the laboratory. The partial transmutation of the morphologies of two different organisms to each other might be possible if the organisms possess common portions of the conserved genome.

If also the future phylogeny is coded to the recent DNA, both mice and men would possess enormous evolutionary potential (frog to prince effect!). Perhaps the explosive cultural evolution of civilization during last centuries has been accompanied by a corresponding shift in the activated portion of memone. This shift could also occur during the lifespan of individual and the idea about personal growth would have a genetic justification. The evolutionary potential might be some day be utilized by the artificial activation of memone and genome. Of course, the activation of higher memetic programs would be possible only if the genes coding for the needed hardware are also present and activated. Again the computer metaphor would work: I have used only a minor portion of the potential of my text processing program to write this piece of text.

Gene activation by electrostatic fields?

The basic question concerns the method of activation. The discovery of chemists Guido Ebner and Guido Schuerch [28] , [6] raises the hope that these ideas might be more than over-active imagination and their work also provides a concrete proposal for the activation mechanism. These findings are briefly described in the article of Hardmuth Mueller [28] who proposes quite different explanation for the strange findings. Ebner and Schuerch studied the effect of electrostatic fields on the growth and morphogenesis of various organisms. Germ, seeds, or eggs were placed between conducting plates creating an electric field in the range .5-2 kV/m: note that the Earth's electric field is in the range $.1 - 4$ kV/m and of the same order of magnitude.

The outcome was rather surprising and in the year 1989 their employer Ciba Geigy (now Novaris) applied for a patent "Method of enhanced fish breeding" [6] for what is called Ciba Geigy effect. The researchers describe how fishes (trouts) develop and grow much better, if their eggs have been conditioned in an electrostatic field. The researchers report [6] that also the morphology of the fishes was altered to what seems to represent an ancient evolutionary form: this was not mentioned in the patent.

The chemists founded their own Institute of Pharmaceutical Research near Basel, where Guido Ebner applied for another very detailed patent, which was never granted (it is not difficult to guess the reasons why!). In the patent he describes the effect of electrostatic fields on several life forms (cress, wheat, corn, fern, micro-organisms, bacteria) in their early stage of development. A clear change in the morphogenesis was observed. For instance, in one example fern had all sort of leaves in single plant apparently providing a series of snapshots about the evolution of the plant. The evolutionary age of the first leaf appeared to be about 300 million years whereas the last grown-up leaf looked close to its recent form.

If one takes these finding seriously, one must consider the possibility that the exposure to an electrostatic field can activate passive genes and change the gene expression so that older morphologies are expressed. The activation of not yet existing morphologies is probably more difficult since strong consistency conditions must be satisfied (activation of program requires activation of a proper hardware).

It is known that the developing embryo has an electric field along the head-tail axis and that this field plays an important role in the control of growth. These fields are much weaker than the fields used in the experiment. p-Adic length scale hierarchy however predicts an entire hierarchy of electric fields and living matter is indeed known to be full of electret structures. The strength of the electric field in some p-adic length scale related to DNA might somehow serve as the selector of the evolutionary age. The recapitulation of phylogeny during the ontogeny could mean a gradual shift of the activated part of the memone and be controlled by the gradually evolving electric field strength.

The finding that led Ebner to his discovery was that it was possible to "wake up" ancient bacteria by the exposure to an electrostatic field. This would suggest that in the case of primitive life forms like bacteria the electric field strength of Earth controls the state of bacterium whereas in higher life forms endogenous electric fields have taken the role of Earth's electric field.

Electric fields and healing

Wound healing is very much like morphogenesis and already Becker discovered that electric field induces a healing of wounds [15] . More recent studies of the effects of electric fields on healing and on embryos are discussed [33] and one can find useful quantitave information from this article. The typical strengths of the electric fields appearing in organisms are in the range .01-.1 kV/m: the upper bound of this field is the lower limit of Earth's recent electric field strength and considerably below the field yielding Ciba Ceigy effect. There are however also much stronger fields present: the voltage over epithelium (double cell layer) is in the range 30-50 mV and would make 6-10 kV if the thickness of epithelium were 5 μm. In the 1950s it was discovered that the direction of external electric field determines whether a flatworm which has been cut in two pieces develops head or tail. A natural voltage gradient exists between the severed worm's tail and the place where its head once was. A naturally occurring electric field of strength 40 V/m has been found to play a vital role in the wound healing in the cornea of rats: it is found that the cells divide in the plane orthogonal to the field and pushing new cells to the wound.

A further finding reported in [33] was that a voltage of 2 mV over cell diameter (1 kV/m if cell radius is 2 μm and in the same range as the field applied in Ciba Geigy effect) alters the front back orientation of the neuroblast. The proposed interpretation of these findings is that electric field provides only directional information whereas the findings of Ebner suggest that much more profound meme/gene level effects might be involved. For instance, one can ask whether the exposure to an appropriate external electric field could induce the return of a differentiated cell to the stem cell stage realized as a shift in the activated portions of memone and genome.

Generalized four-wave mechanism and the concrete mechanism of gene activation by static electric fields

Concerning the concrete mechanism behind the activation there are several constraints. The activation mechanism must be localized at the level of DNA. On the other hand, a given region of DNA must activate only in an electric field of a particular strength coding for its evolutionary age. The basic finding of Ebner about "wake-up" of ancient bacteria in a static electric field suggests that the activation must be a kind of "wake-up" process for an appropriate part of DNA. "Wake-up" corresponds to the generation of self-organization pattern getting its metabolic energy by sending negative energy photons absorbed by some system with corresponding excitation energy. This mechanism is indeed non-local since only the strength of the electric field matters. The transfer of an electron in an electric field through a distance not larger than the size of nucleus by absorbing negative energy photon is a good candidate here.

The generalized four-wave mechanism for remote metabolism requires the existence of generalized standing waves taking care of themselves by sending negative energy (phase conjugate) photons at the energy defined by the frequency of wave. The ideal situation corresponds to a dispersion relation for which the frequency of the oscillation does not depend on wave vector at all: plasma oscillations satisfy this conditions. In the chapter [37] a model for the coherent electric dipole oscillations was constructed. In this case the frequency depends only on the angle between the wave vector and the direction of the electric field. Same applies to magnetostatic oscillations [26] for which the Larmor frequency of electron gives the maximum value of frequency. The frequency is constant for effectively 2-dimensional oscillation patterns with wave vectors at the surface of a cone and periodically recurring oscillation patterns able to represent simple 2-dimensional self-sustaining mental images become possible.

Quantitative estimate support this model. In a field of .5-2 keV/m the electron gains a kinetic energy of $5 - 20$ μeV while travelling a distance of 10 nm corresponding to the thickness of cellular membrane. This corresponds to photons with microwave frequencies in the range .12-.48 GHz and wave lengths in the region .6-2.5 m so that the energy can be sucked from quite large spatial volume by inducing transfer of electron through this distance without a gain of kinetic energy. These frequencies corresponds to the nanosecond scale assigned with the coherent electric dipole oscillations whose importance was first realized by Fröhlich [154] . In the above mentioned model of coherent dipole oscillations as analogs of magnetostatic oscillations these frequencies correspond the p-adic length scale $L(151) = 10$ nm associated with cell membrane thickness which is of central importance in the coiling hierarchy of DNA.

Also magnetostatic waves in a magnetic field associated with some level of the hierarchy of DNA

space-time sheets could be in question. In this case the Larmor frequency of electron defines the maximal oscillation frequency. From the assignment of $L(169) \simeq 5$ μm to the Earth's magnetic field, the length scale associated with the needed field varying in the range $.05 - .1$ Tesla is in the range .1-.2 μm.

4.4.5 Where did those 223 genes pop up?

The reports of the Public Consortium about human genome in Nature, Feb 15, 2001 [122] and of Celera Genomics in Science of Feb 16th, 2001, [157] contained two big surprises.

Are we really so near to fruit flies?

The first astonishing discovery was that the amount of human genome differs relatively little from those of lower organisms: we have only about 30,000 genes, little more than twice the number 13,601 of genes for fruit fly. This paradoxical finding forces to think that our genome is not solely responsible for what we are and that the intronic portion of DNA (only about 1 per cent codes of human DNA codes or amino-acid sequences), is not "junk DNA", but contains important biological information and expresses it non-chemically.

In TGD Universe introns would express memes as the classical field patterns associated with MEs ("topological light rays") responsible for the basic expressions of language understood in an extremely general sense. This language includes body language and even cellular signalling, and could quite well make possible (not necessarily conscious) interspecies communications based on memes expressed by communicating species and forming a common vocabulary. All eukaryotes (cells with nuclei), even bacteria, would possess part of the vocabulary of this universal language. The memetic code word is predicted to consist of a sequence of 21 DNA triplets and carries 126 bits of information instead of 6 bits of genetic code. Of course, also genes are expressed in terms of MEs and define a lower level language.

In this framework the actual role of DNA can be understood using the computer analogy. Memes represent the program modules written using the programming language defined by the memetic code, and realized in terms of the field patterns associated with MEs. Genes represent the necessary hardware needed to realize these programs. System builds only the hardware needed, that is cell expresses only part of the genome. DNA engineering requires besides the addition of the new programs (memes, introns) also the insertion of the necessary hardware (new genes). Memes and corresponding genes should have very intimate relationship. In this conceptual framework the standard view is wrong since it identifies the build-up of a new hardware as the sole activity at the DNA level. This would be like identifying the addition of a net card to a computer as the fundamental activity related with computers.

The head-scratching discovery

The "head-scratching discovery" by the public consortium, as Science termed it, came when the genome was compared with the genomes of our predecessors. It was found that human genome contains 223 genes not possessed by invertebrates. Contrary to what one might expect, these 223 genes could make an enormous difference. The reason is that this number is more than two thirds of the number of the 300 genes differentiating between humans and chimpanzees so that these genes could be the main determinant of the dramatic difference between humans and chimpanzees in standard genetics.

Of course, in TGD framework the most important differences would probably relate to the intronic portion of the DNA responsible for language. Dramatic differences between our intronic DNA that of our invertebrate and perhaps even vertebrate predecessors, in sharp conflict with the idea of continuous evolution, should be discovered.

Are the enigmatic genes a horizontal gene transfer from bacteria?

Biologists can explain the presence of the enigmatic genes only by a "rather recent horizontal transfer from bacteria". Here "rather recent" refers to the evolutionary time scale.

This explanation can be challenged on various grounds.

1. The simplest working hypothesis is that the transfer from bacteria is a probabilistic process. The problem is however why the horizontal transfer did not occur to the genomes of other vertebrates and invertebrates and gradually through the whole evolution. One could argue that something characteristic to the vertebrate genome should have made this process possible. In TGD framework one could imagine that the intronic portion of the vertebrate genome could have contained something which made the transfer possible: a common part of memone with the bacteria involved and making possible language based communications ("language" understood in a generalized sense) at DNA level perhaps?

2. The enigmatic genes are involved with important physiological functions. In particular, they are responsible for important neurological enzymes which stem from mitochondria having its own genome. According to my non-professional interpretation this statement means that also mitochondrial genome contains these enigmatic genes. Thus both mitochondrial and nuclear genomes would have been altered by this horizontal transfer from bacteria. Simultaneous double horizontal transfer does not however look a probable event.

3. Only 113 of the 223 enigmatic genes are widespread in bacteria: it would be easier to believe in the horizontal transfer if all of them were widespread. These 113 widely occurring genes are not encountered in invertebrates at all. As a matter fact, this finding suggests that the transfer occurred from the vertebrate genome to the bacterial one and only partially, rather than vice versa. The analysis of proteins expressed by the enigmatic genes demonstrated that out of 35 identified, only 10 had counterparts in other vertebrates. 25 of them were unique to humans. This suggests that a considerable part of the horizontal transfer has occurred relatively recently and together with associated introns might even distinguish us from chimpanzees.

Horizontal transfer as DNA engineering?

The objections against the horizontal transfer from bacteria force to consider seriously the possibility that the horizontal transfer represents an intentional DNA engineering, both memetic and genetic. The most important transfer should have been to the intronic part of the DNA. The addition of memes would be like adding a new program to a computer. The addition of genes would be like adding a new hardware (say net card or data cable) required by the program to run. The comparison of the intronic portions of DNA of humans and lower vertebrates might thus lead to futher "head-scratching" discoveries. The data are consistent with the assumption that genetic/memetic engineering activities have occurred in several steps during the evolution of the vertebrates although a considerable portion of the enigmatic genes and associated introns, perhaps even two thirds, have been "injected as a single dose".

The evolution of the hominides in Africa had a stagnation period of about 1.5 million years as demonstrated by the study of the ancient stone tools. Then, for about 50 thousand years ago, a sudden jump to creativity occurred. The first ornaments appeared meaning that hominides had become artists and started to express their position in the social hierarchy by clothing and ornaments. This signals about development of highly refined social structures. A general belief is that also language began to develop rapidly and made possible a cumulation of knowledge. It seems that modern human was born and started to migrate from Africa to North. Could it be that memetic engineering induced this crucial step in evolution? Could it be that Neanderthals had to leave because they were not subject to this memetic engineering? Also the emergence of the first civilizations for about 10 thousand years ago might have involved memetic engineering. The ancient Sumerian myths about Gods who came from Heaven and made us their images might be memetic fossils reflecting what occurred.

Who performed the (memetic and) genetic engineering?

One can imagine two identifications for the ancient genetic/memetic engineers.

1. The guess that the engineers were extra-terrestrials (ETs) is supported by ancient myths. The Sumerian and Akkadian texts found inscribed on clay tablets, in which the role of the Elohim in Genesis is performed by the Anunnaki, tell about "Those Who From Heaven to Earth Came". These myths would relate to the last step in the sequence of engineering activities.

2. The second guess is that genetic engineering is due to a highly advanced civilization of a remote geometric future, perhaps futuro-terrestrials, and applying highly advanced technology based on time mirror mechanism and possibly utilizing simpler life forms, perhaps plasmoids, as their couriers. Abduction experiences might relate to genetic manipulations using plasmoids to do the hard job. In this case encounters with aliens would be based on sharing of mental images.

3. The third guess is that genetic engineering is self engineering. The work of Yu. Chen Kangeng gives evidence that the transfer of the genetic information by electromagnetic means is possible [5] . According to [111] , where the method is summarized, the successful transfer of the genetic information from a donor bio-system to an acceptor system was achieved via high-frequency electromagnetic fields feed repeatedly through the optically-active donor bio-system and then delivered over a long period of time to the receiving bio-system in its early developmental stages. The hybrids created through the irradiation of eggs and seeds with such "genetically loaded" fields are claimed to show very specific mixed characteristics that were transferred to the next generation without need for further irradiation. This idea is discussed in [78] on basis of a proposed realization of genetic code at the level of dark matter.

It would seem that the donor genome or parts of it are imprinted to the electromagnetic field pattern in the process and that this field pattern is able to modify the target genome.

Nothing precludes the possibility that genes/supergenes/hyper genes at some level of dark matter hierarchy can also code for genetic self engineering since these activities are after all very similar to other genetically coded bio-chemical activities. The computer analogy would be programs writing programs. The engineering genes would be activated by W MEs inducing plasma oscillation patterns. The claimed effects could be understood if the interaction with genetically imprinted electromagnetic field pattern activates genes inducing genetic self engineering yielding the genetic modifications consistent with the pattern represented by the em radiation.

Magnetic body would receive information about the desired outcome as electromagnetic field patterns emitted by other organisms, most naturally members of the same species. If these modifications are successful, the magnetic body is exposed to this information for long enough time to react and activate W MEs inducing the genetic program inducing the genetic program leading to the suggested genetic modification.

Hyper-genes integrating groups of organisms to larger wholes would be naturally involved with the mechanism. This mechanism would guarantee a rapid propagation of successful genetic modifications to the entire population and would be much more effective than the slowly occurring selection of random mutations. The possibly existing genes responsible for the genetic self engineering could be also introns and express themselves by activating nuclear RNA and process like reverse transcription.

Books related to TGD

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Chapter 5

Many-Sheeted DNA

5.1 Introduction

The problems of how genes code information about the morphology of organism and how this information is expressed, belong to the great puzzles of developmental biology. A closely related mystery is the differentiation of cells. The notion of genetic program is far from precise and it is not clear how close the analogy with a computer program is. There are also several problems which challenge the basic dogmas of genetics.

1. Only 1 per cent of DNA of human genome actually codes polypeptides. Eukaryote genes contain intron sequences which are transcribed into hnRNA but snipped off when hnRNA is transformed mRNA in a process called slicing. The higher the evolutionary level of organism, the higher the fraction of introns is. Molecular Darwinists see introns as "junk DNA" but there is evidence that introns are far from junk. For instance, the splicing of the intron contribution from hnRNA to give mRNA can give several different outcomes depending on the stage of the development of the organism and introns are crucial for the effectiveness of the immune system [110] . Hence one can wonder whether intron mRNA and exon mRNA could both form the real output of gene subprograms serving in some sense as input for other gene subprograms. This interpretation obviously conflicts with "gene-single protein" dogma in its basic form.

2. There are large amounts of highly repetitive DNA which is silent. One can wonder whether there is some fundamental mis-understanding involved. Could it be that this DNA is analogous to control DNA not transcribed to RNA and therefore not at all useless. There is also active repetitive DNA.

3. There is large amount of silent DNA in control sections between genes. Could it be that this silent DNA expresses itself in some nonchemical manner? Chemical expression is very slow, translation rate being twenty aminoacids per second, and one can wonder whether life might have invented faster modes of gene expression and control of gene expression. Also the question whether there is a relation to the typical frequency scales of brain consciousness of order 10 Hz, which can be related to the magnetic and Z^0 magnetic transition frequencies, can be raised.

4. Plant genome is often by a factor of hundred longer than human genome. One could argue that the complexity of organism is measured by the length of the shortest program coding the organism. It is however not at all obvious how the genome of plants could be more redundant than human genome since repetitive sequences common to all animals are present. Introns are actually more frequent in human genome. This suggests that some new unidentified degrees of freedom giving rise to complexity might be present and that the chemistry of DNA in the sense of standard physics is perhaps not all that is needed to understand genetic program.

5. Various self-organization process such as self-assembly and de-assembly are very frequent in living systems. The problem how genes give rise to morphology of the organism is poorly understood. This forces to challenge the dogma of genetic determinism. One should be able to understand what is determined by genes what is determined by self-organization and whether the genes of the standard physics are enough.

The reason why the above mentioned problems have turned out to be so untractable might be due to a wrong view about space-time. Many-sheeted space-time concept of TGD might be absolutely crucial for the expression of genetic code. DNA itself might involve many-sheeted space-time structures coding faithfully the topology of the body parts. This many-sheeted structure of DNA could allow to understand the miraculous looking features of DNA replication and differentiation of cells. TGD based view of evolution as p-adic evolution implied by the basic quantum theory, should be a crucial element of the picture. Together with the p-adic length scale hypothesis it leads to precise quantitative predictions and a general model for genetic program based on the many-sheeted space-time concept. The model explains also why introns are present only in eukaryotic genome. Most importantly, it seems that the statements represented by the dynamical intron-exon decompositions of genes and defining Boolean algebra, could represent our conscious beliefs and thus affect our behavior as conscious beings. Notice the beautiful connection between matter and mindgenes code the information, not only about the material structure of organism, but also about its belief system. Thus without introns, the pariah class in the society of bio-molecules regarded as 'junk DNA' by always-so-imaginative reductionistic materialists, we would have no world views and belief systems! In this chapter TGD based view about genetic code and its realization are discussed in detail.

5.1.1 Many-sheeted DNA

The replacement of the DNA of standard physics with many-sheeted DNA suggest surprisingly simple model for how organism's morphology is coded and decoded to DNA.

1. How the morphology of body is coded?
   The most striking feature of DNA is its one-dimensionality. According to work of Mae-Wan Ho, living systems are liquid crystals [3] . Liquid crystals are effectively one-dimensional since the layers of the liquid crystal consist of homogenous liquid phase determined by macroscopic characteristics such as pH, temperature, ionic concentrations and electric fields. This suggests that the structural information coded into DNA could be essentially information about the macro- properties of the layers of liquid crystal. This would make 1-dimensional coding of the body plan using DNA sequences very natural. Kind of contraction of the body parts to DNA sequences having many-sheeted structure could be in question! This coding would preserve the topological structure of the many-sheeted space-time surface representing the expression domain of the gene. The structure of the expression domains of maternal genes and Hox genes [156] controlling morphogenesis supports this picture.

2. How DNA is expressed?
   The very naive first guess is that during growth various thin space-time sheets associated with DNA gradually grow and are glued together by the join along boundaries contacts and form the space-time sheets associated with their expression domains. Somewhat exaggerating, many-sheeted DNA would represent only a particular developmental period of organism in which it is contracted to a thin thread. For instance, the cells determined to develop into eye are glued to the space-time sheet representing future eye and replication products belong also to this space-time sheet. Clearly, the gluing to the space-time sheet of the future expression domain would generate the needed long range correlation between cells in the expression domain. It must be emphasized that self-organization should play key role in this process: for instance, liquid crystal nature of the living matter should determine morphology to a high extent.

3. What makes differentiation and control of the morphogenesis possible?
   Differentiation must be explainable as a selective activation of transcription and although a local process, involves also top-down control making possible a precise timing. Concentration gradients for the transcription factors, that is proteins controlling transcription, are certainly crucial in this respect. When the concentration of the protein falls below a critical value, the truth value of a statement representing input to some gene program modules changes. This leads obviously to spatial patterns of gene expression resulting from branching of gene programs. For instance, the development of organs should result as a combination of genetic control of this kind plus self-organization. Join along boundaries bonds between gene space-time sheets and larger space-time sheets or genes and control regions of chromosome make possible quantum control of genetic expression based on phase gradients of the super conducting order parameters and

resonant Josephson frequencies which correspond to magnetic transition frequencies of genes, control regions or related substructures. It could also be that the # contacts (wormhole contacts) from genes to various space-time sheets representing body parts provide the interaction with the classical fields of the macroscopic space-time sheets representing body arts and controlling the activity of a particular gene. In any case, the fact is that the action mechanisms of transcription factor proteins in eukaryotes are not understood. The mechanism is not purely chemical one since transcription factors are often located quite far from the promoter region. Electromagnetic oscillations with resonant frequencies could be in question. In absence/presence of oscillation gene is activated.

5.1.2 Realization of the genetic program

TGD suggests also ideas about how organism can act as a conscious computer. Genome represents possible statements consistent with a fixed atomic statement (single element set in set-theoretic representation of Boolean algebra) represented as sequences of DNA. DNA triplets define basic axioms of the axiom system in question. Active genes which have coded some minimum about of intronic mRNA and protein coded by the exon part of the gene give rise to conscious experience about the truth of the statement represented by the gene. Otherwise the truth value of this statement is ill-defined and not consciously experienced. Truth values of the statements representing conclusion of the statement represented by gene in turn act as premises for the statements represented by some genes and these genes in turn activate and give rise to experience of the truthness of corresponding statements. In this manner genetic program proceeds and gives rise to a sequence of experiences about truthness of statements represented by the genome. Note however that the experiences of truthness at DNA level need not correspond to our conscious experiences: entire hierarchy of selves having connection to DNA level is involved.

The beautiful feature of this realization of genetic program is that no cables for signal transmission are needed. The genetic program is also extremely robust and flexible unlike ordinary symbol based programs in which the change of the value of single binary digit can lead to a catastrophe. Furthermore, spatial patterns of gene expression develop naturally: gene in give cell producing transcription factor affects only finite region of space since subcritical concentration of the transcription factor means effectively its total absence. This can lead to intricate structural patterns of gene expression and determination of cells making possible differentiation. The translation of average protein requires 20-60 seconds and the cognitive processes of ours which possibly occur at DNA level must be rather slow. Time scale of emotions is however slow as is also higher level abstract thinking.

Both introns and exons represent statements which are true if the premises of the gene statement are true. Simple model for how introns can be separated from the exon part of the genetic module explains the many mysterious properties of introns elegantly and introns become an absolutely essential element of the genetic program. In particular, addition or subtraction of "comment sign" to nucleotide changes the nucleotide from exonic to intronic or vice versa. Thus comment sign serves essentially as a binary digit telling whether nucleotide belongs to exon or intron. Unless physical realization of comment sign poses any additional constraints, comments signs can be dropped anywhere in gene and this means that same gene can be expressed in 2^N manners, where N denotes the number of basic units in the maximal decomposition into exons and introns. Obviously, an interpretation as a representation for the statements of Boolean algebra for statements about N basic statements suggests itself strongly: perhaps each eukaryotic gene represents Boolean algebra! If also intron-exon decomposition is assumed to be dynamical then the number of exon-intron decompositions in gene consisting of N DNA triplets is

$$M = \sum_{k=1}^{N} \left(\begin{array}{c} 3N \\ 3k \end{array} \right) \quad .$$

The premises of the gene statements are represented in the operator sequences associated with the gene. Intron $\leftrightarrow$ exon transformation induced by the addition or cancellation of "comment signs" associated with nucleotides leads to a generalization of the operon model for the regulation of gene transcription. The protein coded by introns acting as an exon part of gene serves as a repressor of the gene expression. The shifting to a mode in which exons are coded to protein means that the coding of the supressor protein stops and the genes whose activation depends on the output of the gene in question are automatically activated.

The model of cognition [33] suggests that the presence or absence of "comment sign" , which is mathematically a value of binary digit telling whether nucleotide belongs to intron or exon, could correspond to spin direction of cognitive antineutrino determined by magnetization in strong Z^0 magnetic field along chromosome. In fact, the temporal sequences of cognitive neutrino pairs realizing memetic code and possible exon-intron decompositions become different aspects of cognition in the sense that memetic codewords could have interpretation as integers providing quantitative measures for qualia and exon-intron decompositions would represent beliefs. Thus it seems that many-sheeted genes could represent a hierarchy of conscious beliefs: genome would be a collection of Boolean algebras represented by genes. In case of prokaryotes these Boolean algebras contain only one expressed element; in case of eukaryotes number of elements can be much larger but again totally intronic gene is not expressed. DNA could code thoughts and proteins emotions associated with them.

5.1.3 Are nonchemical transcription factors and nonchemical gene expression possible?

Enhancers and silencers affect gene expression in a nonlocal manner difficult to understand purely chemically. There are also tissue specific transcription factors. The notion of many-sheeted DNA suggests the possibility of nonchemical transcription factors. Classical em and Z^0 fields are especially interesting possibility as far as gene expression and its control in long length scales are considered. The general quantum control and coordination mechanisms based on Josephson currents flowing between gene space-time sheets and larger space-time sheets and making possible comparison circuits, clocks, alarm clocks and novelty detectors, suggest themselves. Indeed, the frequency scale 20 aminoacids per second for the translation process corresponds to a typical scale for the magnetic transition frequencies, which lie at the heart of the TGD based theory of brain consciousness. Classical fields affect various macroscopic quantum phases and one cannot exclude the possibility that gene level is involved with cognition and sensory experiencing even in the time scales shorter than the long time scales associated with the neural transmitter action.

Neural level could control genetic level (this is known to occur chemically) via nonchemical control mechanisms. Nuclear matrix, cytoskeleton and the collagen network associated with connective tissues are liquid crystals and ideal tools for transforming electrical signals to mechanical (say conformational wave s) and vice versa. The massless extremals associated with the micro-tubules connecting neuronal cell membrane with the nuclear region could make possible the information transfer from neural level to gene level: in fact, the nondispersive vacuum currents associated with the massless extremals are optimal for communication purposes. This suggests that nerve pulse patterns could be transferred into genome along cellular matrix.

The idea that information from the genetic level would be transferred to neural level and that genetic level could even control neural level chemically is consistent with experimental facts. One could even consider the possibility that genome plays the role of neuronal brain. One can indeed play with idea that possible "this is true" experiences associated with the active genes could be expressed as our emotions. As noticed, the time scale of chemical gene expression is .05 seconds and is much slower than the millisecond time scale of nerve pulse so that direct translation of genes to nerve pulse patterns is not plausible. This is however consistent with the realization of "this is true" experiences as emotions which are characterized by slow time scales. Thus the statements "If A then B" expressed by genes B and the control structures A associated with them could give rise to neural activity translating these experiences to sensory experiences about the internal state of brain accompanied by and often identified with emotions, which in turn could be expressed as internal speech. Music metaphor does not however require any precise coding to nerve pulse patterns. The idea that this communication could occur also non-chemically is much more speculative and not actually supported by the most stringent form of the master slave hierarchy. It is also difficult to imagine how the coding of DNA sequence to, say nerve pulse patterns, could be achieved. In principle, memetic code could be realized as sequences of 21 DNA triplets. The idea about direct one-to-one mapping of DNA level to memetic level seems however implausible.

The large amount of silent DNA suggest that some nonchemical gene expression mechanisms might be at work. This does not necessitate communication between genomes although also this is possible in principle. The extreme would be that neuronal genomes could form neuronal democracy communicating to each other their "If A then B" opinions with conclusion B depending on what the exon-intron decomposition of gene B is for particular gene. This would make possible neuronal

voting. Assume that the sub-selves of self are neuron groups with identical synchronized inputs A. This means that same genes are activated and output depends only on the intron-exon decomposition of the individual gene and that sub-self experiences entire spectrum of opinions about what A implies. Self experiences the neuron group sub-self as the average over the opinions "If A then ..." of individual genome subsub-selves. One can also consider the possibility of Boolean 'machines'. Gene B receives the premises A of "If A then B" as nerve pulse pattern acting to the control sequence associated with B and generate as ouput the nerve pulse pattern representing statement B when premises are satisfied.

5.1.4 Model for the genetic code

The basic numbers of genetic code are probably not accidental. This led for ten years ago to an attempt to construct a model for abstraction process reproducing the basic numbers of the genetic code. The simplest model for an abstraction process is based to a repeated formation of statements about statements starting from two basic statements. If one drops at each step of construction the statement corresponding to empty set in the set theoretic realization of Boolean algebra, one obtains a hierarchy allowing to understand the basic numbers of genetic code.

What one obtains is so called Combinatorial Hierarchy [32] consisting of the Mersenne numbers $2, M(1) = 3, 7$,$127, 2^{127} - 1, ..$ constructed using the rule $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$. The explicitly listed ones are known to be primes. Combinatorial Hierarchy emerges from a model of abstraction process as subsequent transitions from level to metalevel by forming Boolean statements about Boolean statements of level n and dropping one statement away. Combinatorial Hierarchy results also by constructing the sets of all subsets with empty set excluded starting from two element set. The set of statements at level n can be given a structure of Finite Field $G(M(n), 1)$ if $M(n)$ is prime. The multiplicative groups $Z_{M(n)-1}$ form a nested hierarchy and the coset spaces $Z_{k_n} \equiv Z_{M(n+1)-1}/Z_{M(n)-1}$ are cyclic groups. Combinatorial Hierarchy based model of Genetic Code explains the number of DNA:s and aminoacids and the representation of words of the GC as triplets of 4 different codewords. Aminoacids correspond to $k_{n=3} = 21$ axioms of a formal system defined by $n = 3$ level of Combinatorial Hierarchy having a unique imbedding as the group $Z_{k_n} \subset Z_{M(n)-1} = Z_{126}$ and DNA:s correspond to the set $X_{N(DNA)} \subset Z_{M(n)-1}$ of $N(DNA) = (M(n)+1)/2 = 64$ statements consistent with a given atomic statement at level n regarded as special cases of general theorems. GC corresponds to the mapping $x \to x^{k_{n-1}} = x^6$ in $Z_{M(n)-1}$ mapping DNA type statements to aminoacid type statements. The numbers of DNA:s coding single aminoacid are reproduced in a symmetry breaking mechanism involving the finite groups $Z_{p_{n-1}}$ and Z_{k_n} and symmetry breaking is in a well defined sense minimal. The infinite hierarchy of possible genetic codes suggests the possibility of an infinite hierarchy of increasingly complicated life-forms.

The physical model of the genetic code leads to a beautiful interpretation of the genetic code as mapping the fundamental 64 truths to 20 basic conscious experiences, perhaps the emotion about truthness. The fact that hormones correlate with emotions suggests that this map assigns to a logical statement an emotion and that even our emotions could relate to DNA level. Note however that TGD predicts entire hierarchy of selves. Aminoacid P corresponds to the emotionally experienced truth $G_1(P)$ or $G_2(P)$.. or $G_n(P)$ is true, where G_i code for protein P. 3 stopping sign codewords cannot be experienced emotionally as truths not non-truths (holy trinity!).

Cognitive neutrino pairs play an absolutely essential role in the genetic program of eukaryotes in the proposed model. It must be emphasized that these cognitive neutrino pairs need not have anything to do with our cognition.

5.1.5 The relationship between genetic and memetic codes

TGD leads to a model of Boolean mind in terms of the temporal sequences formed by cognitive neutrino pairs with vanishing total energy. As noticed, the model for abstraction process predicts entire hierarchy of genetic codes [33] . This leads to the idea that our cognition might correspond to the level next to the genetic code. The hypothesis that memetic code corresponds to the next level of Combinatorial Hierarchy characterized by Mersenne prime M_{127}, when combined with p-adic length scale hypothesis, leads to a prediction of about .1 seconds for the duration of the 'wake-up' period of sub-self corresponding to the codeword of the memetic code. This codeword consists of 126 bits represented by cognitive neutrino pairs with two possible spin directions corresponding to two values

of Boolean statement. This implies that one millisecond should be the duration of single bit: this time scale is indeed fundamental for nerve pulse activity.

One can construct rather detailed model for cognitive consciousness in terms of the memetic code. In particular, a detailed model for how nerve pulse flips the spin of the cognitive antineutrino is possible [33] . This picture suggests the following general framework. Memes and genes correspond to two levels in the hierarchy of conscious intelligence and genetic programs could be perhaps seen as subprograms called by the higher level memetic programs. One could even see higher level life as symbiosis of memes and genes. This raises several questions. Does genetic code determine the evolution of the organism or is the development of organism some kind of 'social process' in which the genetic level interacts with the memetic level? Do genes code the space-time sheets representing the hardware of the memetic level or do higher level organisms represent symbiosis of two almost independent life forms? Does memetic level control genetic level or vice versa or is the interaction between these levels bi-directional? Despite that these questions which remain open, it seems that the three approaches to understand cognition based on the Combinatorial Hierarchy model of abstraction process, to fermionic Boolean algebra as a model of logical mind and to genetic and menetic programs as a model for conscious intelligence seem to combine to form single "holy trinity" of cognition.

5.1.6 Mersenne hypothesis

The hierarchy of dark matter levels is labeled by the values of Planck constant having quantized but arbitrarily large values TGD inspired quantum biology and number theoretical considerations suggest preferred values for $r = \hbar/\hbar_0$. For the most general option the values of $\hbar$ are products and ratios of two integers n_a and n_b. Ruler and compass integers defined by the products of distinct Fermat primes and power of two are number theoretically favored values for these integers because the phases $exp(i2\pi/n_i)$, $i \in \{a, b\}$, in this case are number theoretically very simple and should have emerged first in the number theoretical evolution via algebraic extensions of p-adics and of rationals. p-Adic length scale hypothesis favors powers of two as values of r.

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1+i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that all the four p-adic length scales sith $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm) define scaled up copies of electro-weak and QCD type physics with ordinary value of $\hbar$ and that these physics are induced by dark variants of corresponding lower level physics leads to a prediction for the preferred values of $r = 2^{k_d}$, $k_d = k_i - k_j$, and the resulting picture finds support from the ensuing models for biological evolution and for EEG [23] . This hypothesis - to be referred to as Mersenne hypothesis - replaces the earlier rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant. The background necessary for understanding what is involved is described in [12, 13, 23] .

5.1.7 Fractal hierarchy of magnetic flux sheets and the hierarchy of genomes

The notion of magnetic body is central in the TGD inspired theory of living matter. Every system possesses magnetic body and there are strong reasons to believe that the magnetic body associated with human body is of order Earth size and that there could be an entire hierarchy of these bodies with even much larger sizes. Therefore the question arises what one can assume about these magnetic bodies. The quantization of magnetic flux suggests an answer to this question.

1. The quantization condition for magnetic flux reads in the most general form as $\oint (p - eA) \cdot dl = n\hbar$. If supra currents flowing at the boundaries of the flux tube are absent one obtains $e \int B \cdot dS = n\hbar$, which requires that the scaling of the Planck constant scales up the flux tube thickness by r^2 and scaling of B by $1/r$. If one assumes that the radii of flux tubes do not depend on the value of r, magnetic flux is compensated by the contribution of the supra current flowing around the flux tube: $\oint (p - eA) \cdot dl = 0$. The supra currents would be present inside living organism but in the faraway region where flux quanta from organism fuse together, the quantization conditions $e \int B \cdot dS = n\hbar$ would be satisfied.

2. From the point of view of EEG especially interesting are the flux sheets which have thickness $L(151) = 10$ nm (the thickness of cell membrane) carrying magnetic field having strength of endogenous magnetic field. In absence of supra currents these flux sheets have very large total

transversal length proportional to r^2. The condition that the values of cycloctron energies are above thermal energy implies that the value of r is of order 2^{k_d}, $k_d = 44$. Strongly folded flux sheets of this thickness might be associated with living matter and connect their DNAs to single coherent structure. One can of course assume the presence of supra currents but outside the organism the flux sheet should fuse to form very long flux sheets.

3. Suppose that the magnetic flux flows in head to tail direction so that the magnetic flux arrives to the human body through a layer of cortical neurons. Assume that the flux sheets traverse through the uppermost layer of neurons and also lower layers and that DNA of each neuronal nuclei define a transversal sections organized along flux sheet like text lines of a book page. The total length of DNA in single human cell is about one meter. It seems that single organism cannot provide the needed total length of DNA if DNA dominates the contribution. This if of course not at all necessarily since supra currents are possible and outside the organism the flux sheets can fuse together. This implies however correlations between genomes of different cells and even different organisms.

These observations inspire the notion of super- and hyper genes. As a matter fact, entire hierarchy of genomes is predicted. Super genes consist of genes in different cell nuclei arranged to threads along magnetic flux sheets like text lines on the page of book whereas hyper genes traverse through genomes of different organisms. Super and hyper genes provide an enormous representative capacity and together with the dark matter hierarchy allows to resolve the paradox created by the observation that human genome does not differ appreciably in size from that of wheat.

5.2 Background

The foundations of genetics were discovered by George Mendel in 1866, but remained generally unknown until 1900. During the first half of nineteenth century it was gradually realized that genes play major roles in the functioning and evolution of organisms. The discovery of DNA revealed the principles of heredity and how genes store hereditary information and transmit it from generation to next. Hereditary information is contained within the nucleotide sequence of DNA.

Organization, expression and evolution of the hereditary information are the main aspects of genetics. Hereditary information is organized into chromosomes consisting of DNA sequences. It is expressed via transcription to mRNA followed by a translation to protein. The evolution of the hereditary information involves basically sexual breeding in one chromosome from the chromosome pairs of both parents combine to form chromosome pair. Also recombination of the members of the chromosome pairs is possible during meiosis. Also other mechanisms, such as fusion or fission of chromosomes and modification of DNA sequences, are possible. There are excellent books about topics [110] but for the convenience of the reader the basics of genetics are very briefly summarized in the following.

5.2.1 DNA and RNA

DNA add RNA provide a manner to store and organize genetic information [110] .

1. Genetic information is stored in nucleic acids, which are long sequences of nucleotide serving as letters of genetic code: three nucleosides form single world of code. There are four different nucleotides so that the number of different words is 64.

2. Nucleotide consists of three basic units joined by covalent bonds: nucleotide= nucleoside+sugar+$5'$-phosphate. The units are sugar, which is deoxiribose in case of DNA and ribose in case of RNA, phosphate and nucleoside (nucleic acid). Nucleosides are the information carrying part of DNA and RNA.

3. DNA and RNA sequences contain 4 different nucleosides. In case of DNA they correspond to C(ytocine), T(ymine), A(denine) and T(ymine). In case of RNA T is replaced by U(racil). U, T and C are purines containing one carbon ring and A and G are pyrimidines containing two carbon rings.

4. DNA molecules/nucleic acids/polynucleotides are formed as very long sequences of nucleotides bound together by phospho-diester bonds.

DNA double helix consists of two DNA strands , which are conjugates of each other, conjugation being defined as $A \leftrightarrow T$, $C \leftrightarrow G$. The helices are bound by hydrogen bonds between A and T and C and G respectively.

Sequences of DNA triplets form genes, which represent basic units of hereditary information revealed as traits of the organism. Each gene involves also additional DNA sequences serving as control structures in the transcription of gene to mRNA. In prokaryotes there is only single chromosome in the form of a circular double strand. In eukaryotes the chromosomes are located in nucleus and appear in homologous pairs. Eukaryotic chromosome is a complicated helical structure resembling beads in thread formed by DNA. DNA is wound around nucleosomes with diameter $d \simeq 10$ nanometers. Nucleosomes consist of octamer formed from 4 different histones. Chromosome structure will be considered in more detail later.

RNA appears both inside nucleus and cell. There are several types of RNA.

1. Messenger RNA (mRNA) is the outcome of transcription of DNA inside nucleus and is translated to proteins outside the nucleus.

2. Transfer RNA (tRNA) is involved in the translation of mRNA to protein: tRNA molecules bind specific aminoacids and glue them to specific mRNA triplets in a manner dictated by genetic code. rRNA appears as a building block protein of ribosomes playing the role of reading head in the translation of mRNA to proteins.

3. In case of eukaryotes transcription involves intermediate state in which DNA is transcribed to hnRNA which contains also the transcriptions of introns ("junk DNA"), which are split in so called splicing process cutting away intron RNA to form RNA-protein complexes which remain inside nucleus.

5.2.2 Proteins

Proteins are in a vital role in organisms. The diversity and complexity of life is largely due to the diversity and complexity of proteins. Some proteins act as transcription factors controlling genetic expression. Some proteins are used by cells in chemical communication between cells: hormones serve as signalling proteins; various receptor proteins serve as receptors of chemical signals and hormone-receptor complexes serve as transcription factors. Neural transmitters appear in the synaptic communication between neurons. Some proteins act as enzymes catalyzing biochemical reactions. Other proteins serve as structural building blocks, either by themselves or in association with nucleic acids (nucleoproteins), polysaccharides (glycoproteins) or lipids (lipoproteins). Some proteins, such as myoglobins and hemoglobins are associated with metal-containing organic molecules.

Proteins consists of polypeptides, which are polymers of 20 different aminoacids. Genetic code assigns unique polypeptide to a given gene. With single exception aminoacids share the same basic structure. Hydrogen atom H, carboxyl group COOH and amino group NH_2 and radical R linked to carbon atom. R determines exclusively the chemical properties of protein. 8 aminoacids are nonpolar (hydrophobic) and 12 of them are polar (hydrophilic). Of the twelve polar aminoacids 7 are neutral, 3 are basic (tending to become positively charged) and 2 and acidic (tending to become negatively charged) under physiological conditions. Carboxyl and amino groups tend to become ionized at physiological pH; -COOH group tends to lose its proton and NH_2 group tends to gain a proton.

In polypeptides, which are products of gene translation, aminoacids are linked to each other by peptide bonds formed when NH_2 group of one aminoacid and $COOH$ group of next aminoacid are linked (H_2O molecule is snipped away in this process). Polypeptide chains spontaneously adopt so called secondary structure determined by the nature of the R groups along the backbone. Backbone forms alpha helix, a coil containg 3.6 aminoacid redidues per turn. Another secondary structure is the beta pleated sheet configuration consisting of rows of polypeptide chains hydrogen bonded with each other. Polypeptide can also adopt the form of a random coil. Proline, because of its unique structure, causes a kink in the polypeptide backbone. Polypeptides have also tertiary structure. How the tertiary structure is determined by the chemistry of aminoacids is poorly understood. One of the big problems of biology is to understand who protein is able to fold to such a unique configuration. TGD suggests

that tertiary structure might not be determined solely by the standard chemistry and that many-sheeted nature of protein might be crucial in determining the final result of the folding. There is also quaternary structure associated with proteins formed by polypeptide sequences. The formation of higher level structures, such as micro-tubules, micro-filaments, cell membranes and collagen fibers involves self-organization and living matter seems to behave as a liquid crystal whose basic properties depend only on very general properties of protein.

5.2.3 Replication, transcription, translation

Information processing in living matter involves three basic processes: replication, transcription and translation. Replication of DNA means replication of DNA double helices and is essentially copying of genetic information. Replication involves unwinding of the parental strands of DNA double helix. They serve as templates on which the growing complementary daughter strands are synthesized. The direction of the synthesis is opposite for the two strands and only the second (leading) strand can be synthetized continuosly whereas the synthesis of the second strand occurs discontinuously and results in disjoint pieces of DNA containing approximately 1000 nucleotide pairs (Okazaki fragments of length about 34 nanometers), which later combine to form connected DNA strand.

DNA can be transcribed to mRNA molecules (messenger RNA) translated to proteins; to tRNA (transfer RNA), which is the RNA molecule affecting the coding of RNA triplets to aminoacids and to rRNA, which is the building block of the machinery affecting the translation. In case of prokaryotes the transcription of DNA to mRNA occurs directly. The rules for the transcription are

$$\begin{aligned} A \to U \ , \quad T \to A \ , \\ C \to G \ , \quad G \to C \ . \end{aligned}$$

In case of eukaryotes the transcription involves two steps since eukaryote genes in general decompose into exons translated to protein plus introns. First the entire gene is transcribed to hnRNA sequence. After this so called splicing occurs and gives rise to mRNA, which corresponds to the DNA sequence formed by the exons. In the splicing process intron sequences are split off and wind around specific proteins which do not leave the nucleus. There are different pathways for slicing meaning that the decomposition to exons and introns is not unique. Dynamical exon-intron decomposition is essential for the working of immune system.

Transcription is a complicated process involving the action of several enzymes. RNA polymerase I is involved in the transciption of large rRNA molecules, RNA polymerase II with the transcription of hnRNA, RNA polymerase III with transcription of small 5S-rRNA molecules and tRNA molecules. Usually so called heavy strand is transcribed. Light strand can be transcribed to some tRNA molecules at least. Gene is preceded by AUG triplet. In eukaryote cells RNA polymerase II copies sequences containing 6000-8000, sometimes even 20.000 nucleotides. The average length of mRNA sequence is 1500 nucleotides and the aminoacid corresponds to a sequence of average length of 1200 nucleotides.

RNA II polymerase binds to the promotor region preceding the gene. Promotor region contains at least two binding sites, so called TATA block and CCAT sequence regognized by RNA polymerase. Between promotor site and gene are operator site in which repressor enzymes bind and make translation impossible. TAC sequence denotes the beginning of that part of gene which is translated to protein (apart from introns). At the end of the gene there is rather long $A \cdots AAA$ control sequence preceided by TGA sequence signifying the end of the part of the gene to be translated. Introns which are not translated begin with AC and end with CA.

The translation of mRNA to polypeptide occurs outside the nucleus. Translation involves tRNA molecules, which are about 80 nucleotides long. Each tRNA contains a specific triplet which is anticodeword for the corresponding codeword in mRNA and binds only to this codeword in translation process. Each tRNA molecule binds with a specific aminoacid molecule and each aminoacid has at least one tRNA binding to it. The allowed bindings of tRNA and aminoacid molecules define genetic code. In translation tRNA carrying aminoacid attaches to an mRNA codeword to its own anticodeword and the aminoacid forms a peptide bond with the polypeptide sequence already translated at rRNA.

Genetic code assigns to 64 RNA triplets 20 aminoacids so that there is a considerable degeneracy involved. The largest number of DNA codewords mapped to same aminoacid is six. Three codewords are interpreted as stoppping sign for the translation. Genetic code is universal for the nuclear DNA of all eukaryotes and prokaryotes. The mitochondrial genetic codes of various eukaryotes however differ slightly from the universal genetic code. For instance, 4 DNA triplets can correspond to stopping sign.

Replication, transcription and translation are not the only information transfer processes occurring in living matter.

1. Reverse transcription $RNA \to DNA$ is known to occur in some cases and is also involved with the homing phenomonen of introns. Reverse transcription might have led from a system of RNA and proteins to system involving DNA sequences and primitive form of genetic code. The simplest starting system of this kind would consist of DNA coding RNA coding a protein which catalyzes both transcription and reverse transcription. This kind of system might have gradually evolved to a more complex DNA sequences.

2. RNA replication can occur in cells infected by viruses. What happens is that viral RNA strand which can be either single or double stranded, is replicated to its complement which in turn serves as a template for the synthesis of progeny RNA molecules.

3. Direct translation of DNA to protein without transcription has been observed only in vitro. This process probably never occurs in living cells.

5.2.4 Introns, pseudogenes, repetitive DNA, silent DNA

The genes in nuclei of the eukaryote cells contain introns, sequences consisting of 10-1000 nuclotides interspersed with the exon parts of DNA which is translated to a protein coded by gene [49] . Molecular Darwinist could compare introns with the commercials appearing between TV program or simply as selfish DNA. One could see them also unused parts of a computer program separated from the program code by comment signs in front of each line corresponding now to DNA nucleotide. The latter metaphor is consistent with the observation that intron can begin even in the middle of DNA triplet and that the transcription to mRNA is not unique so that same gene can give rise to several proteins. The content of intron sequences seem to be unrelated to the exon sequences: as if two separate interspersed computer codes would be in question.

Only one prokaryote cell, photosynthetic cyanobacterium Fischerella, is known to contain introns [49] . Usually also the genes of cell organelles (such as mitochondria of human cell) contain only very few introns. Fungi are however an exception in this respect [110] . The higher the evolutionary level of the eukaryote cell, the higher the fraction of introns in the genome is. For humane genome the fraction of exons is about one per cent. During transcription both introns and exons are transcribed to hnRNA, intron sections are snipped away in a process called splicing and the resulting mRNA for the protein coded by exons is transferred from the nucleus and translated to a protein coded by the gene. It is possible to snip off the introns from genome but the mRNA coded by these genes is not transferred from nucleus, which suggests that introns have some role in genetic program. The addition of introns does not seem to have any dramatic effects on the genetic program.

Introns are a headache of molecular Darwinism. The nickname "junk DNA" tells the basic attitude towards introns. Introns represent selfish DNA living as parasites of the genome. There are two opposite schools concerning how introns have appeared.

1. The first school claims that introns came early. Somewhat surprisinly, this school sees bacteria as results of a long evolution which has gradually snipped off the introns from a primitive cell in order to achieve maximal rate of DNA transcription. One can of course wonder why the same thing has not happened to the cell nuclei also.

2. Second school tells that introns came late: this view conforms with the observations about the fraction of introns in genome. Introns seem to start from preferred sites and exons seem often to correspond to a modular decomposition of the protein they code. On basis of this it has been also proposed that introns separate modular parts of proteins from each other. The facts that introns can appear in the middle of protein module and even split single DNA triplet are not however consistent with this interpretation.

One can criticize the identification of introns as junk DNA.

1. It is difficult to see how human genome containing so high per cent of junk DNA could work with such a fantastic precision while viruses, second form of junk DNA, are often lethal. There are several pathways for slicing. Exon-intron transformation has been found to occur: exon and

intron parts of gene simply change their roles [49, 142] ! This suggest that exon-intron property is additional dynamical degree of freedom in genone and might have deep meaning. Exon↔exon transformation is indeed crucial for the working of immune system.

2. mRNA produced by intronless gene does not get out of nucleus. It seems that the presence of introns somehow initiates a module of genetic program taking care that protein mRNA gets out of the nucleus. Introns seem thus to be necessary for the functioning of the cell and could be in some sense regarded as an output of gene interpreted as a genetic subprogram. Note however that intron mRNA which winds around spherical proteins in the process of splicing, have not been reported to serve as transcription factors.

3. The positions of the intron sequences in similar genes are not same for various species. There are wandering introns which can move even from cell to another one. There is a phenomenon called homing [49, 140] : the RNA coded by intron inserts itself into DNA sequence and builds by inverse transcription its complement in complementary DNA strand. Retrohoming in turn means that introns can carry and install long pieces of RNA to DNA sequences to DNA [123] . This suggests that introns might provide a new mechanism for the evolution of the genome and provide a mechanism for modifying the program code of genetic programs. It is also known that there are long range correlations (in scale of one micro-meter) in genes containing introns [109] . This suggests that introns are essential element in the organization of DNA to larger structures.

All these properties of introns suggest that their role in genetic program is badly misunderstood in the framework provided by molecular Darwinism and the basic dogmas of genetics.

Besides introns there are pseudogenes of various types, which by definition code no proteins. For instance, eukaryote genes from which introns have been snipped off, behave as pseudogenes. Pseudogenes can also contain "programming errors": for instance, the DNA triplet signifying the beginning of gene has changed. Genetic program metaphor suggests interpretation of pseydogenes as unused program modules. The idea about two interspersed program codes could explain the program errors as only apparent program errors. Of course, every experienced computer programmer would suggests the possibility of also genuine program errors! Also the interpretation as control structure affecting transcription via long range interactions rather than via chemical contact interactions might make sense. It is indeed known that so called enhancers and silencers act as transcription factors in this manner.

Genetic code contains large amounts of repetitive DNA.

1. Five per cent of genome of the eukaryotes consists of highly repetitive DNA consisting of 5-300 nucleotides (even 10^6 copies are possible). In particular satellite DNA, containing less than 10 nucleotides belongs to this class. This DNA are active during mitosis and meiosis [110] .

2. 30 per cent of DNA is moderately repetitive. The first class corresponds to rRNA, 5SRNA, tRNA and histogenes (10-100 copies). These genes are concentrated in certain chromosomes. In case of genes coding rRNA, tRNA the repetition of genes is understandable since translation making possible large number of aminoacid copies does not occur. The fact is however that also genes coding proteins appear as very many copies and there is no obvious explanation for this. So called SINE segments have length not longer than 10^3 np and are interspersed through the entire genome as $10^4 - 10^5$ copies. LINE-segements consist about 3×10^3 np: there are about 10^4 copies are interspersed through the entire genome. Part of these sequences are transposons (see below).

3. 65 per cent of DNA are present in only few (1-15) copies. Both exons and introns belong to this group of DNA and exons form only one percent of human genome.

4. The control regions between genes are rather long and seem to contain DNA with no obvious function. Also second strand of DNA can be regarded as silent DNA since its presence is not absolutely necessary for the storage of genetic information. The question is whether this silent DNA has some hitherto unidentified function.

The genome of both prokaryotes and eukaryotes contains transposons, which are movable DNA sequences able to insert themselves to DNA with the help of insertion sequences. Insertion sequences are short (less than 2000 nucleotides) and do not code proteins. Insertion sequences can carry also promotor and repressor sequences with them. Transposons could be important for evolution.

5.2.5 Is Central Dogma an absolute truth?

The Central Dogma of molecular biology states that each gene corresponds to a unique polypeptid. There are several observations challenging Central Dogma.

1. It is known that many alternate pathways of transcript splicing are possible and give rise to different protein outcomes called isoforms. This would suggest that transformation of some introns to exons and vice versa occurs routinely in gene expression. Using computer program analogy, this transformation would mean that the program part represented by introns becomes active and the part represented by exons becomes passive.

2. The phenomenon of superimposed genes [110] . There are genes nested inside genes and translation can start also in the middle of gene producing shorter protein than the gene usually. These phenomena were first observed for bacteriophage $\phi X174$, whose genome is known in its entirety. It is known that gene is transcribed as a whole and that different proteins result from frame shift. Gene can also overlap the DNA sequences formed by two subsequent genes as first observed in bacteriophage $G4$. These observations suggest that the standard notion of gene fails somehow.

3. It is known that also the "nonsense" strand of DNA can serve as template for transcription [110] .

5.2.6 Is life nothing but biochemistry?

It is not at all obvious whether the hypothesis "life is nothing but biochemistry" holds true.

1. It is not known whether protein folding is coded into the chemistry of DNA. The problem is mathematically unattractable due to the occurrence of combinatorial explosion. It seems more probable that folding might be self-organization type phenomenon and thus affected by the conditions of environment: protein development can be regarded as hopping in spin glass type energy landscape leading to some deep valley of free energy valley. TGD suggest that folding is the quantum analog of this kind of process. In particular, p-adic length scale hierarchy and many-sheeted space-time concept suggest that one cannot understand protein folding in terms of DNA chemistry alone.

2. DNA is essentially one-dimensional structure. This suggests that gene codes only one-dimensional skeleton of its expression domain and that self-organization by quantum jumps could take care of the rest. Indeed, the work of Mae-Wan Ho [166] shows that living organisms are liquid crystals which can be regarded as one-dimensional crystals and two-dimensional liquids, whose properties can be characterized by some global parameters. Perhaps genes code the properties of various layers of the liquid crystal. One of the basic characteristics of liquid crystals is self-assembly and de-assembly. Depending on pH, ionic concentrations, temperature, electric fields,... liquid crystals organize to micelle like structures (cell membranes, collagen fibers,....) and effectively one-dimensional layered structures [3] .

3. One can wonder how morphology is coded in DNA and how it is decoded from DNA. It is not at all obvious that DNA chemistry, which is purely local, is enough to code morphology.

4. So called enhancers and silencers are transcription factors, which encourage or disencourage gene expression in eukaryotes. The position of these proteins or orientation in DNA does not seem to be important [110] . For instance, they can bind to introns and the distance of the binding site from gene promotor regions can be thousands of nucleotide pairs. This would suggest that the mechanisms of enhancing and silencing are not purely chemical if chemical at all. This would suggest the generalization of the notions of gene expression and transcription factor. Chemical expression takes place very slowly. Non-chemical expression modes yielding nonchemical transcription factors could make possible very fast running of genetic programs and there could be even connection between many-sheeted genome and nerve pulse activity.

5. The naive expectation is that the size of the genome should correlate with the evolutionary stage of the species. Eukaryotes indeed have genome which is typically 10^3 times longer than prokaroyote genome. The table below however shows that the total length of genome does not

correlate with the complexity of the organism faithfully. The genome of plants is typically 10-100 times longer than human genome. The genome of amoeba is by two orders of magnitude longer than that of human! The genomes of monkeys and men are almost identical. This suggests that there might be some unindentified degree of freedom associated with DNA which explains these differences.

Organism	Human	Mus musculus	Amoeba	Marbled lungfish
$N(DNA)/10^9$	3	3	670	139
Organism	Salamander	Onion	Trumpet lily	
$N(DNA)/10^9$	81	18	90	

Table 1. The amount of total genome measured as the number of DNA triplets.

5.3 Many-sheeted DNA

The notion of many-sheeted DNA suggest a profoundly new manner to understand how the morphology of the organism is coded to and decoded from DNA. p-Adic length scale hypothesis leads to precise quantitative predictions for the number of levels of genetic program as function of a suitably defined size of the organ. The proposed model for introns leads to the interpretation of gene as a representation for Boolean algebra and to the proposal that genes realize not necessarily conscious-to-us Boolean mind at the basic level. What is especially nice is that connection with the realization of Boolean mind in terms of cognitive neutrino pairs is consistent with this picture. Many -sheeted DNA suggests also new forms of gene expression and of control of gene expression. For instance, nerve pulse patterns could affect also genetic program of postsynaptic cell via the classical em and Z^0 field patterns associated with them and genes could affect cell membrane via conformational waves propagating along micro-tubules connecting nucleus to cell membrane.

5.3.1 Many-sheeted DNA as hierarchy of genetic programs

Many-sheeted DNA allows to realize genetic subprogram hierarchy in an elegant manner. Many-sheeted DNA and proteins are like a hierarchy of ordinary DNA and proteins effectively living in different space-times corresponding to body parts. One can consider the possibility that subprograms correspond to p-adic space-time sheets and subprogram hierarchy corresponds to the hierarchy of p-adic space-time sheets. The gene program in a given length scale would selectively activate programs in shorter length scale, etc.. DNA sequences with the same chemical structure correspond to different genetic programs since the many-sheeted structure of DNA affects its functioning. Analogous conclusion is true about proteins.

One can assign to gene a unique p-adic prime as the prime characterizing the largest p-adic sheet at which gene has # contacts. The number of levels in subprogram hierarchy could be deduced from the size of the organism. Gene can have # contacts to several space-time sheets characterized by p-adic primes $p \simeq 2^k$, k power of prime. Denote by k_G the largest value of k associated with gene. k_G characterizes the position of gene in subprogram hierarchy. Gene can have # contacts with space-time sheets $k < k_G$ also. Gene can be characterized by the p-adic k_G labelling the largest space-time sheet to which it has # contacts. "Comment sign" marking each nucleotide of intron could correspond to a direction of classical field at some space-time sheet characterized by p-adic prime $p \simeq 2^k$, $k = k_I$. The only sensible assumption seems to be $k_I = k_G$.

The other # contacts of gene must be assumed to be on space-time sheets with $k < k_G = k_I$. This implies that given program can call only programs which are in the lower level of the hierarchy. This would suggest that programs belonging at the lower level of hierarchy cannot call program at higher level. Does this imply that growth process in which larger and larger space-time sheets are activated can only occur by self-organization? This would mean that DNA space-time sheets with increasing value of k_G expand in phase transition like manner and fuse to form space-time sheets corresponding to various body parts. On the other hand, it is not at all obvious that growth process could not start

from higher level and lead to gradual differentation at lower levels. In fact, embryogenesis seems to occur in this manner [110] .

Also proteins can be classified by the the number k_P characterizing the largest space-time sheet to which protein has # contacts. Proteins must mediate program calls to gene modules G_1 with various values of $k_{G_1} < k_G$. This suggests that protein activating gene characterized by k_{G_1} must have same $k_P = k_{G_1}$. This would automatically guarantee that chemically identical proteins activate only the genes belonging to the level of the fractal hierarchy they represent.

The notion of many-sheeted DNA has immediate applications.

1. Many-sheeted DNA provides a possible explanation for why DNA triplets act as codewords of the genetic code. If members of each DNA triplet are glued to space-time sheet containing only # contacts from the nucleotides of the triplet, codewords have a clear geometrical meaning.

2. The notions of many-sheeted DNA and many-sheeted protein suggests also an explanation for how enhancers and silencers are able to regulate gene expression. Interaction with classical em or Z^0 fields via wormhole contacts provides a nonchemical interaction mechanism. Second mechanism is based on Josephson currents running along join along boundaries contacts. Since interaction with much larger length scale is involved, these interaction mechanisms are not too sensitive to the position of the transcription factor and the distance of the binding site from gene promotor regions can be thousands of nucleotide pairs. This mechanism explains also the observe issue specificity of some transcription factors. Proteins with same chemical structure can be quite different trascription factors if they have contacts to different space-time sheets.

5.3.2 Possible answers to the basic questions

Many-sheeted DNA suggests stupifyingly simple coding of body's morphology. The genes would be obtained by simply contracting the many-sheeted space-time representing expression domains of genes to one-dimensional structure. Decoding of the morphology means the growth of this structures to their orginal size. Of course. this hypothesis is oversimplified but its extreme simplicity makes it worth of testing.

How the structure of expression domain of the gene is coded in the structure of gene?

The p-adic length scale of the gene correlates trivially with the p-adic length scale of the protein coded by it. Already protein folding implies that the correlation with the size of the structure coded by DNA is not so straightforward. Furthermore, proteins are not mere building blocks but can have quite abstract functions like regulating gene expression of genes.

Consider now various aspects of the idea that expression the domain of gene is coded into the structure of gene and this that correspondence could be also realized at functional level.

1. The first thing that comes into mind is that the p-adic length scale of the gene correlates with the p-adic prime of the space-time sheet which corresponds to the expression domain of the gene during early phases of the embryogenesis. Gene clusters, say Hox cluster, would represent kind of a miniature of the body and every gene of Hox cluster would give rise to a space-time sheet which would be a scaled down model of the expression domain of the gene. Thus the expression domains of various genes in the genome could correspond to the extended space-time sheets at the level of the genome and the topology of these genome level expression domains, in particular, their ordering, would be consistent with that for the actual expression domains. Expression domain corresponds most naturally to a join along boundaries condensate generated by the formation of the join along boundaries bonds between the extended space-time sheets associated with the genes. This means that the p-adic prime of the expression domain can be much smaller than one could conclude it to be on basis of its size.

2. One could test the hypothesis that the total length of the region occupied by gene and by the DNA controlling its activity in the genome could correlate with the size of its expression domain at the stage of the development when the gene is expressed. Note that many genes affecting morphogenesis are expressed in a very early stage: many of them in the embryonic stage when no cell formation has yet occurred. This stage corresponds to the p-adic length scale of a fertilized

cell about 10^{-4} meters. Of course, the correlation between the content of the gene program and the size of its expression domain, is not necessary and might be even un-desirable.

3. Fractality suggests that the communication by expression factor proteins at the level of genome might mimick the hormonal communication occurring at the level of the entire organism. This could mean that the hormonal communication between the expression domains of two genes is equivalent with the presence of a transcription factor communication between corresponding genes at the level of nucleus. Hormonal communication between cells involves the formation of hormone-receptor complex acting as a transcription factor.

The length of human genes ranges to thousands of nucleotides. This would mean that the longest p-adic length scales of human gene would correspond to $L(173) \sim 16$ micro-meters. The total length of a human chromosome is about 75×10^6 DNA triplets. The corresponding p-adic length scale is $L(193) \sim 2$ cm. The next length scales correspond to the pair $(197, 199)$ and correspond roughly to the size of brain hemisphere and brain. The total length of DNA in chromosomes is $48 \times L(193) \sim 1$ meter, the size scale of human body.

Many-sheeted space-time concept suggests that genes actually correspond to DNA sequences glued to a larger space-time sheet defining the gene. Hox clusters could be one example of this. The geometry of the organism might be coded to these secondary, tertiary, etc. space-time sheet structures of the DNA sequence guaranteing the coding the topology of the body plan to the topology of the multi-sheeted DNA. These structures are be labelled by p-adic primes and their number would be quite limited.

The linearity of DNA suggests that also the plan of the expression domain should be essentially linear such that each cross section of each module of the expression domain is essentially homogenous phase and its structure is determined by a self organization process constrained by the p-adic length scale hypothesis rather than purely genetically. According to Mae-Wan [166, 167] living systems are liquid crystals and the basic characteristic of the liquid crystals is that they have crystal like structure in one dimension and are liquids in transversal dimensions [3] forming. thus layer-like structures. This suggests that p-adic self-organization determines the size of the transversal layer and that DNA only codes some general properties of the liquid phase for a given layer.

The sizes for the expression domains of the genes should form a hierarchy. Effective expression domain can be much larger than the p-adic length scale characterizing it since join along boundaries condensates are possible. For instance, the modularization of the genetic programs of plants is perhaps stopped at the level $k = 167$ so that expression domains for plant cells could be regarded as join along boundaries concept of of $k = 167$ plant cells. At the level of organism this perhaps corresponds to the emergence of cell walls hindering the formation of higher level structures formed from cells: plant could perhaps be regarded as a large join along boundaries condensate of $k = 167$ plant cells surrounded by a wall. Besides the length of the genome, the number of the p-adic hierarchy levels in the space-time sheet hierarchy of DNA is a natural candidate for a measure of the complexity of the organism.

How the information about morphology is expressed?

One of the fundamental questions of the developmental biology is how the information of genes stored into DNA is translated to the geometry and topology of the organism. The idea of many-sheeted DNA suggests an immediate answer to this question. Expression is 'nothing but' the reversal of the coding. The expression domain of the gene contracted effectively to one-dimensional DNA-thread grows back to the expression domain with non-uniqueness and flexibility brought in by self-organization depending on external parameters. This means that various space-time sheets associated with DNA grow during grow to space-time sheets representing actual organs. This process involves the formation of join along boundaries bonds between growing space-time sheets associated with various DNA molecules so that coherent macroscopic quantum phases become possible.

One can ask how the growth plan is coded into DNA. Or how much of it is coded into the chemistry of DNA? The idea that DNA is essentially body contracted to a thin thread suggests that the chemical control of DNA is restricted to the local properties of tissues. The space-time sheets of replicating DNA at various body parts simply grow and fuse to form join along boundaries condensates growing and giving rise to various organs. The replication of DNA would in turn be quantum self-organization process involving essentially self-hierarchy starting from atomic level and ending up the level of entire organism.

What makes cell differentiation possible?

Cell differentiation is one of the great mysteries of biology. It is known that only part of DNA is active in a cell located in a given part of body and that selective activation of the genome gives rise to differentiation. The problem is to understand the mechanism of activation. Especially difficult challenge for the view about life as mere chemistry is the interaction between large length scales with gene level making possible precise timing of genetic activity.

In TGD framework cell differentiation should correspond to a selection of branch in the the flow diagram describing genetic program. This occurs during the growth since the concentrations of the proteins representing the inputs of the gene programs evolve during the growth and generate also spatial gradients. Therefore different branches of the genetic program are activated in different parts of the developing organism. Also the genes associated with space-time sheet of increasing size are activated during growth and this brings in new and higher control levels.

Very probably the mechanism involves interaction between microscopic degrees of freedom for DNA and between macroscopic degrees of freedom representing body part where DNA resides. The control and coordination based on Josephson currents between gene space-time sheets and larger space-time sheets is very probably involved as is suggested by the general time scales of genetic activity. Also the interaction with the classical fields of the space-time sheet of the body part to which DNA has wormhole contacts provides an obvious mechanism of activation. The frequencies of the coherent oscillations of em fields involved could be important in both interaction mechanisms. This kind of interactions with larger space-time sheets makes possible to understand induction phenomenon, which corresponds signalling between cells and entire cells groups. This kind of signalling could be crucially important for morphogenesis. Many-sheeted space-time thus provides explanation for the ability of cells to form organs. The notion of cell cohesion is introduced to explain this: the cohesion would correspond to the formation of join along boundaries condensate of extended gene space-time sheets.

5.3.3 What is the number of the levels in program hierarchy?

The obvious idea is that the size of the organism determines the largest p-adic prime contributing to the program hierarchy. It is however not obvious whether to define the size of organism as the 'physical', visible size or as electromagnetic size, which is well defined notion in TGD framework.

Does the visible size of the organism determine the number of hierarchy levels?

The simplest working hypothesis is that the number of the levels in the program hierarchy is the number of p-adic length scales between atomic length scale and body size. The larger the visible size of the organism, the larger the number of the levels in the genetic program hierarchy, if this hypothesis is correct. This number is testable characteristic of species and could be valuable guide in attempts to understand how genetic code functions. One can identify the hierarchical level of the gene by looking how many genes it activates before building block protein is coded. It must be however emphasized that visible size need not be a correct criterion: the point is that join along boundaries condensates are possible and give rise to a much larger body size than one might conclude from the value of largest p-adic prime involved.

It is instructive to look the numbers of hierarchy levels in some specific examples assuming that the visible size of the organism determines the number of hierarchy levels. It is assumed that $k = 139$ is the first level which counts as a hierarchy level.

1. Viruses could have 4 hierarchy levels if $k = 139, 149, 151, 157$. Proteins, lipid layers of cell membrane and cell membrane and genes coding building block proteins. It could be that only k=149 is present for the simplest viruses since the formation of the envelope is self-organization process.

2. Bacteria should have 5 levels. $k = 139, 149, 151, 157, 163$.

3. Home fly should have 12 levels since its size is below $L(197) \simeq 1.6$ cm.

4. Animals with size between $L(199) \simeq 16$ cm and $L(211) \simeq 10$ m have 15 hierarchy levels. Note the large gap between $L(199)$ and $L(211) = 64L(199)$.

5. The next level corresponds to the level of dinosauri and whales having sixteen levels unless they correspond to join along boundaries condensates formed from smaller structures which is quite possible. The next level is $L(223)$ and corresponds to size of 640 m!

Does the electromagnetic size of of organism determine the number of hierarchy levels?

There is a large gap between $L(199)$ and $L(211)$ and the next twin length scale corresponds to a length scale of one kilometer. This suggests that new levels of hierarchy possibly emerged after $L(199)$ cannot correspond to the physical growth of body. Mere large size does not guarantee intelligence. Furthermore, if the visible size of the organism determines the number of the hierarchy levels, then dinosauri would have been in a well defined sense more intelligent animals than we! These arguments suggest that the visible size of the organism need not determine the number of genetic program levels.

1. It could be that DNA codes and even controls also the electromagnetic structure of the organism realized as topologically quantized electromagnetic field, "aura", characterizing the organism.

2. An alternative option inspired by the notion of memetic code, which is next level in the hierarchy of genetic codes predicted by the TGD inspired simple model of abstraction process, is that there are higher hierarchy levels present but they are not controlled by the genetic program but call it as a subprogram.

A natural working hypothesis is that EEG correlates with the electromagnetic size of the organism. EEG has emerged rather lately in the evolution and is possessed only by vertebrates. In case of humans it becomes fully developed only at the age of 18. Meditation in general tends to increase the amplitudes of low frequency waves with 8 Hz (alpha wave s) and also waves with lower frequencies (theta wave s). This suggests that growth in electromagnetic degrees of freedom can continue all the lifetime and could be identified as what is called "spiritual growth". It could continue also after the physical death so that the protein based state of life would be only a part of much longer lasting process of self-organization analogous to the development of butterfly. Indeed, in TGD based picture about geometric time the death of the physical body does not mean the end of life.

Schumann resonances are resonances of em fields in the wave cavity defined by the 80 km thick layer between Earth's surface and ionosphere. The frequency range in question correspond to the frequency range of EEG. A hypothesis worth of considering is that human body generates via Schumann resonances topological field quanta, which define electromagnetic sub-selves having the size of Earth. One could even consider the possibility that the highest value of k_G depends on individual and people having tendency to have religious and mystical experiences have exceptionally large value of k_G.

The length scale corresponding to alpha waves is 3.8×10^7 meters and corresponds is roughly 3.75 times the length scale $L(251)$. If levels up to $L(257)$ are present in the human genome then the number of hierarchy levels is 22, not too large number. $L(251) \sim 10^7$ m corresponds to a frequency of 37.5 Hz and is quite near to the 40 Hz frequency claimed by Koch and Crick to be crucial for the visual consciousness! The frequency associated with $k = 257$ corresponds to the frequency of 5 Hz, which also belongs to EEG.

The electromagnetic size of the organ increases rapidly with the number of levels present in the hierarchy as the following table demonstrates.

k	227	229	233	239	241
L_p/m	$2.5E+3$	$5E+3$	$2E+4$	$1.6E+5$	$3.2E+5$
k	251	257	263	269	271
L_p/m	$E+7$	$8E+7$	$6.4E+8$	$5E+9$	$E+10$

Table 2. Table of p-adic length scales above $L(211) \simeq 10$ meters. $L(151) = 10^{-8}$ meters is assumed.

There are even more explicit observations about the importance of ELF em fields for the functioning of living matter and these observations finally led to a breakthrough in TGD based model of conscious brain. The observations about the special effects of ELF em fields on brain at cyclotron frequencies of ions Na^+, Cl^-, K^+ and Ca^{++} in endomagnetic fields $B_{end} = 2B_E/5 = .2$ Gauss were made already at 1983 [46] . These experiments suggest that these ions/their Cooper pairs form are confined in the magnetic field of Earth and form bound states with macroscopic size of order cell size and with

extremely small binding energy corresponding to frequency of order 10 Hz. This is impossible in the standard physics framework but can be understood as resulting from the dropping of ions and electrons from the atomic space-time sheet to the space-time sheet of the cell where the density of the matter is very low.

Also electron Cooper pairs of high T_c electronic super conductor as well as Cooper pairs of neutrino super conductor are important. Besides magnetic cyclotron frequencies Z^0 magnetic cyclotron frequencies and wormhole cyclotron frequencies make sense: Z^0 currents for ions indeed induce automatically also ionic currents.

One can argue that there is very cold, dry and silent at the cellular space-time sheets and this makes possible macroscopic quantum phases formed by Cooper pairs of ions Na^+, Cl^-, K^+ and electron as well as well as Ca^{++} ions. Later the argument was modifiedthe large values of Planck constant [27, 23] imply that cyclotron energy scale is above thermal energy at room temperature even if thermal equilibrium of dark space-time sheets with ordinary ones is allowed. Also other ions are possible but these ions are especially important for nerve pulse generation. These super conductors must be effectively one-dimensional (otherwise gap energy is extremely small) and the needed confinement in the transversal degrees of freedom is caused by the presence of B_{end} which could be in TGD framework interpreted as the dark companion of the Earth's magnetic field responsible for controlling biomatter possibly also associated with the personal magnetic body. One could regard these super conductors as associated with the flux quanta of B_{end} having radius 25 μm (the size of a large neuron) by flux quantization and serving as templates for the formation of biostructures.

When the Josephson frequency (potential difference) associated with the weakly coupled super conductors of this kind corresponds to a magnetic transition frequency, quantum jumps between states of either super conductor occur and change the charge distributions and hence potential differences associated with other Josephson junctions associated with either super conductor. Quantum jumps can lead to 'wake-up' of either or both super-conductor sub-self giving rise to a mental image. Also emission of ELF photons with resonance frequency is involved. The topological field quanta associated with these photons have typically size of order Earth's circumference. The fact that multiples of the cyclotron frequencies correspond directly to the most important frequencies of EEG and also to some important Schumann frequencies suggests very strongly that the 'ELF selves' associated with these topological field quanta represent also selves in our self hierarchy. This leads to a general model for quantum control and for how the space-time sheets representing the self-hierarchy are coupled by join along boundaries bonds serving as Josephson junctions, to a detailed model for the quantum correlates of the sensory qualia and to a model of Boolean mind. ELF selves are a crucial factor of all these models [31, 33] .

The work of Michael Persinger shows that ELF em fields and ELF modulated em fields, affect also gene expression [29] . Thus it seems that ELF levels, rather than being controlled by gene level, actually control and coordinate gene level rather via the formation of join along boundaries bonds between gene space-time sheets and ELF space-time sheet. Whether gene level actually *codes* also ELF levels of the organism is an interesting question. The idea about genome as the entire many -sheeted organism contracted to a thin thread would support this view. On the other hand, the notion of the memetic code identified as the next level of abstraction hierarchy suggests that ELF level corresponds to something genuinely new not reducible to gene level. ELF level could be even seen as a different life form next to the biological life living in symbiosis with biological life. One must also remember that higher levels could couple with gene level only via join along boundaries contacts and that the development of organism could be seen as a 'social' process in the sense that growing organism gradually builds join along boundaries contacts to the space-time sheets representing higher level selves.

Whether the number of the hierarchy levels in the genetic program hierarchy is larger than the visible size of organism, might be perhaps tested sooner or later by deciphering the number of hierarchy levels in the genetic program. To check the hypothesis about EEG, it is enough to study simplest verterbrates possessing EEG. The identification the levels of various genes in program hierarchy would mean a tremendous boost in the understanding of genetic code and dramatic change in world view.

5.3.4 Band structure of chromosomes as an evidence for many-sheeted DNA?

In prokaryotes DNA is arranged in single chromosome forming closed circular double strand whereas in eukaryotes DNA genome is organized into chromosome pairs. Chromosome is believed to correspond to single DNA thread which has beads in thread structure. Beads are spherical nucleosomes of diameter 10^{-8} meters ($L(151)$!) consisting of histones of 4 different types forming histone octamer. DNA is wound very tightly around nucleosomes, there is about 70 nanometers (slightly less than $L(157)$ of DNA per nucleosome. chromosome forms a helical coil with diameter found to be 30 nm. In interphase chromosomes are coiled once more to a hollow tube of diameter 200 nm (slightly less than $L(167)$) a helix of thickness about 10^{-7} meters. The transition from interphase chromosome to metaphase chromatid is accompanied by a winding to a helical coil of diameter about 600 nm (slightly more than $L(169)$). A possible interpretation of these transformations is as generation of new space-time sheets.

Chromosome banding was discovered already in eighteenth century by Metzner. Chromosome banding characterizes both the chromosome and the method used to produced the banding structure and there are many methods for revealing the band structure. Increasing resolution implies the division of band structures to smaller structures in fractal like manner. The band structures can be divided into two classes.

1. The highly localized heterochromatic bands, nucleolar organizers and kinetochores appear in all organisms. The latter two structures seem to reflect the purely geometrical organization, "packing", of genome rather than the internal organization of genome. The main features of heterochromatic banding are its universality, diversity and variability. Heterochromatic banding is present in all eukaryotes and can differ widely for closely related species and be very similar to widely different species. Heterochromatin seems to correspond to highly repetitive short DNA sequences of 10 nucleotid pairs (10^6 copies) located near the centromere of the chromosome. This DNA is not transcribed to DNA. Pairs are often duplicated and duplication leads to various physiological defects. Soma cells of some organisms appear to have ability to get rid of of heterochromatin whereas it is present in germ cells. These facts suggest that the regions of chromosome near its center regulate gene expression and that highly repetitive DNA sequences represent sites for genes at which repressor proteins bind. Abnormally large duplication of repressor sites would lead to stronger repression is more effective and could lead to abnormal development.

2. The chromosomes of the eukaryotes contain also non-localized bands called euchromatic bands. Patterns of euchromatic bands resemble closely to the patters of DNA replication and patterns correlate very strongly with species. Thus euchromatic bands correspond to active RNA. The moderately repetitive DNA which is transcribed corresponds corresponds to euchromatin. It is known that there are several types of euchromatic banding. Banding patterns can be used as diagnostic tools to identify various chromosome fusions and splittings. Various bandings are of enormous value in providing manner to locate genes in genome.

In TGD framework a natural interpretation of various types euchromatic banding provide evidence for the many-sheeted DNA. Thus euchromatic banding should reflect the modular structure of the genetic program as well as the interspersing of control regions and transcribed regions of genes corresponding to the basic structure "If A then B" of the gene.

5.4 Model for the genetic program

The model for the genetic program is based on the interpretation of DNA sequences as statements of a formal system. 64 basic statements represented by DNA triplets correspond to axioms which are identically true. Gene G is interpreted as a theorem of type "If I_1&....&I_n true then O_1&O_2...&O_n true" or generalizations thereof obtained by adding several input statements and allowing also negations of the input statements. It could be that complementary DNA strand represents statements of type "If I_1&....&I_n true then O_1&O_2...&O_n not true". If given DNA sequence has been translated to give rise to some minimum concentration of protein coded by it, the truthness of this statement is emotionally experienced by the genetic computer. Otherwise the truth value of the statement is ill defined.

The information about truthness of I_k is represented by the catalytic action of the enzyme coded by I_k on those parts of gene which are not transcibed, in particular on the promotor sequence of the gene. They give rise to experiences about the truth values of the statements $I_1...I_n$. The conclusion "$O_1\&,..,\&O_n$ is true" represents the output of the gene. These statements appear as the premises for the statements represented by some other genes. Thus the running of genetic program represents a sequence of becoming conscious about various kinds of truths of the formal systems represented by genome.

5.4.1 Genes as statements of conscious formal system

The assumptions for the model of genes as statements of a conscious formal system are following.

1. DNA sequences are assumed to represent axioms of some formal system. There are 64 basic triplets of DNA, which correspond to basic independent statements, axioms, from which higher level statements are built using many-sheeted DNA making possible the construction of statements about statements about....

2. Genes are assumed to represent statements of type "If $I_1\&...\&I_m$ then $O_1\&...\&O_n$ true." or "If $I_1\&...\&I_m$ then $O_1\&...\&O_n$ not true." depending on which strand of DNA double helix is transcribed.

3. The output of gene is either true or ill defined gene can only be conscious about truthness of a statement or be unconscious. The logic of our conscious experience (which need not have anything to do with the possible gene level mind) is consistent with this. We can have conscious experience about truth values of a very limited set of statements and have no experience about the infinitely of all possible logical statements. Note that the experience with standard logic would suggest that the value of the statement is either true or false. The experience with ordinary computers would in turn suggest that the value of outputs could be true, false or ill defined.

4. Gene expression is the counterpart for the emotional experience about truthness of the statement represented by the gene. One can say that the output of the gene is true or ill-defined. The output of the gene G generated by gene expression appears as an input for those genes G_i, which represent statements whose premises depend on the statements appearing in the output of G. This implies that the evolution of the genome involves a sequence of conscious emotional experiences about truthness of some statements, which in turn make possible to become conscious about truthness of some other statements.

5. The formal system represented by DNA and many-sheeted DNA sequences has certain Gödelian flavor in it. The truthness of the stopping sign DNA triplets UAA, UAG and UGA cannot be expressed in terms of proteins coded by exons. They are like undecidable statements in an axiomatic systems whose truth value cannot be deduced from the axions. Introns however can contain stopping sign and if mRNA-protein complexes represent truthness of intronic statemenets, then it is possible to experience the truthness of also the statements containing stopping sign DNA. The analogy with "holy trinity" of mystic and religious thinking is obvious: whether "holy trinity" exists is not decidable by human means! Proteins clearly have finite expressive power. Given aminoacid coded by DNA triplets X_i tells only that the statement $\vee_i X_i$ is true so that the number of emotionally experiencable basic truths reduces to 20.

A more precise but less general model for genome as a conscious formal system is based on the following assumptions.

1. Exon part G of gene and its intron parts I_i are interpreted as logical statements G and I_i. Together they represent the conclusion of a theorem. Hence the running of genetic program means generation of a sequence of conscious experiences of type "*...then* $G_1\&...\&G_n$ is true" or *...then* $G_1\&\cdots\&G_n$ is false" depending on which DNA strand is involved in transcription.

2. The statement represented by a gene G is experienced to be true if G has generated some minimum concentration of the corresponding protein $P(G)$. Under what conditions the intronic

statements $I_1, \cdots I_n$ are experienced as being true, is not clear. The basic dogma of genetics suggests that also now overcritical values for the proteins $P(I_i)$ translated from intronic mRNA inside nucleus make possible conscious experience about the truthness of these statements.

3. mRNA-protein complexes are not able to regulate directly the activity of genes having intron statements as premises. The regulation mechanism, if present, must be indirect. Simplest regulation mechanism is based on the observation that gene can be in states in which the roles of some introns and exons are changed. In particular, each gene has complementary gene for which exons and introns (with stopping sign excluded) have changed their roles. If the protein coded by complementary gene has the role of a silencer for the expression of gene protein, the production of mRNA-protein complexes means that the translation of the silencer molecules does not occur anymore. Since the existing silencer molecules gradually decay, these genes are activated. Thus the activation of a gene by intron-exon transformation activates automatically also the genes whose input depends on the output of the gene. Note that exons would code what is very much analogous to "printed output".

It is important to notice that cognition represented basically by a genetic program is not restricted to brain. All cells of body have DNA and elementary cognitive abilities. Perhaps the special role of the frontal lobes in cognition is due to the fact that DNA in cortex has wormhole contacts with topological field quanta representing electromagnetic part of our body not visible to bare eyes. The electromagnetic size of our body could be given the size of entire Earth as suggested by the fact that EEG frequencies correspond to Schumann frequencies associated with the resonances of the wave cavity between Earth's surface and ionosphere.

5.4.2 Genes as modules of a genetic program

Genes can be also regarded as modules of genetic program. The input of module consists of the premises of the statements $I_1 \cdots I_n$ and conclusions represent the statements "$O_1 \cdots ...O_n$ true" or "$O_1 \cdots ...O_n$ not true". $O_1 \cdots O_n$ serves as input for other genes and running of genetic program continues as long as premises of some genes are true.

Ordinary programs "If A then B" and "While A do B" as basic control structures. Also genetic program should have some control structures and it seems that both these structures appear in genetic programs.

1. Assuming that genes represent theorems, the general form of statements appearing in genetic program is indeed "If A then B". A is represented in terms of enzyme concentrations and possibly intron mRNA-protein complexes activating or repressing some genes. B is represented by the protein and intronic mRNA-protein complexes transcripted from gene.

2. "While $N > 0$ do $\cdots$ and $N \to N - 1$" is the basic structure of loop in computer program. The simplest function of this loop is to circumvent infinite loops, which are nightmare of programmer. The counterpart of an infinite loop is member of species, which never dies. The presence of too many sufficiently intelligent (and, as one could bet, selfish) individuals of this kind would be a catastrophe from the point of view of species. It seems that this kind of condition is represented. Certain genes crucial for the survival of higher organisms contain certain amount of telomere which is reduced every time when the gene is active. This means that the gene modules effectively contain additional condition "While the amount of telomere $> 0 \cdots$ and reduce the amount of telomere by one unit".

One can understand basic rules of Mendel easily if the conditions guaranteing the activity of gene depend on both members of chromosome. For instance, in the case that two traits are such that second on dominates, the output of gene realizing the property is logical AND function having as its arguments the truth values of the statements represented by related genes in the chromosomes. If G_1 in chromosome 1 and G_2 in its partner chromosome have coded sufficient amounts of their specific enzymes then some third G codes the enzyme giving rise to the nondominant trait, otherwise the dominate trait appears. Second situation is the one in which traits are not yes/no properties but have discrete specrum like red, white and pink. In this case there are two genes G_1 and G_2 coding red and white directly. Various combinations of color would correspond to three combinations G_1G_1 (red), G_2G_2 (white) and G_1G_2, G_2G_1 (pink).

The notion of many-sheeted DNA implies that gene submodules should correspond to body parts. This raises several interesting questions about what the bodily correlates of the "body part =subprogram calls second body part=subprogram". Is there some kind of communication occurring between body parts also? Perhaps chemical communication based on the same enzymes that regulate gene transcription? Gene modules call gene modules corresponding to smaller sized body parts: is this true also for the communication between body parts? Or does signal transfer occur in dual manner from small body parts to larger ones?

If this kind of correspondence exists, say, at hormonal level, one could directly deduce information about the structure of genetic program from the topology of the hormonal communications. For instance, genome should have central unit analogous to brain receiving information from controlling the activities of the rest of the genome. An obvious candidate for the brain of chromosome is centromere. Centromere seems to be analogous to brain in the sense that lot of repetitive DNA presumably controlling gene expression is situated near the centromere.

5.4.3 How gene expression is regulated?

In case of prokaryotes the regulation of transcription is quite satisfactorily understood. The problem is to understand how transcription is regulated in case of the eukaryotes and here the notion of many-sheeted DNA could be crucial.

Operon theory for the regulation of gene expression in prokaryotes

Jacob, Monod and Pardee [110] suggested operon theory for the regulation of the transcription of genes responsible for lactose production in E. coli. The presence of lactose induces E. coli to produce 3 enzymes needed in the production of lactose. The enzymes correspond to three structure genes x, y, z of lactose. The mechanism is following.

1. So called i gene regulates the production of the building block proteins of the repressor protein which self-assembles as tetramer of the repressor protein.

2. Repressor protein binds to a specific site next to the promotor and hinders the binding of the RNA polymerase so that transcription becomes impossible.

3. Inductor, in the present case lactose, binds to the repressor protein and hence hinders the formation of the repressor tetrameres so that transcription becomes possible.

4. The transcript contains not only the gene but also the entire operon so that several genes are translated simultaneously.

How eukaryotes differ from prokaryotes?

Operon theory does not generalize as such to eukaryotes. Although the notion of the promoter generalizes, there is no clear-cut evidence for operons [110] . Rather, silencers and enhancers could take the role of the inducers and repressors in the eukaryotic gene expression. The action of a silencer/enhancer is not sensitive to its precise location or orientation and the distance from promoter can be more than thousand nucleotide pairs. TGD based explanation is based on the notions of many-sheeted DNA and protein. Silencers and enhancers mediate the interaction of the atomic space-time sheet of DNA with the classical fields of some larger space-time sheet. This interaction makes possible top-bottom type control analogous to the control of slave by master in Haken's theory of self-organization. Both classical em and Z^0 fields can control the gene expression in this manner. In eukaryotes classical Z^0 fields could have especially important role. Classical Z^0 fields are believed to be crucial for the model of cognition and this suggests that "mind-matter" interaction could at least partially relay on classical Z^0 fields and enhancers/silencers. Silencers and enhancers could make also possible Josephson junctions between gene space-time sheet and some larger space-time sheet and thus realize 'biofeedback'.

Second difference is related to introns. It is known that introns and exons can change their roles and it is known that there are several pathways for splicing leading to different proteins, isoforms. The replacement of single-valued gene→ polypeptide map with many-valued map obviously increases the information content of gene. The interpretation of introns and exons as two interspersed computer

codes with intron lines of code separated from exons by "comment signs" marking each nucleotide of intron is attractive model for the situation. Dropping of some comment signs changes the result of the splicing process. Comment sign distribution could be dynamical and tissue specific so that one could say that genome is not invariant of species but only of a particular tissue type. This obviously reduces the genetic determinism and gives organism better abilities to survive. In human genome 1 percent of gene corresponds to exons in the "normal" state (in whatever manner that state is defined). The number of various combinations of exon and intron combinations is 2^N where N denotes the numbers of basic components of gene (perhaps coding proteins having no decomposition to modular proteins). The number of combinations increases exponentially with N and provides huge flexibility.

The interpretation of various exon-intron decompositions as statements of Boolean algebra of statements about N basic statements suggests strongly itself. In particular, exonic and intronic proteins for same intron-exon decomposition would naturally correspond to a statement and its negation. Thus one could regard eukaryotes as representing higher levels in the hierarchy of abstractions in which prokaryotes represent the lowest level. Eukaryotic genome would be a collection of genes identifiable as Boolean algebras and the running of the genetic program would mean that at given moment some statement in some of these Boolean algebras is experienced to be true. This kind of identification would mean effectively understanding of the logical meaning of the genetic code. The dominance of particular exon-intron decomposition over its complement would simply mean that this Boolean statement is true while its complement is not true. This suggests the possibility that only those 2^{N-1} exon-intron configuration which represent statements consistent with a given atomic statement are usually realized (atomic statement corresponds to a one-element subset in the set theoretic representation of Boolean algebra).

The fact that introns and exons are set theoretical complements of each other raises the possibility that the proteins coded by introns and exons have opposite effects as transcription factors. For instance, exons could code enhancer and introns could code silencer. This implies that same gene can act as both enhancer and silencer. The only thing needed is that the roles of introns and exons are changed. When this occurs, the production of intron-RNA complexes begins and the production of the composite protein coded by introns acting as exons stops. When the production of silencer protein coded by introns ceases, the silencer proteins associated with the operator sites gradually decay and gene expression also enhanced by enhancer proteins can start. Thus the activation of the gene module activates automatically the gene modules which it calls and genetic program runs.

This would suggests rather general mechanism of gene expression.

1. There exists 2^{N-1} exon-intron decomposition plus their complements. Depending on the state of gene with given exon-intron decomposition, exons or introns are translated to protein. Both introns and exons represent statements. The modular decomposition of protein to sub-proteins often represented by the decomposition to exons corresponds to the decomposition of the statement E to $E = E_1 \& E_2 ... \& E_n$. Same holds true for I: $I = I_1 \& I_2 ... \& I_n$.

2. The proteins coded usually by exons activate some genes and these proteins appear as prerequisites of type

$$IF\ [E_1\ OR\ E_2 \cdots\ OR\ E_n]\ THEN \cdots\ .$$

   The presence of all activators is not necessary.

3. Introns correspond to repressors quite generally. The proteins coded by introns in the "abnormal" state of the gene correspond to prequisites of type

$$\cdots IF\,[NOT(I_1) \& NOT(I_2) ... \& NOT(I_n)]\ THEN \cdots\ .$$

   This means that the absence of all repressors from operator site is necessary. The general form of gene statement is

$$IF\ [E_1\ OR\ E_2 \cdots\ OR\ E_n] \& IF\,[NOT(I_1) \& NOT(I_2) ... \& NOT(I_n)]\ THEN \cdots\ .$$

   Various E_k:s and I_k:s represent proteins in turn having modular decomposition to a product of more primitive statements.

The role of the hierarchy of Josephson currents

The control– and coordination hierarchy formed by super conductors represented by space-time sheets coupled to each other by join along boundaries bonds suggests new quantum level control mechanisms for genetic expression. Josephson currents at resonant frequencies corresponding to some magnetic transition of gene or its substructure could 'wake-up' the gene self and initiate the self-organization process leading to the gene activity. Silencers and enhancers could correspond to proteins which have join along boundaries to larger space-time sheets serving as masters. This would explain why neither the exact position nor orientation of the silencer or enhancer is not important for their functioning.

Various genes and and associated control structures have mutual Josephson junctions controlling gene expression. This would mean the presence of extremely weak longitudinal electromagnetic fields (the potential differences over Josephson junctions would be in 10^{-14} eV range). The control mechanisms behind morphogenesis are poorly understood and phase gradients along chromosomes and along the growing organism could be involved with the control of morphogenesis. The fact that the rate of the translation process is about 20 aminoacids per seconds is in accordance with the idea that this process is controlled by a Josephson current associated with some ion having this frequency.

5.4.4 Model for the physical distinction between exons and introns

A priori one can imagine an endless number of possibilities for the physical realization of the binary digit distinguishing between exons and intron. The assumption that the basic picture deduced from the model of neural cognition combined with some empirical constraints however allows to fix the picture to a high degree.

Constraints on the identification of the physical distinction between exons and introns

Introns seem to begin with CT and end with TC: the assumption that this is the sole signature of the beginning of intron is however not consistent with the observation about the change of the roles of intron and exons. Furthermore, this criterion is obviously not sufficient for telling where intron begins and ends since also ordinary genes can contain similar section. This suggests that single bit of information completely analogous to a comment sign in front of the line of computer code, distinguishes between intronic and exonic nucleotides and the problem is to identify the physical representation for this bit. Subsequent physical considerations indeed suggest that exonic and intronic nucleotides are distinguished by different direction of magnetic or Z^0 magnetic field along chromosome.

There are several constraints on the comment sign mechanism defining the decomposition of the gene to exons and introns.

1. Comment signing should be copied automatically from DNA to mRNA and the splicing mechanism should also rely on the comment sign mechanism. This requires that the enzymes responsible for the splicing bind to introns only. For instance, binding probability could depend crucially on the direction of a magnetic or Z^0 magnetic field associated with the DNA.

2. Introns can start and end in the middle of DNA triplet. Total length of the intronic and exonic parts of gene must correspond to an integer multiple of DNA triplets. This suggests that there is some mechanism forcing exon and intron sections to contain integer multiple of DNA triplets.

3. The tranformations of genes involving transformation of exons and introns to each other are known to occur. This suggests that there is a physical mechanism, perhaps a pulse propagating along DNA sequence, changing the value of the comment sign.

Realization of the intron-exon distinction in terms of cognitive neutrino pairs

Hints concerning the possible realization of the marking mechanism comes from the model of EEG and nerve pulse and cognition realized in terms of cognitive neutrino pairs. The assumption that DNA is involved with our long term cognition suggests that the mechanism is basically the same and that the spin direction of the cognitive neutrino pairs basically tells whether intron or exon portion is in question.

1. The first observation is that chromosomes, having thickness equal to the cell membrane thickness, could correspond to defects of a neutrino super-conductor and contain cognitive neutrino pairs. DNA thread has molecular thickness of few Angstroms and winds around the nucleosomes having diameter $L(151)$. The naive expectation is that defects must correspond to DNA threads with a thickness of few Angstroms characterized by p-adic length scales $L(k = 139)$. This need not be however the case since many-sheeted space-time concept allows DNA threads to have thickness of, say, $L(149)$, (nucleosomes around which DNA thread winds correspond to $k = 149$ and have radius $L(149)$). This looks somewhat strange. There is however additional support for this identification. Many-sheeted space-time concept suggests a rather science fictive solution to the problem how DNA replication is possible on the surface of the nucleosome: since nearby portions of DNA thread do not correspond to same space-time sheet, the opening of DNA double strand can occur without any problems. In fact, the condition that cognitive antineutrino rest mass at $k = 149$ space-time sheet and negative Z^0 interaction energy of neutrino at $k = 169$ space-time sheet cancel each other for cognitive neutrino pair, allows only $k = 149$ option [33] .

2. Memes correspond to time like sequences of cognitive neutrino pairs such that the spin direction codes for a bit. Since genes correspond to space like sequences, this suggests that genes are accompanied by spatial sequences of cognitive neutrino pairs such that the spin direction of the cognitive antineutrino codes for whether given nucleotide is exon or intron. The DNA counterpart of the nerve pulse propagating along double DNA helix with a duration corresponding to the time scale defined by the spin flip frequency of the cognitive antineutrino would indeed give rise to the exon-intron transformation. The change of the roles of exons and introns has been indeed observed [142] and is only special case of the change of roles of introns and exons. Pulse could also be restricted to single intron or exon so that much more general modifications of the exon-intron structure are possible. Since DNA double strand forms binary structure similar to the double lipid layer structure of cell membrane, the pulse could be very much analogous to nerve pulse and be perhaps induced by propagating soliton of appropriate super-conductor [57] .

3. Cognitive antineutrinos, which have large Z^0 magnetic moment, serve as sources of an axial Z^0 magnetic field and the direction of this field depends on the direction of the spin of the antineutrino. If cognitive antineutrinos are the only sources of axial Z^0 magnetic field (also wormhole contacts could serve as sources), then introns and exons carry Z^0 magnetic of opposite sign. The direction of the Z^0 magnetic field, which is rather strong by the quantization of Z^0 magnetic flux and by the large value of the Z^0 magnetic moment of neutrino, would serve as a physical marker of exon and intron sections of the gene and thus signify the presence/absence of the comment sign.

4. Z^0 magnetization induces also nuclear Z^0 magnetization of DNA nucleotides. Nitrogen and phosphor nuclei possess odd number of neutrons and presumably have Z^0 magnetic moment so that they can indeed suffer spontaneous Z^0 magnetization. The interaction energy is however by 7 orders smaller than for neutrinos at $k = 151$ space-time sheet so that cognitive neutrinos would serve as the masters of the dynamics. Note that Z^0 magnetization induces ordinary magnetization but due to the large mass of nucleons the magnetization is by the ratio $m_p/m(\nu, 149) \sim 10^{-7}$ smaller than Z^0 magnetization, which would mean that magnetic field would be about 10^{-7} Tesla for chromosomal Z^0 magnetic field of order Tesla.

5. Flux quantization for the strength of the Z^0 magnetic field associated with the micro-tubular surface gives idea about the neutrino density per unit length needed assuming that cognitive antineutrinos serve as the source of the Z^0 magnetic field. The conditions

$$g_Z B_Z 2q_Z(\nu) = \frac{m\times 2\pi}{S} \quad , m = 0, 1, 2, \cdots \quad ,$$

$$g_Z B_Z = \frac{1}{4\pi} g_Z \frac{\mu_Z(tot)}{V} = \frac{1}{4\pi} g_Z \frac{dN(\nu)}{dL} \frac{1}{S} \frac{g_Z Q_Z(\nu)}{2m(\nu,k)}$$

give

$$\frac{dN(\nu)}{dL} = \frac{m\times 4\pi}{\alpha_Z} m(\nu, k) \quad ,$$

$$\alpha_Z = \frac{\alpha}{sin(\theta_W)cos(\theta_W)} \quad , \quad \alpha \simeq \frac{1}{137} \quad , \quad sin^2(\theta_W) \simeq .23 \quad .$$

Using the values of the fine structure constant and Weinberg angle, one obtains the estimate for the number of cognitive antineutrinos per Angstrom for the minimal value of the Z^0 magnetic field. If DNA space-time sheet carrying cognitive antineutrinos has thickness of DNA thread of about 2.5 Angstroms, the criterion would give linear density of 64×21 antineutrinos per Angstrom, which is nonsensible and the only possibility would be that Z^0 magnetic field is wormhole magnetic field having Z^0 wormholes as sources [84] . If DNA thread has radius $L(149)$, there are $k = 42$ cognitive antineutrinos per Angstrom, which looks rather reasonable. The rather large number of cognitive antineutrinos means that DNA molecules can be regarded as Z^0 magnetized objects. This means that spin flip for cognitive antineutrinos must be a phase transition like process.

6. One could also consider the possibility of ordinary magnetization controlled by electrons having mass by 3 orders of magnitude smaller than proton mass. The objection against this model is that presence of ordinary magnetization of DNA would presumably have been observed.

What forces exons to contain integer multiple of 3 nucleotides?

One should also understand the physical mechanism forcing the lengths of the intron and exon sections to be integer multiples of three nucleotides. A possible mechanism is based on the existence of a phase gradient along the intron such that the increment of the phase Φ corresponds to an integer multiple of $\Delta\Phi = n2\pi$ for introns and possibly exons and even DNA triplets.

1. For arbitrary value of $\Delta\phi$, splicing process would not be possible since the phase associated with the resulting DNA sequence would be discontinuous at the point where exonic portions of the gene are glued together. If the phase gradient along intron and exon is such that it increases by 2π along single DNA triplet, the condition is achieved automatically if intron and exon consist of integer multiple of DNA triplets. The phase gradient could correspond to the phase difference associated with the weakly coupled super conductors formed by the two DNA strands or the phases of the supra currents flowing in DNA strands.

2. An attractive possibility is that the phase gradient is related with the helical structure of DNA double helix: the mimimum number of DNA triplets giving rise to a multiple of 2π rotation of the helix is 10 and corresponds to the p-adic length scale $L(151)$ defining the thicnkess of the cell membrane. The helix can be characterized by the tangent vector of helix having axial and azimutal components:

$$K = (1, \frac{d\phi}{dz}) = (1, 10 \times 2\pi) \times \frac{1}{L(151)} \quad .$$

The phase gradient would be naturally a multiple of this vector

$$\frac{d\Phi}{dz} = nK \quad .$$

For $n = 10$ the increase of Φ would be 2π per single DNA triplet. For $n = 1$, $n = 2$, $n = 5$ and $n = 10$ the allowed lengths would come in multiples of periods 10, 5 and 2 and 1 DNA triplets respectively. Note that 5 triplets corresponds to the p-adic length scale $L(149)$ associated with the lipid layer of the cell membrane. The presence of this gradient would naturally define the splitting of the nucleotide sequence to DNA triplets and might be important in the dynamics of DNA translation and transcription.

Does DNA level contribute to our consciousness

The splitting of Z^0 wormhole contacts yields cognitive neutrino pairs and the annihilation of cognitive neutrino pairs to Z^0 wormholes are in fundamental role in TGD based model of cognition. Boolean thoughts are identifed as the fermionic Boolean algebra defined by the Fock states of the cognitive neutrinos [33] . The model for intron-exon transformation in terms of cognititive neutrinos has very close relationship with the model of cognition at neural level: this suggests that the contents of our

consciousness could have direct coupling to DNA expression. Each intron/exon section of gene could perhaps be identified as a value of single Boolean statement such that the direction of the spin of the cognitive antineutrinos determined by the direction of the spontaneous Z^0 magnetization tells the truth value of the statement in question.

This suggest that some part of neuronal genome, whose dynamics is slow as compared to neural dynamics but consistent with the slow dynamics of the belief system as required, stores information, not only about the physical structure of organism, but also about our belief structures, intentions and long term goals. These beliefs become conscious when gene is activated, perhaps by neural activity: neural transmission is indeed known to induce effects at gene level. The statements represented by genes would correspond directly to our conscious beliefs at various levels of the space-time sheet hierarchy! Perhaps the memetic codewords consisting of the temporal sequences of 126 cognitive neutrino pairs at the level of cell membrane could have interpretation as bit sequences representing integers in the range $(1, 2^{126})$ and genuine Boolean thought resides basically at the genome level.

This mechanism becomes possible only at p-adic length scales longer than $L(169)$ since neutrinos suffer primary topological condensation at this space-time sheet. Therefore the emergence of genes with a total length larger than $L(169)$ should correspond to the emergence of the eukaryotes, introns and Boolean consciousness. Thus only some large enough bacteria (at least Fischerella) can have cognitive abilities. The absence of mitochondrial introns is probably due to the short length of the mitochondrial genes. The mitochondrial DNA of fungi is known to contain introns and the reason is perhaps that the length of DNA is longer than the critical length. Obviously, the proposed scenario implies a relationship between DNA level and logical thinking and partial reduction of language structures to DNA level.

In this picture genome is a collection of genes which can be regarded as Boolean algebras. Prokaryotes would represent only $B(1)$ algebra and only single statement would be associated with gene: the only possible conscious experience associated with gene statement would be experience about the truthness of the corresponding statements. Higher level Boolean mind realized as Boolean algebras $B(N)$, $N > 1$ are present only in eukaryotes since only their DNA can have Z^0 wormhole contacts to space-times sheets $k \geq 169$. Also the genes associated with cell organelles corresponds almost as a rule to the smallest possible Boolean algebra.

5.4.5 Are the properties of the introns consistent with the proposed model?

The proposed interpretation of introns is consistent with the basic facts about introns.

1. It has been found that the precise positions of introns in gene does not seem to affect gene expression. Introns can start in the middle of protein building block or even in the middle of codeword. The content of intron DNA does not correlate with the content of protein DNA. This is just what the model predicts. Introns are known to wander around genome and between cells. One could interpret their presence as some kind of experimentation with small modifications of the genetic program. An interesting question is how much intron distribution affects genetic during the evolution of individual and how large the differences between members of species are. The addition of intron to the gene does not in general have any dramatic consequences. This can be understood if I does not represent input of the program modules activated by already existing intron proteins. Addition of intron only leads to a more flexible organism.

2. In the proposed picture the evolutionary step leading from prokaryotes to eukaryotes was the emergence of the introns and gene programs having also intronic mRNA as output. This was perhaps necessitated by the emergence of the cell nucleus since introns were needed as input by the genetic program transferring mRNA out of nucleus. The emergence of the cell nucleus as $L(163)$ structure could in principle have occurred already for a cell of size $L(k) = 167$. It seems that in cells of animals the size of the nucleus corresponds to $L(163)$ or perhaps even $L(167)$. Cell nucleus is however not all that is needed for the emergence of introns: the model requires the presence of $k = 169$ level in the hierarchy.

3. What is beautiful is that homing [140] and retrohoming [123] phenomena can be regarded as modification of the genetic program in a manner which is automatically internally consistent! The addition of intron or new exon does not spoil the running of the genetic program. One can quite well consider the possibility that organisms are continually experimenting with various

modifications of genetic program. It might even be that homing and retrohoming phenomena make possible the evolution of the genetic program during the lifetime of individual.

Also the situation in which intron correspond to the entire protein is possible. This means that mRNA binds with protein and remains remains inside nucleus in the first case whereas it leaves the nucleus in the second case. These genes might indeed appear in cells. On the other hand, since these genes do not activate other genes and are thus dead ends of gene expression, selection could lead to a situation in which these genes themselves are not activated. Part of silent DNA could correspond to purely intronic genes.

1. Histones form the basic protein building block of chromosomes. Histone genes are known to contain no introns. The interpretation is that the gene coding histone is in exon state permanently. If histone genes contained intron parts, histones could act as repressor genes and regulate gene activity. Since histones appear as building block proteins of nucleosomes of chromosomes, this would mean that hardware could become software: obviously a highly undesired situation. Second consequence would be that the basic hardware for transcription could change: this could have catastrophic consequences. Also interferons are known to have no introns. The explanation might be similar. This explains also why the DNA of mitochondria contains no introns.

2. It is known that the pseudogenes obtained by splitting the introns are not active. For instance, the mRNA coded by gene is left inside the nucleus. One can imagine at least two manners to understand this. The first possibility is that the gene in purely intronic state and when active, products only mRNA-protein complexes left inside teh nucleus. There is also a second mechanism involved in case that gene is pure exonic state. The intronic output of gene module represents either statements I_k which are not true or have ill defined truth value. This means that the subsequent behavior of the genetic program is dramatically changed. In particular, the program module taking care that mRNA is taken out of nucleus, is not started.

5.4.6 The phenomenon of superimposed genes

Before the discovery of the structure of the genome of $\phi X174$, it was thought that the Central Dogma is absolute truth. It has however turned out that genes within genes and even overlapping genes are possible [110] . Bacteriophage $\phi X174$, which is virus with single stranded circular DNA, contains two genes, denoted by A and D, containing genes B and E within them. A gene contains also gene A^* which starts in the middle of A and ends in the same codeword. Also the translation of a gene overlapping with A and gene C next to it have been observed in G4 bacteriophage having genome very similar to that of $\phi 174$.

To understand how the translation of mRNA can give rise to genes inside genes, one is forced to introduce the notion of reading frame shift. This concept is somewhat ad hoc since it requires that the translation of a gene within gene does not obey the usual rules since reading is stopped without stopping sign.

The geometric realization of the subprogram structure might make possible to understand gene superimposition.

1. Geometrically gene would a linear model for its expression domain obtained by thinning it to DNA thread. Two subsequent genes G_1 and G_2 are like two subsequent body parts. If gene superposition occurs, there is third body part having overlap with both and "glued" to both: kind of joint connecting two body parts.

2. These 'body parts' represent subprograms. Transcription generates protein which refers to some other program module realized as body part. If the requirement that each body part generates program call to existing body part, is satisfied, then gene superimposition is possible. This requirement is actually very natural consistency condition. That our body is full of this kind of joints would suggest that gene superposition is a general phenomenon.

A concrete model is obtained in terms of many-sheeted DNA and many-sheeted versions of various RNA:s using the intuition provided by the TGD based model of intron-exon transformation.

1. An obvious idea is to generalize the idea about the direction of chromosomal Z^0 magnetic field as indicator for whether nucleotide corresponds to intron or exon. Of course, Z^0 magnetic fields are not possible since entire genome of $\phi X174$ consisting of 5386 nucleotides which corresponds to a total DNA length about 1.8 micro-meters far below $L(169)$. Thus ordinary magnetic field must be in question. Magnetic field could be generated by magnetized electrons.

2. Gene can have sub-genes, which correspond to various space-time sheets. Ribosome which acts on mRNA must somehow know the beginning and the end of the gene or sub-gene. Magnetic field indeed makes this discrimination possible and can also serve as indicator whether given space-time sheet corresponds to intronic or exonic DNA. Magnetic fields can reside on several space-time sheets and in general gene can decompose to gene and set of nested sub-genes corresponding to em charged wormhole to various space-time sheets.

There are reasons to hope that this model could explain the peculiarities related to the translation of $\phi X174$ genes since mRNA can contain several nested genes. This picture seems to require that stopping sign RNA:s are interpreted as stopping signs only in case of "main gene".

5.4.7 About genetic evolution

The proposed general model of genetic program provides nontrivial insights to evolution of genome.

ORP and the structure of the genetic program

An interesting question is whether "ontogeny recapitulates phylogeny" principle in its original form (to be distinguished by its TGD based analog applying much more generally) could give nontrivial constraints on the structure of the genetic program.

1. One could argue that the structure of the genetic program must reflect its evolution. In the beginning of development only the lowest level genes are activated and in turn activate more evolved genes which in turn $\cdots$. The gradual emergence of new hierarchy levels would have interpretation as emergence of new abstraction levels: statements about statements about... are formed. These levels correspond to emergence of higher level selves having more abstracted experiences about the state of organism or its organs.

2. One can also defend quite different point of view. The evolution starts from simple main program corresponding to, say the length scale of a fertilized egg. Gradually subprograms corresponding to the emergence of smaller length scale structures are activated. In growth stage simple replication of the basic structure together with the activation of the lower level programs giving rise to differentiation occurs. This leads to join along boundaries condensates of the fundamental expression domains having some finite size determined by the metabolic resources available and by self-organization. In fact, the general structure of embryogenesis supports this view.

3. Option 2) suggests that genetic program modules call only modules associated with shorter length scales so that higher levels cannot be activated by program call. If this is the case new levels should emerge when some space-time sheet associated with DNA expands in phase transition like manner and fuses with corresponding space-time sheets associated with neighboring cells. These phase transitions would represent the self-organization aspect of development.

4. Cell differentiation could be understood as resulting from the branching of genetic program in position dependent manner caused by diffusion gradients of transcription factors. For instance, these transcription factors would correspond to hormones which bind to receptors to form a complex binding to gene.

Homeostasis, loops, tautologies

If P then P is the simplest loop one can imagine and corresponds to a gene coding protein activating the gene itself. Biologically this represents endless cancer like growth limited only by lifetime of protein and resources and hence possible breakdown of the system! More complicated statement structures of this type represent n-fold tautologies: *If* P_1 *then* P_2 , *If* P_2 *then* P_3 ,..., *If* P_n *then* P_1 . These systems

are also self-amplifying and correspond to a cyclic reaction in which genes code enzymes activating other genes in the cycle.

This kind of cycles might be involved with the very early evolution of life. For instance, DNA-RNA-protein trinity might have developed from a situation in which RNA coded protein which catalyzed both the reverse transcription of RNA to DNA and transcription of DNA to RNA. Thus simplest life form would have represented tautology *If P then P*! Reverse transcription such that the reverse transcriptase also catalyzes transcription is indeed known to occur. Certain plant viruses contain inverse transcriptase synthetizing in infected cell DNA from its RNA and then DNA complementary to this. This double strand joins to the genome of the host cell and duplicates itself.

More complicated cycles involving several equivalent statements would have evolved gradually (note the parallel with the generation of mathematical theorems stating equivalence of statements!). Bacteria replicate endlessly and might perhaps be regarded as example of life form which corresponds to n-fold tautology.

The role of chromosomes

An interesting question is whether the organization of the genome to chromosomes could have some deeper organizational meaning. The fact that chromosome fusions and splittings are possible, suggests that chromosomes as a whole cannot have direct identification in terms of any body structure. Indeed, the realization of genetic program in terms of protein concentrations representing inputs and outputs of genes interpreted as subprograms is very flexible as far as the location of gene subprograms is considered. Only genes which form larger program structures should form geometrically connected units and the relative locations of these units could be rather free. As already found, genes seem indeed form clear geometrical subunits.

Chromosomes could be identified as a set of mutually interacting parallely running genetic programs. One can of course consider the possibility that chromosomes mean the composition of body part to N_c linear structures, N_c being the number of chromosome pairs. Parallel interacting processing would bind these structures to single coherent hole. This division to N_c parts should be detectable at all levels of body organization. One can also consider the possibility is that the structure of chromosome parallels the structure of body and that centrosome corresponds in some sense to the brains of chromosome and the branches of chromosome correspond to right and left halves of the body. Genetic programs associated with different chromosomes are known to run in very precise synchrony. Many -sheeted DNA could explain this synchrony naturally as resulting from the interaction of genes with with classical em fields with space-time sheet containing the chromosomes.

The table below gives chromosome numbers for some animals. For the home fly the number of chromosome pairs is 6 whereas the number of the p-adic hierarchy levels determined by the size of the home fly is 12. For fruit fly the number of chromose pairs is 4. Horse has 32 pairs of chromosomes and dog has 39 pairs of chromosomes whereas Homo sapiens has 23 chromosomes. The large number of chromosomes can be understand as a manner to produce large number of outcomes in breeding. The number of possible combinations of chromosomes in sexual breeding is 2^{N_c}, 2^{16} more than in case of Homo Sapiens. There are indeed very many different looking dogs barking around! The number of chromosomes varies wildly. For instance, the number of chromosomes in Harpalinae is $18+x$ [40] ! The size of this insect is about one centimeter.

Animal	Man	Chimpanzee	Cow	Dog	Cat
N_c	23	24	30	39	19
Animal	Horse	Rat	Rabbit	Alligator	Frog
N_c	32	21	22	16	13
Animal	House fly	Fruit fly	Honeybee	Flatworm	Harpalinae
N_c	6	4	16	8	$18+x$

Table 3. Chromosome numbers for some species.

The natural expectation is that the size of chromosomes has gradually grown during evolution when new p-adic space-time sheets have emerged. This process could correspond to insertion of introns to the basic DNA. The possibility coming first in mind is that the value of k_G in genes of given chromosome tends to increase as a function of the distance from the second end of gene. Genetic program realized in terms of many-sheeted space-time concept does not however require this. The

genes involved in the coding the structure of given body part are known to be linearly arranged according to the structure of body part itself. This is certainly consistent with TGD picture in which body parts grow from space-time sheets associated with DNA. It seems that the highest activated space-time sheets in genes must correspond to brain, in particular frontal lobes, in case of human. This would suggest that also in chromosome the largest active length scales correspond to the region around centrosome.

p-Adic evolution of DNA

p-Adic evolution should involve two aspects.

1. The increase of the p-adic length scale characterizing the basic DNA modules. This suggest the classification of the basic building blocks of the genome by the p-adic length scale associated with the corresponding DNA sequences.

2. The fractal evolution involving emergence of longer p-adic length scales characterizing the size of the space-time sheets to which basic DNA sequences had # contacts. Thus the lengths of introns and exons are not expected to correlate with the p-adic scale of the space-time sheet to which they possibly have # contacts. Rather, same gene can have # contacts to arbitrarily large space-time sheets.

Consider first the critical lengths of the basic program modules. The lengths $L(149), L(151), L(157), ...$ of gene or DNA sequence might mean the emergence of something genuinely new in the evolution. This length scale hierarchy expressed in terms of $L(137)$ comes in powers of 2 as $N_{137} = 1, 2, 64, 128, 2^{10}, 2^{13}, 2^{15}, ...$

Single nucleotide pair corresponds to in double helix to distance of .34 nanometers which is larger than the length scale of $L(139)$. The structure of the double helix is such that there is a periodicity of 3.4 nanometers: this means that basic period corresponds to 10 nucleotides. This implies that 5 DNA triplets correspond to a length of 5.05 nanometers, which equals to p-adic length scale $L(149)$ if $L(151)$ is defined to be $L(151) = 10.2$ nm. $L(149)$ corresponds to the thickness of the lipid layer of cell membrane and $L(151)$ corresponds to 10 DNA triplets, to the thickness of the cell membrane and the basic period of DNA sequence when DNA triplet is regarded as a basic unit. Perhaps this periodicity is not accident but has deeper meaning possibly related to the periodicity of phase variable associated with DNA. The lengths of DNA sequences corresponding to p-adic length scale $L(k)$, $p \simeq k$, k power of prime are $N(DNA) = 2^{k-149} \times 5$ DNA triplets.

This means that the critical numbers of DNA triplets possible leading to the emergence of qualitatively new properties of organism are given by

$$\begin{aligned} N(DNA) &= 2^{(k-149)/2} \times 5 \ , \\ k &\in \{149, 151, 157, 163, 167, 169, 174, 179, 181, 191, 193, ..\} \end{aligned} \tag{5.4.1}$$

The few lowest critical values of DNA triplets in gene are

$$N(DNA) = n \times 5 \ ,$$
$$n = 1, 2, 2^4 = 16, 2^7 = 128, 2^9 = 512, 2^{10} = 1024, 2^{12}, 2^{15}, 2^{16}, \cdots$$

The steps of this hierarchy resembles bring in mind the evolution for the length of the basic memory unit of computer memory! One must however notice that 5 DNA triplets seems to serve as a basic unit.

The emergence of new p-adic length scales could have meant emergence of new levels of modularization in the genetic program and it is interesting to look these numbers from this point of view.

1. One could think that short sequences of precursors of DNA, mRNA and tRNA molecules were generated spontaneously by self-assemly. This implied automatically the generation of aminoacids by the more primitive counterparts of transcription and translation processes. The lengths of DNA molecules began gradually grow and at the critical lengths of DNA corresponding to p-adic length scales dramatic new effects emerged. Also new space-time sheets emerged in the genome and the first guess is that this occurred for the critical sizes of the organism given by p-adic length scales.

2. Formation of lipid layers might have been the revolution occurring at this stage and since lipids should have had size of order $L(149)$. This revolution should have occurred when the length of the genome became longer than 5 DNA triplets and meant formation of lipid layers by self organization process known to occur in all liquid crystals: these layers were perhaps formed in the surface of water such that hydrophobic ends of proteins would have pointed out of water. Self organization presumably led simultaneously to the formation of double membranes having thickness $L(151)$ such that the hydrophobic ends of proteins pointed in the interior of the double membrane. Second revolution became possible when the number of DNA triplets became larger than 10 triplets so that proteins connecting cell interior of the double membrane to its exterior became possible and the control of ion concentrations became in principle possible. Transfer RNA (tRNA) has length of at most 27 triplets. Third revolution should have occurred $L(157)$, which corresponds to 80 triplets.

3. Smallest viruses possessing single strand of DNA have lengths between 15-100 nanometers and this suggest that genome correspond to p-adic length scales $L(149)$, $L(151)$ and $L(157)$. These length scales could characterize largest space-time sheets also present in genome. The building blocks of the envelope of viruses are genetically coded separately and self-assemble spontaneously so that only building blocks need to be coded. Therefore p-adic prime associated with the genome of virus could be smaller than that determined by the size of the virus. Viruses with two DNA strands have sizes between $250 - 1000$ nanometers. This suggest that the emergence of $k = 163$ length scale in the genome of virus was accompanied by the emergence of double stranded DNA. $k = 163$ is perhaps the largest p-adic length scale associated with virus genome.

4. Bacteria have typically sizes of $1 - 10$ micro-meters. This suggests that $k = 163, 167, 169$ are the possible space-time sheets associated with the bacterial genome. The emergence of $k = 169$ could have meant the emergence of multicellulars and generation of epithelial sheet like structure consisting of two cell layers as well as emergence of introns and DNA cognition.

Consider now the typical lengths for the structures of the eukaryotic genome.

1. The presence of introns means that the length of a gene coding given protein plus introns is much longer than the DNA coding only the protein. The higher the evolutionary level of species, the larger the fraction of introns. For human genome the fraction of exons is roughly 1 per cent. The typical length of hnRNA in nucleus is 6.000-8.000 np (nucleotide pairs) which corresponds to 18 micro-meters and length scale $L(163)$ and $L(167)$. Even genes with length 20.000 np are possible and correspond to $L(169)$. The lengths of mRNA vary between 500-3.000 nucleotides corresponding to interval 1.7×10^{-7}-10^{-6} meters and length scales $L(157)$ and $L(163)$. RNA sequences coding typical protein consisting of roughly 300 amino acids are about 3×10^{-7} meters and correspond to $L(159)$.

2. Most of the highly repetitive DNA has rather short length between $5 - 300$ nucleotides. Introns having typically lengths between $10 - 1000$ nucleotide pairs. The length of ribosomal DNA is not longer than 10^3 nucleotides. These examples suggests that the basic program modules correspond to p-adic length scales between $L(139)$ and $L(157)$ and that introns and genes are built as fractal versions of the basic program modules possibly present in all plants and animals. The basic programs are chemically identical. They could however have wormhole contacts to increasingly larger space-time sheets so that organism possesses fractal like structural hierarchy. Alternatively, the contacts are on space-time sheets with same p in all animals but the sizes of the join along boundaries condensates formed by fundamental expression domains depend on organism. The frequent occurrence of Hox genes in the genetic code of body parts of various sizes in the entire animal kingdom is consistent with both options.

5.4.8 Possible explanations of the silent DNA

Genome contains large amounts of silent DNA which is not transcribed. One can consider several explanations of silent DNA in TGD framework.

1. Each gene consists of a transcribed part and control part contained in region between gene and its predecessor. It might be that highly repetitive DNA located near the centromere corresponds

actually to a control part of DNA and is therefore not transcribed. Enhancers and silencers could be in question and they could have contacts to larger space-time sheets and take care of the control in long length scale enhancing or silencing a large number of genes simultaneously.

2. Genome can be regarded as a large collection of program modules calling each other. Large programs typically contain a great number of modules not used by the average user. There is also a larger number of program modules whose output is not visible to the user. Silent DNA could correspond to program modules of this kind. The counterpart of unused program modules are genes which are permanently repressed. This kind of permanent repression certainly occurs during differentiation and most of DNA in given part of organism is this kind of DNA.

3. Silent DNA could also correspond to purely intronic genes which correspond to dead ends of the genetic program and are decoupled from genetic program by selection.

4. The most radical possibility is that silent DNA corresponds to genes which are expressed non-chemically and corresponding control regions affected by nonchemical transcription factors. A possible test for the existence of nonchemical gene expression is to modify the silent part of, say, neural genome and find whether and how this affects the behavior of the organism.

5.5 TGD inspired ideas about the regulation of morphogenesis

The understanding of morphogenesis provides a challenge for the TGD inspired notion of the many-sheeted DNA. The difficult task is to separate chemistry from geometry and identify those features of morphogenesis necessitating the concept of the many-sheeted DNA. Also the role of quantum control mechanisms must be understood. In the sequel general ideas about the quantum control of morphogenesis are discussedand a very brief review about the morphogenesis in Drosophila is given to provide bird's eye of view about genetic control. Also Hox genes and TGD based model for Hox genes is discussed.

5.5.1 Biological alarm clocks and morphogenesis

Gene expression is known to involve nonchemical transcription factors (enhancers silencers), whose underlying interaction mechanism is not not known. TGD suggest an extremely general mechanism of quantum control and coordination based on Josephson currents flowing between space-time sheets representing various levels of the biological self-hierarchy [52, 53] . Josephson currents themselves act as clocks. In case that the potential difference over Josephson junction corresponds to the difference of the energies for the states of charge carriers localized inside either super conductor, Josephson current 'wakes-up' 'clock self' and initiates self-organization process. Therefore alarm clock is in question. Besides clocks and alarm clocks one can build pattern recognizers and novelty detectors and these circuits could serve as building bricks of complicated Boolean circuits controlling the functioning of living systems and also morphogenesis. Potential differences between gene space-time sheets and some larger space-time sheets, such as growing organs serving as the controllers of the gene expresion, would act as transcription factors in the sense that suitable input supra-current would 'wake-up' gene self and activate self-organization process leading to gene expression.

Some examples are in order to show that this idea might have relevance.

1. The replication of the cell is an extremely complicated process but could be understood as quantum self-organization process leading to final state patter which only very mildly depends on the initial state. This process must be initiated by a 'wake-up' self representing perhaps the cell. The alarm clocks must now be contained to the membrane surrounding the cell nucleus and probably also to the cell membrane since the cell membrane is known to be coupled to the division process of the cell nucleus, too [208] . The reference currents are generated, when the new cell is born. The process leading to the replication of the cell involves a reduction in the density of super conducting charge carriers in the critical region and this could initiate the replication of the cell. This is achieved if Josephson currents run away from certain region of the membrane of the cell nucleus implying depletion of charge carriers.

2. The generation of completely new spatial structures during the morphogenesis is second extremely complicated process which should be understandable in terms of quantum self-organization. An example is afforded by the generation of somites [39] , which later give rise to brain and spinal cord. The homogenous longitudinal cell mass divides in a phase transition like manner into somites with clock wise regularity and the number of the somites is a constant characteristic for the species in question [39] . The catastrophe theoretic models proposed in [39] are based on the assumption that the pulse triggering the formation of somites is coupled to a biological clock, so that the motion of the boundary between differentiated and undifferentiated cell mass alternately slows down or fastens up and implies the generation of discrete regions, where the formation of the somites takes place.

A qualitative TGD based description is provided by the alarm clock model:

1. There is certain biorhythm realized using Josephson junctions (rhythms (minute scale) of this kind have indeed been identified [39]) at cell level.

2. Josephson currents flow between the cells belonging to the longitudinal cell mass and neighboring cells in transversal direction. Due to the presence of the cell level reference currents, Josephson currents interfere destructively and variations in density of charge carriers are small.

3. There is slow dependence of the phase of the order parameter ψ along the linear cell mass implying a phase lag between the clocks.

4. Reference current dissipates gradually through phase slippages and when the time is ripe the amplitude of the Josephson current becomes large and makes the density of charge carriers small inside the longitudinal region. The formation of the somites begins since the stability criterion implies that the stable size of topological field quantum decreases.

5. Time regulation is achieved through the presence of the biological clock: nothing happens unless the phase of the clock is correct since Josephson current runs to a "wrong" direction.

6. The process begins from the cells, which were born first since the clocks associated with them were created first and propagates in the order, in which the cells were born. In fact, the spatial dependence of the phase of the order parameter might code this order. The spatial dependence of the phase means that the rate for the propagation of the somite formation varies with position and guarantees in this manner the formation of spatially separated structures (compare with clock wave front model of [39]). The number of the somites is just the multiple of 2π:s that the phase of the order parameter increases along the longitudinal cell mass.

5.5.2 Could vacuum quantum numbers control gene expression via Josephson currents

Controlled and synchronized gene expression is the most fundamental aspect of morphogenesis and implies surprising determinism of the development. When developing organism achieves certain level of development, certain gene activates. This requires feedback mechanism from long length scales of size of order organ to the gene level. In standard physics, the most plausible mechanisms are chemical. Whether this is the case is an unanswered question yet. In any case, it is very difficult to imagine how chemical concentrations which carry purely local information, could code information about the size of the organ and how the evolution could have led to a chemical kinetics initiating gene expression for critical values of the various chemical concentrations. The notions of many-sheeted space-time and general hypothesis about bio-control and coordination based on a hierarchy of weakly coupled super conductors provides a fresh and more promising approach to this process. This hypothesis is discussed in detail in [52, 53] .

Many-sheeted space-time concept suggests hierarchies of biological alarm clocks whose ringing induces ringing of some clocks at a lower level of hierarchy so that finally the alarm clock waking-up and activating definite gene, rings. One mechanism causing the ringing would be a situation in which the potential difference associated with the Josephson junction becomes equal to the energy difference for states associated with either super conductor: cyclotron resonance, which seems to be crucial for brain functioning and EEG, is basic example of this. This could at DNA level lead to the activation

of gene and start up of a self-organization process. One could imagine complicated circuits in which ringing would occur only provided all the required conditions are achieved.

The correlation of gene expression with the size of the growing organ could be achieved as follows. Topological field quanta are characterized by a handful of vacuum quantum numbers associated with the dependence of the phases of the two CP_2 complex coordinates ξ^i on space-time coordinates (Appendix). In particular, two frequency type quantum numbers emerges. If the potential difference corresponds to the difference of the vacuum frequencies ω_1 associated with the coupled super conductors and if ω_1 correlates with the size of the corresponding structures, the ringing of the clock occurs when the size difference is critical. If the first super conductor corresponds to some structure with a fixed size (say gene) and second super conductor corresponds to the growing organ, this mechanism could indeed initiate new kind of gene expression when the growing organ reaches critical size.

5.5.3 Early morphogenesis of Drosophila

During the last years the understanding about the regulation of morphogenesis has grown dramatically [156, 113] . For instance, in case of Drosophila (fruit fly) surprisingly detailed knowledge about the regulatory cascade occurring during embryogenesis exists. It is known that genetic program with 6 hierarchy levels is in action.

1. The so called maternal factors act before the onset of cellularization and lead to the segmentation of embryo. This cascade begins with the diffusion of transcription products of maternal-effect (coordinate-) genes from the anterior and posterior poles of the embryo during oögenesis. These genes define anterior-posterior polarization.

2. Maternal factors control the spatial pattern for the transcription of gap genes which are expressed in domains along the anterior to posterior axis of the embryo. Gap genes divide embryo to anterior, middle and posterior parts.

3. Gap genes regulate each other and the next set of genes in the hierarchy, pair-rule genes. These are expressed in 7 stripes of cells coresponding to every other segment.

4. At the next level of hierarchy are segment polarity genes, many of which are expressed in 14 segmentally repeated stripes. Segment polarity genes include also proteins other than transcription factors (i.e. secreted signaling molecules, receptors, kinases, etc.) and they mediate interactions between cells.

5. During cellular phase (blastula) hox genes controlling the formation of various body parts are expressed. The lowest level of the hierarchy is represented by tissue specific genes.

The expression domains of these genes are indeed two-dimensional slices in accordance with the idea that genes can be regarded as obtained by compressing the expression domain of gene to DNA thread. This principle might be realized quite generally in the sense that the expression domains of all genes expressed inside particular body part are also slices formed as join along boundaries condensates of fundamental expression domains whose size corresponds to some p-adic length scale.

5.5.4 Hox genes

The discovery of the universality of so called hox (homeo box) genes has been one of the great discoveries in genetics during last few years years [156, 113] . Surprisingly, animal species with widely different morphologies (hydra, flies, leeches, mouses and humans) seem to obey very similar body plan coded by hox genes. Hox genes contain highly conserved nucleotid sequence called homeobox coding protein consisting of 61 aminoacids (which corresponds to DNA length of about 61 nanometers which is slightly below $L(157)$). Hox genes are also known as "selector" genes because their expression within a region of the embryo causes its cells to select a particular route of morphogenetic development determined by detailed nuclotide content of Hox gene. Hox genes function by coding what are called transcription factor proteins: these proteins bind to and activate all downstream genes necessary for the production of, say leg. Hence hox gene for leg functions like a main program for the development of leg. Obviously, Hox genes provide a possibility to test and develop TGD based ideas about the coding and decoding of the morphology in terms of the many-sheeted DNA.

5.5.5 Evolution of Hox genes

The conserved nature of the homeobox sequence indicates that all Hox genes are homologous, having arisen by divergence from a common ancestral gene. Note however that the control parts of genetic program (promoter and operator regions at which various activating and repressing proteins bind) involved with Hox genes seem to vary widely. Second basic feature of hox genes is their clustering. The development of this clustering has been studied and it has been found that all animals species must have inherited their Hox genes from a common ancestor.

1. Already plants possess single homeobox unit in their hox gene. Doubling of the hox gene meant the emergence of a primitive head-body structure and thus of primitive animals (hydra, which are freshwater polypes, represent one studied example). Next step was doubling of this gene pair, which lead to the formation of nematode worms. The further doublings lead gradually to more complicated animals. For instance, beetle possesses 8 Hox genes, amphioxus, which is almost vertebrate, has 12 hox genes.

2. The next step in the evolution was the doubling of the entire chromosome containing Hox cluster. The next doubling led to vertebrates with four Hox clusters located in four chromosomes. Each cluster contains a subset of 13 nonhomologous Hox genes. These clusters are labelled as Hox-A, Hox-B, Hox-C, Hox-D. n:th gene in, say cluster A, is denoted by Hox-A-n, $n = 1, .., 13$. The homologous Hox genes in various chromosomes, Hox-A-n,...,Hox-D-n, whose number is never larger than four, form 13 groups called prologues. The maximum number of Hox genes is 52 but some of genes are missing. Each vertebrate has its own Hox-bode telling which Hox genes are absent and which are not. For instance, human 39 Hox genes.

Doubling of Hox clusters led to a more flexible gene expression since the conditions associated with gene statements involve protein outputs from all four Hox clusters. For instance, the condition in genetic program could have the form *IF [Hox-A-n or Hox-B-n] then...* This implies that the mutation of Hox gene in single cluster, which otherwise might be lethal, need not have any dramatic consequences. Doubling of the Hox cluster leads also to a multiplication of possible Hox patterns in breeding by a factor of 4 and hence to the large variation of the progeny, which is selective advantage. It is known that doublings of Hox clusters where followed by an emergence of large number of Hox-codes and only some of these codes have survived.

The presence of 4 Hox clusters in vertebrates could relate to four different tissue types corresponding to epithelial, connective, muscular and nervous tissues. Certainly this correspondence is not simply tissue-type $\leftrightarrow$ Hox cluster although there is some evidence that given Hox cluster dominates the expression of given tissue type under normal circumstances. For animals with 2 or 1 Hox clusters this kind of correspondence cannot hold true.

5.5.6 Characteristic features of Hox genes

The characteristic features related to the expression of Hox genes give clues as how many-sheeted DNA is expressed.

Posterior Hox genes dominate over anterior Hox genes

Posterior Hox genes dominate over more anterior genes. For instance, if posterior hox gene is removed to more anterior position the phenotype is more posterior. A simple illustrative example is based on a toy model of insect based on 3 Hox genes. The protein product of the Hox 1 gene instructs the formation of the head. The cells in the middle of body respond to both Hox1 and Hox2 genes. The protein product of Hox gene 2 is however believed to instruct the cells in this region not to not respond to Hox gene 1 so that Hox 2 genes determine the resulting structure. In the similar manner Hox 3 gene dominates over Hox 1 and Hox 2 genes in the tail part of the fictitious insect. Actually this picture is oversimplified but gives a good grasp of the idea.

This corresponds to a simple recursive control structure in genetic program.
P(n-1): IF protein coded by n:th Hox gene is the highest Hox protein present then DO B(n) ELSE DO P(n+1).
B(n): Form the n:th body part.

The problem is to understand how this control structure is realized. If Hox gene corresponds to program B(n) and does not serve as repressor of lower level Hox gene expression then it would seem that control structure must involve some "new genetics".

1. Hox genes select genetic programs. The mechanism of selection is based on attachment of the protein products to the control regions of corresponding genes could be such that gene program n is activated only if Hox proteins Hox-m $m \leq n$ are attached to the gene program.

2. One possibility involving introns in essential manner is that the activation of n:th Hox gene deactivates lower level Hox genes automatically. One possibility is that activation corresponds to the change of roles of introns and exons in Hox gene. Before activation Hox-n gene would be in "abnormal" state so that its intron parts would code protein. This protein could enhance the expression of the lower level Hox genes. After the activation this protein product would be absent and lower level Hox expression would not be enhanced anymore.

Hox expression domains are co-linear with the gene ordering inside Hox cluster

The development of embryo occurs in anterior to posterior (head to tail) direction. In all species hitherto examined, there is a strict correspondence between the ordering of the Hox genes inside clusters and the anterior boundaries of the expression domains along the head-tail axis of the developing embryo. Presence of the anterior boundary means that gene is not expressed above this boundary. The anterior boundaries of homologous genes in different clusters are same.

Establishment of Hox gene expression patterns in vertebrates

It is known that in vertebrates Hox gene expression patterns in developing embryo are established by waves propagating in posterior-anterior direction (tail to head). This means that there is also temporal co-linearity. Wave proceeds and ultimately stops at the anterior boundary of the expression domain. These anterior boundaries are characteristics of Hox genes and their ordering is the same as the ordering of Hox genes.

It is known that this pattern is not due to a forward spreading of cells. The presence of chemical signalling during the wave propagation is also excluded by the result of an experiment in which embryo was transversally sectioned [156] . What happened that the wave propagated through the sectioning. Of course, it could be that chemical concentration gradient has been formed in earlier stage of development.

5.5.7 TGD based model for Hox genes

The attempt to understand the known facts about Hox genes and their expression provides strong constraints on the general TGD based model of many-sheeted DNA and the results might be generalized to build more general models of gene expression during morphogenesis.

Hox cluster as a set of many-sheeted Hox genes?

Hox genes define division of developing embryo to slices of roughly same size. This suggests strongly that the largest space-time sheets associated with Hox genes correspond to the same p-adic prime $p \simeq 2^k$, k prime or power of prime. It could be that Hox genes are glued on same space-time sheet to form Hox cluster. Dominance of the posterior genes over anterior genes and spatial and temporal co-linearity reflect some kind of hierarchical ordering of Hox genes. This hierarchical ordering does not however seem to reflect the hierarchy of space-time sheets but gene program hierarchy.

Does activation of Hox gene involve a phase transition?

In vertebrates the activation of Hox genes occurs as a wave propagating from tail to head. A possible TGD based identification for the wave is as a phase transition leading to an expansion of a new space-time sheet associated with the many-sheeted Hox gene propagating in head to tail direction. This phase transition is determined solely by the internal state of the genome in given embryonic cell. In this phase transition the DNA space-time sheets would expand and join to form larger space-time sheet determining the size of the "imaginal disk" associated with the organ in question.

In Drosophila the length of DNA per single Hox gene plus its control region is about 10^{-5} meters. This suggests that the maximal space-time sheets of Hox genes correspond to $k = 173$, and that in activation this space-time sheet grows to its actual size. Of course, this growth could have occurred already in the segmentation stage. This would imply that the cells containing Hox genes are glued together by join along boundaries contacts to form larger space-time sheets which later grow to space-time sheets corresponding to various organs.

How to understand basic facts about Hox gene expression?

There are several aspects involved with Hox gene expression which one should understand.

1. Co-linearity.
   Somehow the activation of n:th Hox gene leads to the activation of n+1:th Hox gene independently of what the n+1:th gene is. One possibility is that there is transcription factor gradient along the Hox gene which grows with time and gradually activates Hox genes in linear order. Perhaps enhancer is in question. Second possibility is that many-sheeted nature of Hox genes is crucially involved. Suppose that activation of Hox gene involves expansion of the largest space-time sheet associated with Hox gene. If the expansion of the space-time sheet of n:th Hox gene is necessary condition for the expansion of n+1:th space-time sheet, co-linearity follows automatically. This looks natural if the expansion of the Hox gene space-time sheet proceeds slowly along the Hox cluster so that expanding space-time sheet of n:th Hox gene is glued with that of n+1:th Hox gene

   This picture explains automatically also why the relocation of the Hox gene to a more anterior position makes Hox expression more posterior. The anterior boundaries in Hox clusters located in different chromosomes are the same. This suggest that the control for the beginning of the Hox expression program is associated with the space-time sheet representing entire embryo. Control could involve classical field affecting acting via enhancer or silencer type transcription factors whose effect is known to be not purely chemical.

2. Temporal co-linearity.
   This is present in vertebrates but not in Drosophila. Chemical signalling between cells cannot explain temporal co-linearity and it must be due to the independent development of the cell genomes. The simplest explanation is that there is lag in the activation time for the genetic program activating Hox genes increasing monotonically as a function of the distance along the anterior-posterior axis. This dependence could be generated by a gradient of corresponding transcription factor concentration, perhaps created already in maternal period. This gradient should be generated by a DNA sequence located at the $5'$ end of the Hox cluster so that transcription factor in question must be repressor: activation takes place when the concentration is subcritical.

3. The presence of the anterior boundaries.
   The presence of the anterior boundaries is most naturally due to determination of cells occurred before the activation of Hox genes. Segmentation genes indeed force various segments to different branches of genetic program and it is quite plausible that the activation of the Hox genes depends on segment. What is needed that the Hox genes above anterior boundary are too far from criticality for the activation to occur. It is also possible that cells in anterior end of the embryo generate repressor concentration which gradually grows and shifts anterior boundary in posterior direction during morphogenesis. If the expansion of space-time sheets associated with Hox genes is responsible for activation, this expansion should stop at n:th gene in n:th expression domain. It is not clear why this should occur without the proposed mechanism.

4. Posterior prevalence.
   An explanation in terms of the control mechanisms of gene programs activated by Hox genes has been already considered. Second explanation for posterior prevalence is that the expansion of the space-time sheet associated with Hox genes to a single space-time sheet common to first n Hox genes somehow represses the expression of all Hox genes expect n:th one. Perhaps only the gene on the boundary of this space-time can be active.

Quantum model for the expression of Hox genes

There are too much unknown factors to allow a construction of a detailed quantum model for the situation. What however seems clear that the differences of the vacuum frequencies representing potential differences over Josephson junctions should effectively appear as transcription factors and control parameters. A quantum model possibly catching some aspects of Hox gene expression might involve at least the following assumptions.

1. Assume that genes along chromosome are characterized by vacuum frequencies ω_i. This frequency does not depend on gene but only on its position in the chromosome. This assumption guarantees spatial co-linearity. The dependence of the gene's vacuum frequency on the position of gene along the chromosome could be understood if chromosome forms linear join along boundaries condensate with Josephson junctions connecting subsequent gene space-time sheets. This would mean that there is electric field along the chromosome. These Josephson junctions could be involved with the activation of the gene by the control DNA section preceding it. Also the effect of the enhancers and silencers might involve resonant Josephson current between control section of DNA and gene leading to the wake-up of the gene.

2. The vacuum frequency Ω characterizing the size of the growing organism increases with time and Ω changes in a phase transition like manner step by step. Temporal co-linearity can be understood if there is some (possibly phase) gradient along the growing organism implying that the phase transition leading to the increase of Ω proceeds from tail to head. The gradient could act like a concentration of a chemical suppressor decreasing in head-to tail direction and established already before the Hox gene expression started.

3. The space-time sheet of the organism and gene space-time sheets form weakly coupled super conductors and potential differences over the Josephson junctions serve as transcription factors. When the frequency $\Omega - \omega_i$, which corresponds to potential difference eV, equals to critical frequency, resonant currents are generated waking-up i:th gene and activating it. Given gene is active only during the time interval when $\Omega - \omega_i$ is critical. With the assumed dependence of ω_i on the position of gene, this implies spatial co-linearity and posterior prevalence.

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Chapter 6

DNA as Topological Quantum Computer

6.1 Introduction

Large values of Planck constant makes possible all kinds of quantum computations [3, 11, 8, 26] . What makes topological quantum computation (tqc) [21, 23, 16, 20, 17] so attractive is that the computational operations are very robust and there are hopes that external perturbations do not spoil the quantum coherence in this case. The basic problem is how to create, detect, and control the dark matter with large $\hbar$. The natural looking strategy would be to assume that living matter, say a system consisting of DNA and cell membranes, performs tqc and to look for consequences.

There are many questions. How the tqc could be performed? Does tqc hypothesis might allow to understand the structure of living cell at a deeper level? What does this hypothesis predict about DNA itself? One of the challenges is to fuse the vision about living system as a conscious hologram with the DNA as tqc vision. The experimental findings of Peter Gariaev [147, 192] might provide a breakthrough in this respect. In particular, the very simple experiment in which one irradiates DNA sample using ordinary light in UV-IR range and photographs the scattered light seems to allow an interpretation as providing a photograph of magnetic flux tubes containing dark matter. If this is really the case, then the bottle neck problem of how to make dark matter visible and how to manipulate it would have been resolved in principle. The experiment of Gariaev and collaborators [192] also show that the photographs are obtained only in the presence of DNA sample. This leaves open the question whether the magnetic flux tubes associated with instruments are there in absence of DNA and only made visible by DNA or generated by the presence of DNA.

6.1.1 Basic ideas of tqc

The basic idea of topological quantum computation (tqc) is to code tqc programs to braiding patterns (analogous to linking and knotting). A nice metaphor for tqc is as dance. Dancing pattern in time direction defines the tqc program. This kind of patterns are defined by any objects moving around so that the Universe might be performing topological quantum computation like activities in all scales.

One assigns to the strands of the braid elementary particles. The S-matrix coding for tqc is determined by purely topological consideration as a representation for braiding operation. It is essential that the particles are in anyonic phase: this means in TGD framework that the value of Planck constant differs from its standard value. Tqc as any quantum computation halts in state function reduction which corresponds to the measurement of say spins of the particles involved.

As in the case of ordinary computers one can reduce the hardware to basic gates. The basic 2-gate is represented by a purely topological operation in which two neighboring braid strands are twisted by π. 1-particle gate corresponds to a phase multiplication of the quantum state associated with braid strand. This operation is not purely topological and requires large Planck constant to overcome the effects of thermal noise.

In TGD framework tqc differs somewhat from the ordinary one.

1. Zero energy ontology (ZEO) means that physical states decompose into pairs of positive and negative energy states at the "upper" and "lower" light-like boundaries boundaries of $CD \times CP_2$, where CD denotes causal diamond identified as the intersection of the future and past directed lightcones (in the sequel CD is used for $CD \times CP_2$ in order to make notations more elegant). Positive and negative energy states have opposite values of conserved quantum numbers. The interpretation is as an event, say particle scattering, in positive energy ontology. The time like entanglement coefficients define S-matrix, or rather M-matrix, and this matrix can be interpreted as coding for physical laws in the structure of physical state as quantum superposition of statements "A implies B" with A and B represented as positive and negative energy parts of quantum state. The halting of topological quantum computation would select this kind of statement.

2. The new view about quantum state as essentially 4-D notion implies that the outcome of tqc is expressed as a four-dimensional pattern at space-time sheet rather than as time=constant final state. All kinds of patterns would provide a representation of this kind. In particular, holograms formed by large $\hbar$ photons emitted by Josephson currents, including EEG as a special case, would define particular kind of representation of outcome.

6.1.2 Identification of hardware of tqc and tqc programs

One challenge is to identify the hardware of tqc and realization of tqc programs.

1. Living cell is an excellent candidate in this respect. The lipid layers of the cell membrane is 2-D liquid crystal and the 2-D motion of lipids would define naturally the braiding if the lipids are connected to DNA nucleotides. This motion might be induced by the self organization patterns of metabolically driven liquid flow in the vicinity of lipid layer both in interior and exterior of cell membrane and thus self-organization patters of the water flow would define the tqc programs.

2. This identification of braiding implies that tqc as dancing pattern is coded automatically to memory in the sense that lipids connected to nucleotides are like dancers whose feet are connected to the wall of the dancing hall define automatically space-like braiding as the threads connected to their feet get braided. This braiding would define universal memory realized not only as tissue memory but related also to water memory [29] .

3. It is natural to require that the genetic code is somehow represented as property of braids strands. This is achieved if strands are "colored" so that A,T,C,G correspond to four different "colors". This leads to the hypothesis that flux tubes assignable to nucleotides are wormhole magnetic flux tubes such that the ends of the two sheets carry quark and antiquark (*resp.* antiquark and quark) quantum numbers. This gives mapping A,T,C,G to u, u_c, d, d_c. These quarks are not ordinary quarks but their scaled variants predicted by the fractal hierarchy of color and electro-weak physics. Chiral selection in living matter could be explained by the hierarchy of weak physics. The findings of topologist Barbara Shipman about mathematical structure of honeybee dance led her to proposed that the color symmetries of quarks are in some mysterious manner involved with honeybee cognition and this model would justify her intuition [30] .

4. One should identify the representation of qubit. Ordinary spin is not optimal since the representation of 1-gates would require a modification of direction of magnetic field in turn requiring modification of direction of flux tubes. A more elegant representation is based on quark color which means effectively 3-valued logic: true, false, and undefined, also used in ordinary computers and is natural in a situation in which information is only partial. In this case 1-gates would correspond to color rotations for space-time sheets requiring no rotation of the magnetic field.

In this framework genes define the hardware of tqc rather than genetic programs. This means that the evolution takes place also at the level of tqc programs meaning that strict genetic determinism fails. There are also good reasons to believe that these tqc programs can be inherited to some degree. This could explain the huge differences between us and our cousins in spite of almost the identical genetic codes and explains also cultural evolution and the observation that our children seem to learn more easily those things that we have already learned [202] . It must be added that DNA as tqc paradigm seems to generalizedDNA, lipids, proteins, water molecules,... can have flux tubes connecting them

together and this is enough to generate braidings and tqc programs. Even water could be performing simple tqc or at least building memory representations based on braiding of flux tubes connecting water molecules.

6.1.3 How much tqc resembles ordinary computation?

If God made us to his own image one can ask whether we made computers images of ourselves in some respects. Taking this seriously one ends up asking whether facts familiar to us from ordinary computers and world wide web might have counterparts in DNA as tqc paradigm.

1. Can one identify program files as space-like braiding patterns. Can one differentiate between program files and data files?

2. In ordinary computers electromagnetic signalling is in key role. The vision about living matter as conscious holograms suggests that this is the case also now. In particular, the idea that entire biosphere forms a tqc web communicating electromagnetically information and control signals looks natural. Topological light rays (MEs) make possible precisely targeted communications with light velocity without any change in pulse shape. Gariaev's findings [147] that the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind of picture. Also the model of EEG in which the magnetic body controls the biological body also from astrophysical distances conforms with this picture.

3. The calling of computer programs by simply clicking the icon or typing the name of program followed by return is an extremely economic manner to initiate complex computer programs. This also means that one can construct arbitrarily complex combinations from given basic modules and call this complex by a single name if the modules are able to call each other. This kind of program call mechanism could be realized at the level of tqc by DNA. Since the intronic portion of genome increases with the evolutionary level and is about 98 per cent for humans, one can ask whether introns would contain representations for names of program modules. If so, introns would express themselves electromagnetically by transcribing the nucleotide to a temporal pattern of electromagnetic radiation activating desired subprogram call, presumably the conjugate of intronic portion as DNA sequence. A hierarchical sequence of subprogram calls proceeding downwards at intronic level and eventually activating the tqc program leading to gene expression is suggestive.

   [147] [147] has found that laser radiation scattering from given DNA activates only genomes which contain an address coded as temporal pattern for the direction of polarization plane. If flux tubes are super-conducting and there is strong parity breaking (chiral selection) then Faraday rotation for photons traveling through the wormhole flux tube code nucleotide to an angle characterizing the rotation of polarization plane. User id and password would be kind of immune system against externally induced gene expression.

4. Could nerve pulses establish only the connection between receiver and sender neurons as long magnetic flux tubes? Real communication would take place by electromagnetic signals along the flux tube, using topological light ray (ME) attached to flux tube, and by entanglement. Could neural transmitters specify which parts of genomes are in contact and thus serve as a kind of directory address inside the receiving genome?

6.1.4 Basic predictions of DNA as tqc hypothesis

DNA as tqc hypothesis leads to several testable predictions about DNA itself.

Anomalous em charge

The model for DNA as tqc assigns to flux tubes starting from DNA an anomalous em charge. This means that the total charge of DNA nucleotide using e as unit is $Q = -2+Q(q)$, where -2 is the charge of phosphate group and $Q(q) = -/+2/3, +/-1/3$ is the electromagnetic charge of quark associated with "upper" sheet of wormhole magnetic flux tube. If the phosphate group is not present one has

$Q = Q(q)$. In the presence of phosphate bonds the anomalous charge makes possible the coding of nucleotides to the rotation of angle of polarization plane resulting as photon travels along magnetic flux tube. The anomalous em charge should be visible as an anomalous voltage created by DNA. It would be relatively easy to test this prediction by using various kinds of DNA:s.

Does breaking of matter antimatter and isospin symmetries happen at the level of DNA and mRNA?

The nice feature of the model is that it allows to interpret the slightly broken A-G and T-C symmetries of genetic code with respect to the third nucleotide Z of codon XYZ in terms of the analog of strong isospin symmetry at quark level at wormhole magnetic flux tubes. Also matter-antimatter dichotomy has a chemical analog in the sense that if the letter Y of codon corresponds to quark u, d (antiquark u_c, d_c), the codon codes for hydrophobic (hydrophilic) aminoacid. It is also known that the first letter X of the codon codes for the reaction path leading from a precursor to an aminoacid. These facts play a key role in the model for code of protein folding and catalysis. The basic assumption generalizing base pairing for DNA nucleotides is that wormhole flux tubes can connect an aminoacid inside protein only to molecules (aminoacids, DNA, mRNA, or tRNA) for which Y letter is conjugate to that associated with the aminoacid. This means that the reduction of Planck constant leading to the shortening of the flux tube can bring only these aminoacids together so that only these molecules can find each other in biocatalysis: this would mean kind of code of bio-catalysis.

The fact that matter-antimatter and isospin symmetries are broken in Nature suggests that the same occurs at the level of DNA for quarks and anti-quarks coding for nucleotides. One would expect that genes and other parts of genome differ in the sense that the anomalous em charge, isospin, and net quark number (vanishes for matter antimatter symmetric situation) differ for them. From Wikipedia [209] one learns that there are rules about distribution of nucleotides which cannot be understood on basis of chemistry. The rules could be understood in terms of new physics. Chargaff's rules state that these symmetries hold true in one per cent approximation at the level of entire chromosomes. Szybalski's rules [209] state that they fail for genes. There is also a rule stating that in good approximation both strands contain the same portion of DNA transcribed to mRNA. This implies that at mRNA level the sign of matter antimatter asymmetry is always the same: this is analogous to the breaking of matter antimatter asymmetry in cosmology (only matter is observed).

It would be interesting to study systematically the breaking of these symmetries for a sufficiently large sample of genes and also other in parts of genome where a compensating symmetry breaking must occur. That the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind of picture. Also the model of EEG in which magnetic body controls biological body from astrophysical distances conforms with this picture.

6.2 Basic concepts and ideas

The following represents a brief overall view about the notions of quantum jump, unitary process described by unitary U-matrix between zero energy states having as its orthogonal rows M-matrices between positive and negative energy parts of zero energy states identifiable as counterpart of ordinary S-matrix and of Negentropy Maximization Principle (NMP) governing the dynamics of state function reduction cascade.

6.2.1 What happens in quantum jump?

Quantum jump involves U process and state function reduction cascade. Negentropy Maximization Principle implies second law for the standard view about state function reduction: second law states that the ensemble entropy increases by the randomness of the outcome of the state function reduction process. When negentropic entanglement possible in what might be called intersection of the real and various p-adic worlds is present the situation is not so clear. Before proceeding to consider the modification of the second law one must define more precisely what U process is.

The simplest view about quantum jump is as a unitary U-process followed by as a cascade of state function reductions proceeding from top to bottom. But what is the top?

1. In positive energy ontology it would be entire Universe. Quantum classical correspondence suggests that one should be able to assign to quantum jump a duration of geometric time. For this proposal this time is most naturally infinite.

2. The vision about fractal hierarchy of selves and quantum jumps together with ZEO suggests a more refined view about quantum jump in which. U-process and subsequence state function reduction cascade could occur independently for disjoint CDs. For a given CD the new sub-CDs (representing mental images of the corresponding self) can be created and old destroyed so that the only constraint would be that only disjoint CDs can perform quantum jumps independently. For this option the duration of geometric time assignable to the quantum jump would naturally correspond to the temporal distance between the tips of CD: p-adic length scale hypothesis and number theoretical vision suggest that this distance comes as an octave of CP_2 time scale (prime or integer multiple is the more general option). For infinitely large CD this would mean infinite duration. This picture is consistent with the TGD view about how the arrow of subjective time induces the arrow of geometric time [4] .

6.2.2 M-matrix

The unitary U-matrix characterizing the unitary process has as its rows orthogonal M-matrices characterized by in general non-unitarity M-matrices. M-matrix decomposes into a product of positive definite diagonal square roots of density matrix and unitary S-matrix measurent in particle physics experiment. M-matrix represents both the time-like entanglement between positive and negative energy parts of zero energy states with opposite quantum numbers and space-like entanglement for the positive and negative energy states.

Time-like and space-like entanglement in zero energy ontology

M-matrix for each summand is product of Hermitian square root of density matrix and unitary S-matrix multiplied by a square root of probability having interpretation as analog for Boltzmann weight or probability defined by density matrix (note that it is essential to have $Tr(Id) = 1$ for factors of type II_1. If factor of type I_∞ are present situation is more complex. This means that quantum computations are highly universal and M-matrices are characterized by the inclusion $\mathcal{N} \subset \mathcal{M}$ in each summand defining measurement resolution. Hermitian elements of $\mathcal{N}$ act as symmetries of M-matrix. The identification of the reducible entanglement characterized by Boltzmann weight like parameters in terms of thermal equilibrium would allow to interpret quantum theory as square root of thermodynamics.

If the entanglement probabilities defined by S-matrix and assignable to $\mathcal{N}$ rays do not belong to the algebraic extension used then a full state function reduction is prevented by NMP. Ff the generalized Boltzmann weights are also algebraic then also thermal entanglement is irreducible. In p-adic thermodynamics for Virasoro generator L_0 and using some cutoff for conformal weights the Boltzmann weights are rational numbers expressible using powers of p-adic prime p.

Effects of finite temperature

Usually finite temperature is seen as a problem for quantum computation. In TGD framework the effect of finite temperature is to replace zero energy states formed as pairs of positive and negative energy states with a superposition in which energy varies.

One has an ensemble of space-time sheets which should represent nearly replicas of the quantum computation. There are two cases to be considered.

1. If the thermal entanglement is reducible then each space-time sheet gives outcome corresponding to a well defined energy and one must form an average over these outcomes.

2. If thermal entanglement is irreducible each space-time sheet corresponds to a quantum superposition of space-time sheets, and if the outcome is represented classically as rates and temporal field patterns, it should reflect thermal average of the outcomes as such.

If the degrees of freedom assignable to topological quantum computation do not depend on the energy of the state, thermal width does not affect at all the relevant probabilities. The probabilities

are actually affected even in the case of tqc since 1-gates are not purely topological and the effects of temperature in spin degrees of freedom are unavoidable. If T grows the probability distribution for the outcomes flattens and it becomes difficult to select the desired outcome as that appearing with the maximal probability.

6.2.3 Hyper-finite factors of type II_1 and quantum measurement theory with a finite measurement resolution

The realization that the von Neumann algebra known as hyper-finite factor of type II_1 is tailor made for quantum TGD has led to a considerable progress in the understanding of the mathematical structure of the theory and these algebras provide a justification for several ideas introduced earlier on basis of physical intuition.

Hyper-finite factor of type II_1 has a canonical realization as an infinite-dimensional Clifford algebra and the obvious guess is that it corresponds to the algebra spanned by the gamma matrices of WCW. Also the local Clifford algebra of the imbedding space $H = M^4 \times CP_2$ in octonionic representation of gamma matrices of H is important and the entire quantum TGD emerges from the associativity or co-associativity conditions for the sub-algebras of this algebra which are local algebras localized to maximal associative or co-associate sub-manifolds of the imbedding space identifiable as space-time surfaces.

The notion of inclusion for hyper-finite factors provides an elegant description for the notion of measurement resolution absent from the standard quantum measurement theory.

1. The included sub-factor creates in zero energy ontology states not distinguishable from the original one and the formally the coset space of factors defining quantum spinor space defines the space of physical states modulo finite measument resolution.

2. The quantum measurement theory for hyperfinite factors differs from that for factors of type I since it is not possible to localize the state into single ray of state space. Rather, the ray is replaced with the sub-space obtained by the action of the included algebra defining the measurement resolution. The role of complex numbers in standard quantum measurement theory is taken by the non-commutative included algebra so that a non-commutative quantum theory is the outcome.

3. This leads also to the notion of quantum group. For instance, the finite measurement resolution means that the components of spinor do not commute anymore and it is not possible to reduce the state to a precise eigenstate of spin. It is however perform a reduction to an eigenstate of an observable which corresponds to the probability for either spin state.

4. The realization for quantum measurement theory modulo finite measurement resolution is in terms of M-matrices defined in terms of Connes tensor product which essentially means that the included hyper-finite factor N takes the role of complex num bers.

As already explained, the topology of the many-sheeted space-time encourages the generalization of the notion of quantum entanglement in such a manner that unentangled systems can possess entangled sub-systems. One can say that the entanglement between subselves is not visible in the resolution characterizing selves. This makes possible sharing and fusion of mental images central for TGD inspired theory of consciousness. These concepts find a deeper justification from the quantum measurement theory for hyper-finite factors of type II_1 for which the finite measurement resolution is basic notion.

Also the notions of resolution and monitoring pop up naturally in this framework. p-Adic probabilities relate very naturally to hyper-finite factors of type II_1 and extend the expressive power of the ordinary probability theory. p-Adic thermodynamics with conformal cutoff is very natural for hyper-finite factors of type II_1 and explains p-adic length scale hypothesis $p \simeq 2^k$, k prime characterizing exponentially smaller p-adic length scale.

6.2.4 NMP and biology

The notion of self is crucial for the understanding of bio-systems and consciousness. It seems that the negentropic entanglement is the decisive element of life and that one can say that in metaphoral

sense life resides in the intersection of real and p-adic worlds.

Generalization of the notion of information

TGD inspired theory of consciousness, in particular the formulation of Negentropy Maximization Principle (NMP) in p-adic context, has forced to rethink the notion of the information concept. In TGD state preparation process is realized as a sequence of self measurements and state preparation for next quantum jump is state reduction for the previous quantum jump. In zero energy ontology one can interpret the state preparation for positive and negative energy parts of the state as reduction and preparation in the sense of standard physics. Each self measurement means a decomposition of the sub-system involved to two unentangled parts unless the system is bound state. The decomposition is fixed highly uniquely from the requirement that the reduction of the entanglement entropy is maximal.

Bound state entanglement is stable against self measurement simply because energy conservation prevents the decay to a pair of free (uncorrelated) subsystems. The generalized definition of entanglement entropy allows to assign a negative value of entanglement entropy to rational and algebraic entanglement, so that this kind of entanglement would actually carry information, in fact conscious information (experience of understanding). This kind of entanglement cannot be reduced in state function reduction. Macro-temporal quantum coherence could correspond to a generation of either bound state entanglement or negentropic entanglement, and is indeed crucial for ability to have long lasting non-entropic mental images. Generation of negentropic entanglement would involve experience about expansion of consciousness and that of bound states entanglement a loss of consciousness.

The mathematical models for quantum computers typically operate with systems for which entanglement probabilities are identical. Also rational numbers are involved. Does this mean that negentropic entanglement makes possible quantum computation? This does not seem to be the case. State function reduction with random outcomes is a central element of quantum computation which suggests that quantum computation must be based on entropic entanglement with large enough value of $\hbar$ to overcome the restrictions caused by the interactions with the external world. The negentropic entanglement in turn would relate to conscious information processing involving experience of understanding represented by negentropic entanglement. Negentropic entanglement would make possible conscious cellular automaton type information processing much closer to that carried out by ordinary computers and this information processing might be equally important in living systems.

Life as islands of rational/algebraic numbers in the seas of real and p-adic continua?

Rational and even algebraic entanglement coefficients make sense in the intersection of real and p-adic words, which suggests that life and conscious intelligence reside in the intersection of the real and p-adic worlds. This would mean that the mathematical expressions for the space-time surfaces (or at least 3-surfaces or partonic 2-surfaces and their 4-D tangent planes) make sense in both real and p-adic sense for some primes p. Same would apply to the expressions defining quantum states. In particular, entanglement probabilities would be rationals or algebraic numbers so that entanglement can be negentropic and the formation of bound states in the intersection of real and p-adic worlds generates information and is thus favored by NMP.

The identification of intentionality as the basic aspect of life seems to be consistent with this idea.

1. The proposed realization of the intentional action has been as a transformation of p-adic space-time sheet to a real one. Also transformations of real space-time sheets to p-adic space-time sheets identifiable as cognitions are possible. Algebraic entanglement is a prerequisite for the realization of intentions in this manner. Essentially a leakage between p-adic and real worlds is in question and makes sense only in zero energy ontology. The reason is that various quantum numbers in real and p-adic sectors are not in general comparable in positive energy ontology so that conservation laws would be broken or even cease to make sense.

2. The transformation of intention to action can occur if the partonic 2-surfaces and their 4-D tangent space-distributions are representable using rational functions with rational (or even algebraic) coefficients in preferred coordinates for the imbedding space dictated by symmetry considerations. Intentional systems must live in the intersection of real and p-adic worlds.

3. For the minimal option life would be also effectively 2-dimensional phenomenon and essentially a boundary phenomenon as also number theoretical criticality suggests. There are good reasons to

expect that only the data from the intersection of real and p-adic partonic two-surfaces appears in U-matrix so that only the data from rational and some algebraic points of the partonic 2-surface dictate U-matrix. This means discretization at parton level and something which might be called number theoretic quantum field theory should emerge as a description of intentional action.

A good guess is that algebraic entanglement is essential for quantum computation, which therefore might correspond to a conscious process. Hence cognition could be seen as a quantum computation like process, a more approriate term being quantum problem solving. Living-dead dichotomy could correspond to rational-irrational or to algebraic-transcendental dichotomy: this at least when life is interpreted as intelligent life. Life would in a well defined sense correspond to islands of rationality/algebraicity in the seas of real and p-adic continua. Life as a critical phenomenon in the number theoretical sense would be one aspect of quantum crticality of TGD Universe besides the criticality of the space-time dynamics and the criticality with respect to phase transitions changing the value of Planck constant and other more familiar criticalities. How closely these criticalities relate remains an open question [62] .

The view about the crucial role of rational and algebraic numbers as far as intelligent life is considered, could have been guessed on very general grounds from the analogy with the orbits of a dynamical system. Rational numbers allow a predictable periodic decimal/pinary expansion and are analogous to one-dimensional periodic orbits. Algebraic numbers are related to rationals by a finite number of algebraic operations and are intermediate between periodic and chaotic orbits allowing an interpretation as an element in an algebraic extension of any p-adic number field. The projections of the orbit to various coordinate directions of the algebraic extension represent now periodic orbits. The decimal/pinary expansions of transcendentals are un-predictable being analogous to chaotic orbits. The special role of rational and algebraic numbers was realized already by Pythagoras, and the fact that the ratios for the frequencies of the musical scale are rationals supports the special nature of rational and algebraic numbers. The special nature of the Golden Mean, which involves $\sqrt{5}$, conforms the view that algebraic numbers rather than only rationals are essential for life.

That only algebraic extensions are possible is of course only a working hypothesis. Also finite-dimensional extensions of p-adic numbers involving transcendentals are possible and might in fact be necessary. Consider for instance the extension containing $e, e^2, .., e^{p-1}$ as units (e^p is ordinary p-adic number. Infinite number of analogous finite-dimensional extensions can be constructed by taking a function of integer variable such that $f(p)$ exists both p-adically and as a real transcendental number. The powers of $f(p)^{1/n}$ for a fixed value of n define a finite-dimensional transcendental extension of p-adic numbers if the roots do not exist p-adically.

Numbers like $log(p)$ and π cannot belong to a finite-dimensional extension of p-adic numbers [30] . One cannot of course take any strong attitude concerning the possibility of infinite-dimensional extensions of p-adic numbers but the working hypothesis has been that they are absent. The phases $exp(i2\pi/n)$ define finite dimensional extensions allowing to replace the notion of angle in finite measurement resolution with the corresponding phase factors in finite measurement. The functions $exp(i2\pi q/n)$, where q is arbitrary p-adic integers define in a natural manner the physical counterparts of plane waves and angular momentum eigenstates not allowing an identification as ordinary p-adic exponential functions. They are clearly strictly periodic functions of q with a finite value set. If n is divisible by a power of p, these functions are continuous since the values of the function for q and $q + kp^n$ are identical for large enough values of n. This condition is essential and means in the case of plane waves that the size scale of a system (say one-dimensional box) is multiple of a power of p.

Evolution and second law

Evolution has many facets in TGD framework.

1. A natural characterization of evolution is in terms of p-adic topology relating naturally to cognition. p-Adic primes near powers of two are favored if CDs have the proposed discrete size spectrum. From the point of view of self this would be essentially cosmic expansion in discrete jumps. CDs and can be characterized by powers of 2 and if partonic 2-surfaces correspond to effective p-adic p-adic topology characterized by a power of two, one obtains the commeasurability of the secondary p-adic time scale of particle and that of CD in good approximation.

2. The notion of infinite primes motivates the hypothesis that the many-sheeted structure of space-time can be coded by infinite primes [71] . The number of primes larger than given infinite prime P is infinitely larger than the number of primes than P. The infinite prime P characterizing the entire universe decomposes in a well defined manner to finite primes and p-adic evolution at the level of entire universe is implied by local p-adic evolution at the level of selves. Therefore maximum entanglement negentropy gain for p-adic self increases at least as $log(p)$ with p in the long run. This kind of relationship might hold true for real selves of p-adic physics is physics of cognitive representations of real physics as suggested by the success of p-adic mass calculations. Thus it should be possible to assign definite p-adic prime to each partonic 2-surface.

3. A further aspect of evolution relates to the hierarchy of Planck constants implying that at dark matter levels rational or at least integer multiples of the favored p-adic time scales are realized. The latter option is favored by the idea that the book like structure with pages consisting of many-sheeted coverings of CD and CP_2, and correlates with the emergence of algebraic extensions of p-adic numbers defined by the roots $exp(i2\pi/n)$ of unity. For the latter option evolution by quantum jumps would automatically imply the drifting of the partonic 2-surfaces to the pages of books labelled by increasing values of Planck constant. For more general option one might argue that drifting to pages with small values of Planck constant is also possible. This would give kind of antizooms of long length scale physics to short scales. Both kind of temporal zooms could be crucial for conscious intelligence building scaled models about time evolution in various scales.

4. The generation of negentropic entanglement between different number fields would of course be the fundamental aspect of evolution. It would give rise to increasingly complex and negentropic sensory perceptions and cognitive representations based on conscious rules coded by negentropic entanglement. This would justify the association concept as it used in neuro-science. Negentropic entanglement could be also crucial for the basic mechanism of metabolism and make possible conscious co-operation even in nano-scales.

Just for fun one can play also with numbers.

1. The highest dark matter level associated with self corresponds to its geometric duration which can be arbitrarily long: the typical duration of the memory span gives an idea about the level of dark matter hierarchy involved if one assumes that the time scale .1 seconds assignable to electrons is the fundamental time scale. If the time scale T of human life cycle corresponds to a secondary p-adic time scale then $T = 100$ years gives the rough estimate $r \equiv \hbar/\hbar_0 = 2^{33}$ if this time scale corresponds to that for dark electron. The corresponding primary p-adic time length scale corresponds to $k = 160$ and is 2.2×10^{-7} meters.

2. If human time scale -taken to be $T = 100$ years- corresponds to primary p-adic time scale of electron, one must have roughly $r = 2^{97}$.

I have already discussed the second law in TGD framework and it seems that its applies only when the time scale of perception is longer than the time scale characterizing the level of the p-adic and dark matter hierarchy. Second law as it is usually stated can be seen as an unavoidable implication of the materialistic ontology.

Stable entanglement and quantum metabolism as different sides of the same coin

The notion of binding has two meanings. Binding as a formation of bound state and binding as a fusion of mental images to larger ones essential for the functioning of brain and regarded as one the big problems of consciousness theory.

Only bound state entanglement and negentropic entanglement are stable against the state reduction process. Hence the fusion of the mental images implies the formation of a bound entropic state- in this case the two interpretations of binding are equivalent- or a negentropic state, which need not be bound state.

1. In the case of negentropic entanglement bound state need not be formed and the interesting possibility is that the negentropic entanglement could give rise to stable states without binding

energy. This could allow to understand the mysterious high energy phosphate bond to which metabolic energy is assigned in ATP molecule containing three phosphates and liberated as ATP decays to ADP and phosphate molecule. Negentropic entanglement could also explain the stability of DNA and other highly charged biopolymers. In this framework the liberation of metabolic (negentropic) energy would involve dropping of electrons to a larger space-time sheets accompanying the process $ATP \to ADP + P_i$. A detailed model of this process is discussed in [29] .

2. The formation of bound state entanglement is expected to involve a liberation of the binding energy and this energy might be a usable energy. This process could perhaps be coined as quantum metabolism and one could say that quantum metabolism and formation of bound states are different sides of the same coin. It is known that an intense neural activity, although it is accompanied by an enhanced blood flow to the region surrounding the neural activity, does not involve an enhanced oxidative metabolism [21] (that is $ATP \to ADP$ process and its reversal). A possible explanation is that quantum metabolism accompanying the binding is involved. Note that the bound state is sooner or later destroyed by the thermal noise so that this mechanism would in a rather clever manner utilize thermal energy by applying what might be called buy now–pay later principle.

If these interpretations are correct, there would be two modes of metabolism corresponding to two different kinds of fusion of mental images.

6.2.5 Generalization of thermodynamics allowing negentropic entanglement and a model for conscious information processing

The possibility of negetropic entanglement in TGD framework means that the second law of thermodynamics must be modified. The most obvious modification means only the replacement $S \to S - N$, where S is thermodynamical entropy and N the negentropy associated with negentropic entanglement. Hence the basic formulas of thermodynamics remain formally as such. The generalization leads to a thermodynamical model for how conscious information is generated and how metabolism relates to this. One can also understand why living matter is so effective entropy producer as compared to inanimate matter and the characteristic decomposition of living systems to highly negentropic and entropic parts.

Modification of thermodynamics to take into account negentropic entanglement

What does the presence of the negentropic entanglement mean from the point of view of thermodynamics? There are two obvious options to consider. The optimistic option is just the standard thermodynamics saying nothing about negentropy generation. The pessimistic option is that the generation of negentropy must be accompanied by a generation of at least the same amount of entropy: the good news is that this entropy can be carried by different system and it is possible to have genuinely negentropic systems. The following consideration is restricted to the pessimistic option which seems to be more realistic view about the world we live in.

1. One must generalize the basic expression for energy differential

$$dE \quad = \quad TdS - dW \to T(dS - dN) - dW \quad . \tag{6.2.1}$$

This means that there are two kinds of energies given out by the system. The useful work dW and negentropic energy TdN. For steam engine only dW is present. For ideal system only negentropic energy would be present.

2. What happens to the second law? The pessimistic guess is that generation of negentropy requires a generation of at least same amount of entropy so that one would have

$$\Delta S - \Delta N \geq \quad 0 \quad . \tag{6.2.2}$$

Here S can be interpreted as a sum of two terms. The first part corresponds to the ensemble entropy generated by the randomness of ordinary quantum jumps, and second part to the entropy assignable as maximal entanglement entropy assignable to the decompositions of bound state to two parts. N corresponds to maximal negentropy for the decompositions of negentropic subsystem to pairs. One can criticize these definitions and a possible modification of could be as as the average for the entanglement entropies over this kind of decompositions.

3. Quite generally, Clausius inequality allowing to deduce extremization conditions for various thermodynamical potentials generalizes to

$$T_0(\Delta S - \Delta N) - \Delta E - P_0\Delta V \quad \geq \quad 0 \ . \tag{6.2.3}$$

where T_0 and P_0 and temperature and pressure of heat bath. Living systems would be entropy producers and this seems to conform with what we see around us.

For instance, for a system in constant volume one would have

$$\Delta S - \Delta N - \frac{\Delta E}{T} \quad \geq \quad 0 \ . \tag{6.2.4}$$

so that systems developing negentropy would also generate thermodynamics entropy. For a system in heat bath one has $T = T_0$ and Clausius inequality gives

$$\Delta F \quad = \quad -\Delta W \tag{6.2.5}$$

stating that increase of free energy at constant temperature requires work done on the system ($dW < 0$): otherwise $\Delta F \leq 0$ holds true.

By using the variable $S - N$ instead of S all formulas reduce formally to standard thermodynamics except that S can be negative.

The analog of Carnot cycle as a simple model for information processing in living matter

Carnot engine transforms heat to work. Costa de Beauregard [7] , [7] has proposed a modification of Carnot engine as a model for information processing. One can consider Carnot engine and its information theoretic analog in this framework.

1. The basic equation for Carnot engine is

$$dW \quad = \quad dQ_{in} - dQ_{out} \geq 0 \ . \tag{6.2.6}$$

Optimal efficiency corresponds to $dS_{out} = dS_{in}$.

2. The information theoretic analog of Carnot engine proposed by Beauregard does not perform work and one would have

$$dW \quad = \quad 0 \ , \tag{6.2.7}$$

and

$$dN = dS_{out} - dS_{in} \geq 0 \ . \tag{6.2.8}$$

The interpretation would be that incoming entropy flow leaves the computer in a state of higher entropy and the difference corresponds to information dN feeded to say printer. The increase of entropy would have interpretation in terms of erasing of data from computer memory.

The problematic aspect of the model is that it requires $T_{in} > T_{out}$ in order to have $dN > 0$. For living systems one has however typically $T_{in} < T_{out}$. Already for $T_{in} = T_{out}$ the situation trivializes since one has

$$dN = 0 \tag{6.2.9}$$

by $dW = 0$ and $dS = dQ/T$.

3. In the recent case however a more general condition

$$T_{in} d(S_{in} - N_{in}) - T_{out} d(S_{out} - N_{out}) \geq 0 \tag{6.2.10}$$

holds true and allows to generate conscious information provided it is compensated by thermodynamical entropy. Note that the temperature of the environment can be even lower than the temperatures of the system.

It is also possible to transform information to work as the expression for the differential $dF = -SdT - TdN - dW$ of the generalized free energy $E = E - TS$ shows. The increase of dW for the work done by the system is compensated by the reduction of information dN so that system loses negentropy in the process keeping dF constant. The loss of negentropy couild be interpreted in terms of a loss of metabolic energy which corresponds to negentropic entanglement for AMP, ADP, and ATP molecules.

Basic biological implications

Some clarifying comments about biological implications are in order.

1. There is no need to restrict the consideration to equilibrium systems. First of all, the environment and living system are in general at different temperatures and temperature difference is typically of wrong sign for the model of Beauregard to work in this context. Beauregard's model is of course a model for computation, not for the generation of negentropic mental images. Maybe cognitive machine might be proper term for what the modified model could describe.

2. Quite generally, self-organization requires a feed of energy to the system so that one has flow equilibrium. In the case of living system this feed of energy is metabolic energy associated with the negentropic entanglement transferred to the system in the ATP-ADP process. Self-organization driven by negentropic entanglement leads to standardized negentropic mental images automatically as asymptotic self-organization patterns in 4-D sense (CDs within CDs within ... : CD denotes causal diamond defined as cartesian produc to the intersection of the future and past directed light-cones with CP_2, which is the key notion in zero energy ontology).

3. No explicit assumptions about computational aspects of the process has been made. Just a generation of conscious information identified in terms of negentropic entanglement is assumed. The basic character quantum jump as U-process followed by the cascade of state function reductions represents a fractal hierarchy of what can be seen as quantum computations and are distinguished from classical computations in that the process proceeds from top to bottom rather than being a local process. The result of computation is represented using statistical ensembles

defined by sub-CDs at various levels of the hierarchy and is in principle communicable by classical fields (say EEG patterns in the case of brain) to higher levels of self hierarchy which in turn can induces the same distributions so that communication of the objective aspects of the experience with the mediation of "medium" is possible. The presence of the "medium" seems unavoidable. Magnetic body would be this medium in TGD inspired biology.

Living matter involves also another aspect made possible by the generalized second law obtained by the replacement $S \to S - N$. Subsystem can have also negative net entropy and split to two highly negentropic and entropic pieces. In the extreme situation this is nothing but excretion, which is absolutely essential element of being alive but sometimes forgotten from the lists of properties distinguishing living matter from inanimate matter. It is not at all clear whether this is possible for standard non-equilibrium systems defining information as a reduction of disorder. At all levels of the fractal hierarchy division into negentropic and entropic subsystems is expected.

This picture seems to be in accordance with basic chemistry of energy metabolism.

1. The process creating both negentropy and entropy would be standardized in living matter and mean a generation of high energy phosphate bonds assignable to AMP, ADP, and ATP containing 1, 2, and 3 phosphates respectively besides the sugar residue. Sugar residue is basic nutrient and would provide the stored metabolic energy transformed to the negentropic energy of the high energy phosphate bonds if the proposed view is correct. Also other DNA nucleotides such as G can appear besides A but in metabolism A has a preferred role.

2. The basic metabolic cycle provides ADP with an additional phosphate energizing it to ATP and the reverse process transfers the metabolic energy and also negentropic entanglement to the acceptor molecule. Also ADP can provide metabolic energy by transforming to AMP when ATP is not available in sufficient amounts. That the catabolism of AMP creates urea excreted out of the system fits with the general picture. The catabolism for nutrients would create the entropy compensating for the negentropy of the high energy phosphate bonds.

3. The backbone of DNA is made of sugar and phosphate residues and corresponds to a sequence of XMP, $X = A, T, C, G$ with each XMP presumably containing single high energy phosphate bond serving as a storage or potential source of negentropy. This conforms with the view that DNA carries conscious information.

Negentropic and entropic entanglement are assumed to generate mental images with opposite emotional colors. This connects information processing with emotions. From neuroscience point of view this is not a news: peptides are molecules of emotions on one hand and molecules of information on the other hand [40] . The well-known specialization of the left and right hand sides of the amygdala to experience positive and negatively colored emotions could be seen as one instance of this connection and representing also an example about fractal negentropic-entropic differentiation.

6.3 How quantum computation in TGD Universe differs from standard quantum computation?

Many problems of quantum computation in standard sense might relate to a wrong view about quantum theory. If TGD Universe is the physical universe, the situation would improve in many respects. There is the new fractal view about quantum jump and observer as "self"; there is p-adic length scale hierarchy and hierarchy of Planck constants as well as self hierarchy; there is a new view about entanglement and the possibility of irreducible entanglement carrying genuine information and making possible quantum superposition of fractal quantum computations and quantum parallel dissipation; there is zero energy ontology, the notion of M-matrix allowing to understand quantum theory as a square root of thermodynamics, the notion of measurement resolution allowing to identify M-matrix in terms of Connes tensor product; there is also the notion of magnetic body providing one promising realization for braids in tqc, etc... This section gives a short summary of these aspects of TGD.

There is also a second motivation for this section. Quantum TGD and TGD inspired theory of consciousness involve quite a bundle of new ideas and the continual checking of internal consistency by writing it through again and again is of utmost importance. This section can be also seen as this

kind of checking. I can only represent apologies to the benevolent reader: this is a work in rapid progress.

6.3.1 General ideas related to topological quantum computation

Topological computation relies heavily on the representation of tqc program as a braiding. There are many kinds of braidings. Number theoretic braids are defined by the orbits of minima of vacuum expectation of Higgs at lightlike partonic 3-surfaces (and also at space-like 3-surfaces). There are braidings defined by Kähler gauge potential (possibly equivalent with number theoretic ones) and by Kähler magnetic field. Magnetic flux tubes and partonic 2-surfaces interpreted as strands of define braidings whose strands are not infinitely thin. A very concrete and very complex time-like braiding is defined by the motions of people at the surface of globe: perhaps this sometimes purposeless-looking fuss has a deeper purpose: maybe those at the higher levels of dark matter hierarchy are using us to carry out complex topological quantum computations)!

General vision about quantum computation

In TGD Universe the hierarchy of Planck constants gives excellent prerequisites for all kinds of quantum computations. The general vision about quantum computation (tqc) would result as a special case and would look like follows.

1. Time-like entanglement between positive and negative energy parts of zero energy states would define the analogs of qc-programs. Space-like quantum entanglement between ends of strands whose motion defines time-like braids would provide a representation of q-information.

2. Both time- and space-like quantum entanglement would correspond to Connes tensor product expressing the finiteness of the measurement resolution between the states defined at ends of space-like braids whose orbits define time like braiding. The characterization of the measurement resolution would thus define both possible q-data and tq-programs as representations for "laws of physics".

3. The braiding between DNA strands with each nucleotide defining one strand transversal to DNA realized in terms of magnetic flux tubes was my first bet for the representation of space-like braiding in living matter. It turned out that the braiding is more naturally defined by flux tubes connecting nucleotides to the lipids of nuclear-, cell-, and endoplasma membranes. Also braidings between other microtubules and axonal membrane can be considered. The conjectured hierarchy of genomes giving rise to quantum coherent gene expressions in various scales would correspond to computational hierarchy.

About the relation between space-like and time-like number theoretic braidings

The relationship between space- and time-like braidings is interesting and there might be some connections also to 4-D topological gauge theories suggested by geometric Langlands program discussed in the previous posting and also in [36] .

1. The braidings along light-like surfaces modify space-like braiding if the moving ends of the space-like braids at partonic 3-surfaces define time-like braids. From tqc point of view the interpretation would be that tqc program is written to memory represented as the modification of space-like braiding in 1-1 correspondence with the time-like braiding.

2. The orbits of space-like braids define codimension two sub-manifolds of 4-D space-time surface and can become knotted. Presumably time-like braiding gives rise to a non-trivial "2-braid". Could also the "2-braiding" based on this knotting be of importance? Do 2-connections of n-category theorists emerge somehow as auxiliary tools? Could 2-knotting bring additional structure into the topological QFT defined by 1-braidings and Chern-Simons action?

3. The strands of dynamically evolving braids could in principle go through each other so that time evolution can transform braid to a new one also in this manner. This is especially clear from standard representation of knots by their planar projections. The points where intersection

occurs correspond to self-intersection points of 2-surface as a sub-manifold of space-time surface. Topological QFT:s are also used to classify intersection numbers of 2-dimensional surfaces understood as homological equivalence classes. Now these intersection points would be associated with "braid cobordism".

Quantum computation as quantum superposition of classical computations?

It is often said that quantum computation is quantum super-position of classical computations. In standard path integral picture this does not make sense since between initial and final states represented by classical fields one has quantum superposition over *all* classical field configurations representing classical computations in very abstract sense. The metaphor is as good as the perturbation theory around the minimum of the classical action is as an approximation.

In TGD framework the classical space-time surface is a preferred extremal of Kähler action so that apart from effects caused by the failure of complete determinism, the metaphor makes sense precisely. Besides this there is of course the computation associated with the spin like degrees of freedom in which one has entanglement and which one cannot describe in this manner.

For tqc a particular classical computation would reduce to the time evolution of braids and would be coded by 2-knot. Classical computation would be coded to the manipulation of the braid. Note that the branching of strands of generalized number theoretical braids has interpretation as classical communication.

The identification of topological quantum states

Quantum states of tqc should correspond to topologically robust degrees of freedom separating neatly from non-topological ones.

1. The generalization of the imbedding space inspired by the hierarchy of Planck constants suggests an identification of this kind of states as elements of the group algebra of discrete subgroup of $SO(3)$ associated with the group defining covering of M^4 or CP_2 or both in large $\hbar$ sector. One would have wave functions in the discrete space defined by the homotopy group of the covering transforming according to the representations of the group. This is by definition something robust and separated from non-topological degrees of freedom (standard model quantum numbers). There would be also a direct connection with anyons.

2. An especially interesting group is dodecahedral group corresponding to the minimal quantum phase $q = exp(2\pi/5)$ (Golden Mean) allowing a universal topological quantum computation: this group corresponds to Dynkin diagram for E_8 by the ALE correspondence. Interestingly, neuronal synapses involve clathrin molecules [23] associated with microtubule ends possessing dodecahedral symmetry.

Some questions

A conjecture inspired by the inclusions of HFFs is that these states can be also regarded as representations of various gauge groups which TGD dynamics is conjectured to be able to mimic so that one might have connection with non-Abelian Chern-Simons theories where topological S-matrix is constructed in terms of path integral over connections: these connections would be only an auxiliary tool in TGD framework.

1. Do these additional degrees of freedom give only rise to topological variants of gauge- and conformal field theories? Note that if the earlier conjecture that entire dynamics of these theories could be mimicked, it would be best to perform tqc at quantum criticality where either M^4 or CP_2 dynamical degrees of freedom or both disappear.

2. Could it be advantageous to perform tqc near quantum criticality? For instance, could one construct magnetic braidings in the visible sector near q-criticality using existing technology and then induce phase transition changing Planck constant by varying some parameter, say temperature.

6.3.2 Fractal hierarchies

Fractal hierarchies are the essence of TGD. There is hierarchy of space-time sheets labelled by preferred p-adic primes. There is hierarchy of Planck constants reflecting a book like structure of the generalized imbedding space and identified in terms of a hierarchy of dark matters. These hierarchies correspond at the level of conscious experience to a hierarchy of conscious entities - selves: self experiences its sub-selves as mental images.

Fractal hierarchies mean completely new element in the model for quantum computation. The decomposition of quantum computation to a fractal hierarchy of quantum computations is one implication of this hierarchy and means that each quantum computation proceeds from longer to shorter time scales $T_n = T_0 2^{-n}$ as a cascade like process such that at each level there is a large number of quantum computations performed with various values of input parameters defined by the output at previous level. Under some additional assumptions to be discussed later this hierarchy involves at a given level a large number of replicas of a given sub-module of tqc so that the output of single fractal sub-module gives automatically probabilities for various outcomes as required.

6.3.3 Irreducible entanglement and possibility of quantum parallel quantum computation

The basic distinction from standard measurement theory is irreducible entanglement not reduced in quantum jump.

NMP and the possibility of irreducible entanglement

Negentropy Maximimization Principle (NMP) states that entanglement entropy is minimized in quantum jump. For standard Shannon entropy this would lead to a final state which corresponds to a ray of state space. If entanglement probabilities are rational - or even algebraic - one can replace Shannon entropy with its number theoretic counterpart in which p-adic norm of probability replaces the probability in the argument of logarithm: $log(p_n) \to log(|p_n|_p)$. This entropy can have negative values. It is not quite clear whether prime p should be chosen to maximize the number theoretic negentropy or whether p is the p-adic prime characterizing the light-like partonic 3-surface in question.

Obviously NMP favors generation of irreducible entanglement which however can be reduced in U process. Irreducible entanglement is something completely new and the proposed interpretation is in terms of experience of various kinds of conscious experiences with positive content such as understanding.

Quantum superposition of unitarily evolving quantum states generalizes to a quantum superposition of quantum jump sequences defining dissipative time evolutions. Dissipating quarks inside quantum coherent hadrons would provide a basic example of this kind of situation.

Quantum parallel quantum computations and conscious experience

The combination of quantum parallel quantum jump sequences with the fractal hierarchies of scales implies the possibility of quantum parallel quantum computations. In ordinary quantum computation halting selects single computation but in the recent case arbitrarily large number of computations can be carried out simultaneously at various branches of entangled state. The probability distribution for the outcomes is obtained using only single computation.

One would have quantum superposition of space-time sheets (assignable to the maxima of Kähler function) each representing classically the outcome of a particular computation. Each branch would correspond to its own conscious experience but the entire system would correspond to a self experiencing consciously the outcome of computation as intuitive and holistic understanding, and abstraction. Emotions and emotional intellect could correspond to this kind of non-symbolic representation for the outcome of computation as analogs for collective parameters like temperature and pressure.

Delicacies

There are several delicacies involved.

1. The above argument works for factors of type I. For HFFs of type II_1 the finite measurement resolution characterized in terms of the inclusion $\mathcal{N} \subset \mathcal{M}$ mean is that state function reduction takes place to $\mathcal{N}$-ray. There are good reasons to expect that the notion of number theoretic entanglement negentropy generalizes also to this case. Note that the entanglement associated with $\mathcal{N}$ is below measurement resolution.

2. In TGD inspired theory of consciousness irreducible entanglement makes possible sharing and fusion of mental images. At space-time level the space-time sheets corresponding to selves are disjoint but the space-time sheets topologically condensed at them are joined typically by what I call join along boundaries bonds identifiable as braid strands (magnetic flux quanta). In topological computation with finite measurement resolution this kind of entanglement with environment would be below the natural resolution and would not be a problem.

3. State function reduction means quantum jump to an eigen state of density matrix. Suppose that density matrix has rational elements. Number theoretic vision forces to ask whether the quantum jump to eigen state is possible if the eigenvalues of ρ do not belong to the algebraic extension of rationals and p-adic numbers used. If not, then one would have number theoretically irreducible entanglement depending on the algebraic extension used. If the eigenvalues actually define the extension there would be no restrictions: this option is definitely simpler.

4. Fuzzy quantum logic [83] brings also complications. What happens in the case of quantum spinors that spin ceases to be observable and one cannot reduce the state to spin up or spin down. Rather, one can measure only the eigenvalues for the probability operator for spin up (and thus for spin down) so that one has fuzzy quantum logic characterized by quantum phase. Inclusions of HFFs are characterized by quantum phases and a possible interpretation is that the quantum parallelism related to the finite measurement resolution could give rise to fuzzy qubits. Also the number theoretic quantum parallelism implied by number theoretic NMP could effectively make probabilities as operators. The probabilities for various outcomes would correspond to outcomes of quantum parallel state function reductions.

6.3.4 Possible problems related to quantum computation

At least following problems are encountered in quantum computation.

1. How to preserve quantum coherence for a long enough time so that unitary evolution can be achieved?

2. The outcome of calculation is always probability distribution: for instance, the output with maximum probability can correspond to the result of computation. The problem is how to replicate the computation to achieve the desired accuracy. Or more precisely, how to produce replicas of the hardware of quantum computer defined in terms of classical physics?

3. How to isolate the quantum computer from the external world during computation and despite this feed in the inputs and extract the outputs?

The notion of coherence region in TGD framework

In standard framework one can speak about coherence in two senses. At the level of Schrödinger amplitudes one speaks about coherence region inside which it makes sense to speak about Schrödinger time evolution. This notion is rather defined.

In TGD framework coherence region is identifiable as a region inside which the modified Dirac equation holds true. Strictly speaking, this region corresponds to a light-like partonic 3-surface whereas 4-D space-time sheet corresponds to coherence region for classical fields. p-Adic length scale hierarchy and hierarchy of Planck constants means that arbitrarily large coherence regions are possible.

The precise definition for the notion of coherence region and the presence of scale hierarchies imply that the coherence in the case of single quantum computation is not a problem in TGD framework. De-coherence time or coherence time correspond to the temporal span of space-time sheet and a hierarchy coming in powers of two for a given value of Planck constant is predicted by basic quantum TGD. p-Adic length scale hypothesis and favored values of Planck constant would naturally reflect this fundamental fractal hierarchy.

De-coherence of density matrix and replicas of tqc

Second phenomenological description boils down to the assumption that non-diagonal elements of the density matrix in some preferred basis (involving spatial localization of particles) approach to zero. The existence of more or less faithful replicas of space-time sheet in given scale allows to identify the counterpart of this notion in TGD context. De-coherence would mean a loss of information in the averaging of M-matrix and density matrix associated with these space-time sheets.

Topological computations are probabilistic. This means that one has a collection of space-time sheets such that each space-time sheet corresponds to more or less the same tqc and therefore the same M-matrix. If M is too random (in the limits allowed by Connes tensor product), the analog of generalized phase information represented by its "phase" - S-matrix - is useless.

In order to avoid de-coherence in this sense, the space-time sheets must be approximate copies of each other. Almost copies are expected to result by dissipation leading to asymptotic self-organization patterns depending only weakly on initial conditions and having also space-time correlates. Obviously, the role of dissipation in eliminating effects of de-coherence in tqc would be something new. The enormous symmetries of M-matrix, the uniqueness of S-matrix for given resolution and parameters characterizing braiding, fractality, and generalized Bohr orbit property of space-time sheets, plus dissipation give good hopes that almost replicas can be obtained.

Isolation and representations of the outcome of tqc

The interaction with environment makes quantum computation difficult. In the case of topological quantum computation this interaction corresponds to the formation of braid strands connecting the computing space-time sheet with space-time sheets in environment. The environment is four-dimensional in TGD framework and an isolation in time direction might be required. The space-time sheets responsible for replicas of tqc should not be connected by light-like braids strands having time-like projections in M^4.

Length scale hierarchy coming in powers of two and finite measurement resolution might help considerably. Finite measurement resolution means that those strands which connect space-time sheets topologically condensed to the space-time sheets in question do not induce entanglement visible at this level and should not affect tqc in the resolution used.

Hence only the elimination of strands responsible for tqc at given level and connecting computing space-time sheet to space-time sheets at same level in environment is necessary and would require magnetic isolation. Note that super-conductivity might provide this kind of isolation. This kind of elimination could involve the same mechanism as the initiation of tqc which cuts the braid strands so the initiation and isolation might be more or less the same thing.

Strands reconnect after the halting of tqc and would make possible the communication of the outcome of computation along strands by using say em currents in turn generating generalized EEG, nerve pulse patterns, gene expression, etc... halting and initiation could be more or less synonymous with isolation and communication of the outcome of tqc.

How to express the outcome of quantum computation?

The outcome of quantum computation is basically a representation of probabilities for the outcome of tqc. There are two representations for the outcome of tqc. Symbolic representation which quite generally is in terms of probability distributions represented in terms "classical space-time" physics. The rates for various processes having basically interpretation as geometro-temporal densities would represent the probabilities just as in the case of particle physics experiment. For tqc in living matter this would correspond to gene expression, neural firing, EEG patterns,...

A representation as a conscious experience is another (and actually the ultimate) representation of the outcome. It need not have any symbolic counterpart since it is felt. Intuition, emotions and emotional intelligence would naturally relate to this kind of representation made possible by irreducible entanglement. This representation would be based on fuzzy qubits and would mean that the outcome would be true or false only with certain probability. This unreliability would be felt consciously.

The proposed model of tqc combined with basic facts about theta waves [30, 45] to be discussed in the subsection about the role of supra currents in tqc suggests that EEG rhythm (say theta rhythm) and correlated firing patterns correspond to the isolation at the first half period of tqc and random firing at second half period to the sub-sequent tqc:s at shorter time scales coming as negative powers

of 2. The fractal hierarchy of time scales would correspond to a hierarchy of frequency scales for generalized EEG and power spectra at these scales would give information about the outcome of tqc. Synchronization would be obviously an essential element in this picture and could be understood in terms of classical dynamics which defines space-time surface as a generalized Bohr orbit.

Tqc would be analogous to the generation of a dynamical hologram or "conscious hologram" [9] . EEG rhythm would correspond to reference wave generated by magnetic body as control and coordination signal and the contributions of spikes to EEG generated by neurons would correspond to the incoming wave interfering with the reference wave.

How data is feeded into submodules of tqc?

Scale hierarchy obviously gives tqc a fractal modular structure and the question is how data is feeded to submodules at shorter length scales. There are certainly interactions between different levels of scale hierarchy. The general ideas about master-slave hierarchy assigned with self-organization support the hypothesis that these interactions are directed from longer to shorter scales and have interpretation as a specialization of input data to tqc sub-modules represented by smaller space-time sheets of hierarchy. The call of submodule would occur when the tqc of the calling module halts and the result of computation is expressed as a 4-D pattern. The lower level module would start only after the halting of tqc (with respect to subjective time at least) and the durations of resulting tqc's would come as $T_n = 2^{-n}T_0$ that geometric series of tqc's would become possible. There would be entire family of tqc's at lower level corresponding to different values of input parameters from calling module.

One of the ideas assigned to hyper-computation [1] is that one can have infinite series of computations with durations comings as negative powers of 2 (Zeno paradox obviously inspires this idea). In TGD framework there can be however only a finite series of these tqc's since CP_2 time scale poses a lower bound for the duration of tqc. One might of course ask whether the spectrum of Planck constant could help in this respect.

The role of dissipation and energy feed

Dissipation plays key role in the theory of self-organizing systems [2] . Its role is to serve as a Darwinian selector. Without an external energy feed the outcome is a situation in which all organized motions disappear. In presence of energy feed highly unique self-organization patterns depending only very weakly on the initial conditions emerge.

In the case of tqc one function of dissipation would be to drive the braidings to static standard configurations, and perhaps even effectively eliminate fluctuations in non-topological degrees of freedom. Note that magnetic fields are important for 1-gates. Magnetic flux conservation however saves magnetic fields from dissipation.

External energy feed is needed in order to generate new braidings. For the proposed model of cellular tqc the flow of intracellular water induces the braiding and requires energy feed. Also now dissipation would drive this flow to standard patterns coding for tqc programs. Metabolic energy would be also needed in order to control whether lipids can flow or not by generating cis type unsaturated bonds. Obviously, energy flows defining self organization patterns would define tqc programs.

Is it possible to realize arbitrary tqc?

The 4-D spin glass degeneracy of TGD Universe due to the enormous vacuum degeneracy of Kähler action gives good hopes that the classical dynamics for braidings allows to realize every possible tqc program. As a consequence, space-time sheets decompose to maximal non-deterministic regions representing basic modules of tqc. Similar decomposition takes place at the level of light-like partonic 3-surfaces and means decomposition to 3-D regions inside which conformal invariance eliminates light-like direction as dynamical degree of freedom so that the dynamics is effectively that of 2-dimensional object. Since these 3-D regions behave as independent units as far as longitudinal conformal invariance is considered, one can say that light-like 3-surfaces are 3-dimensional in discretized sense. In fact, for 2-D regions standard conformal invariance implies similar effective reduction to 1-dimensional dynamics realized in terms of a net of strings and means that 2-dimensionality is realized only in discretized sense.

6.4 DNA as topological quantum computer

Braids [1] code for topological quantum computation. One can imagine many possible identifications of braids but this is not essential for what follows. What is highly non-trivial is that the motion of the ends of strands defines both time-like and space-like braidings with latter defining in a well-defined sense a written version of the tqc program, kind of log file. The manipulation of braids is a central element of tqc and if DNA really performs tqc, the biological unit modifying braidings should be easy to identify. An obvious signature is the 2-dimensional character of this unit.

6.4.1 Conjugate DNA as performer of tqc and lipids as quantum dancers

In this section the considerations are restricted to DNA as tqc. It is however quite possible that also RNA and other biomolecules could be involved with tqc like process.

Sharing of labor

The braid strands must begin from DNA double strands. Precisely which part of DNA does perform tqc? Genes? Introns [49] ? Or could it be conjugate DNA which performs tqc? The function of conjugate DNA has indeed remained a mystery and sharing of labor suggests itself.

Conjugate DNA would do tqc and DNA would "print" the outcome of tqc in terms of RNA yielding amino-acids in the case of exons. RNA could the outcome in the case of introns. The experience about computers and the general vision provided by TGD suggests that introns could express the outcome of tqc also electromagnetically in terms of standardized field patterns. Also speech would be a form of gene expression. The quantum states braid would entangle with characteristic gene expressions. This hypothesis will be taken as starting point in the following considerations.

Cell membranes as modifiers of braidings defining tqc programs?

The manipulation of braid strands transversal to DNA must take place at 2-D surface. The ends of the space-like braid are dancers whose dancing pattern defines the time-like braid, the running of classical tqc program. Space-like braid represents memory storage and tqc program is automatically written to memory during the tqc. The inner membrane of the nuclear envelope and cell membrane with entire endoplasmic reticulum included are good candidates for dancing hall. The 2-surfaces containing the ends of the hydrophobic ends of lipids could be the parquets and lipids the dancers. This picture seems to make sense.

1. Consider first the anatomy of membranes. Cell membrane [15] and membranes of nuclear envelope [69] consist of 2 lipid [52] layers whose hydrophobic ends point towards interior. There is no water here nor any direct perturbations from the environment or interior milieu of cell. Nuclear envelope consists of two membranes having between them an empty volume of thickness 20-40 nm. The inner membrane consists of two lipid layers like ordinary cell membrane and outer membrane is connected continuously to endoplasmic reticulum [31] , which forms a highly folded cell membrane. Many biologists believe that cell nucleus is a prokaryote, which began to live in symbiosis with a prokaryote defining the cell membrane.

2. What makes dancing possible is that the phospholipid layers of the cell membrane are liquid crystals [2] : the lipids can move freely in the horizontal direction but not vertically. "Phospho" could relate closely to the metabolic energy needs of dancers. If these lipids are self-organized around braid strands, their dancing patterns along the membrane surface would be an ideal manner to modify braidings since the lipids would have standard positions in a lattice. This would be like dancing on a chessboard. Note that the internal structure of lipid does not matter in this picture since it is braid color dicated by DNA nucleotide which matters. As a matter fact, living matter is full of self-organizing liquid crystals and one can wonder whether the deeper purpose of their life be running and simultaneous documentation of tqc programs?

3. Ordinary computers have an operating system: a collection of standard programs - the system - and similar situation should prevail now. The "printing" of outputs of tqc would represent example of this kind of standard program. This tqc program should not receive any input from the environment of the nucleus and should therefore correspond to braid strands connecting

conjugate strand with strand. Braid strands would go only through the inner nuclear membrane and return back and would not be affected much since the volume between inner and outer nuclear membranes is empty. This assumption looks ad hoc but it will be found that the requirement that these programs are inherited as such in the cell replication necessitates this kind of structure (see the section "Cell replication and tqc").

4. The braid strands starting from the conjugate DNA could traverse several time through the highly folded endoplasmic reticulum but without leaving cell interior and return back to nucleus and modify tqc by intracellular input. Braid strands could also traverse the cell membrane and thus receive information about the exterior of cell. Both of these tqc programs could be present also in prokaryotes [86] but the braid strands would always return back to the DNA, which can be also in another cell. In multicellulars (eukaryotes [33]) braid strands could continue to another cell and give rise to "social" tqc programs performed by the multicellular organisms. Note that the topological character of braiding does not require isolation of braiding from environment. It might be however advantageous to have some kind of sensory receptors amplifying sensory input to standardized re-braiding patterns. Various receptors in cell membrane would serve this purpose.

5. Braid strands can end up at the parquet defined by ends of the inner phospholipid layer: their distance of inner and outer parquet is few nanometers. They could also extend further.

   i) If one is interested in connecting cell nucleus to the membrane of another cell, the simpler option is the formation of hole defined by a protein attached to cell membrane. In this case only the environment of the second cell affects the braiding assignable to the first cell nucleus.

   ii) The bi-layered structure of the cell membrane could be essential for the build-up of more complex tqc programs since the strands arriving at two nearby hydrophobic 2-surfaces could combine to form longer strands. The formation of longer strands could mean the fusion of the two nearby hydrophobic two-surfaces in the region considered. In fact, tqc would begin with the cutting of the strands so that non-trivial braiding could be generated via lipid dance and tqc would halt when strands would recombine and define a modified braiding. This would allow to connect cell nucleus and cell membrane to a larger tqc unit and cells to multicellular tqc units so that the modification of tqc programs by feeding the information from the exteriors of cells - essential for the survival of multicellulars - would become possible.

Gene expression and other basic genetic functions from tqc point of view

It is useful to try to imagine how gene expression might relate to the halting of tqc. There are of course myriads of alternatives for detailed realizations, and one can only play with thoughts to build a reasonable guess about what might happen.

1. Qubits for transcription factors and other regulators

Genetics is consistent with the hypothesis that genes correspond to those tqc moduli whose outputs determine whether genes are expressed or not. The naive first guess would be that the value of single qubit determines whether the gene *is* expressed or not. Next guess replaces "*is* " with "*can be*".

Indeed, gene expression involves promoters, enhancers and silencers [87] . Promoters are portions of the genome near genes and recognized by proteins known as transcription factors [96] . Transcription factors bind to the promoter and recruit RNA polymerase, an enzyme that synthesizes RNA. In prokaryotes RNA polymerase itself acts as the transcription factor. For eukaryotes situation is more complex: at least seven transcription factors are involved with the recruitment of the RNA polymerase II catalyzing the transcription of the messenger RNA. There are also transcription factors for transcription factors and transcription factor for the transcription factor itself.

The implication is that several qubits must have value "Yes" for the actual expression to occur since several transcription factors are involved with the expression of the gene in general. In the simplest situation this would mean that the computation halts to a measurement of single qubit for subset of genes including at least those coding for transcription factors and other regulators of gene expression.

2. Intron-exon qubit

Genes would have very many final states since each nucleotide is expected to correspond to at least single qubit. Without further measurements that state of nucleotides would remain highly entangled for each gene. Also these other qubits are expected to become increasingly important during evolution.

For instance, eukaryotic gene expression involves a transcription of RNA and splicing out of pieces of RNA which are not translated to amino-acids (introns). Also the notion of gene is known to become increasingly dynamical during the evolution of eukaryotes so that the expressive power of genome increases. A single qubit associated with each codon telling whether it is spliced out or not would allow maximal flexibility. Tqc would define what genes are and the expressive power of genes would be due to the evolution of tqc programs: very much like in the case of ordinary computers. Stopping sign codon and starting codon would automatically tell where the gene begins and ends if the corresponding qubit is "Yes". In this picture the old fashioned static genes of prokaryotes without splicings would correspond to tqc programs for which the portions of genome with a given value of splicing qubit are connected.

3. What about braids between DNA, RNA, tRNA and amino-acids

This simplified picture might have created the impression that amino-acids are quantum outsiders obeying classical bio-chemistry. For instance, transcription factors would in this picture end up to the promoter by a random process and "Print" would only increase the density of the transcription factor. If DNA is able to perform tqc, it would however seem very strange if it would be happy with this rather dull realization of other central functions of the genetic apparatus.

One can indeed consider besides the braids connecting DNA and its conjugate - crucial for the success of replication - also braids connecting DNA to mRNA and other forms of RNA, mRNA to tRNA, and tRNA to amino-acids. These braids would provide the topological realization of the genetic code and would increase dramatically the precision and effectiveness of the transcription and translation if these processes correspond to quantum transitions at the level of dark matter leading more or less deterministically to the desired outcome at the level of visible matter be it formation of DNA doublet strand, of DNA-mRNA association, of mRNA-tRNA association or tRNA-amino-acid association.

For instance, a temporary reduction of the value of Planck constant for these braids would contract these to such a small size that these associations would result with a high probability. The increase of Planck constant for braids could in turn induce the transfer of mRNA from the nucleus, the opening of DNA double strand during transcription and mitosis.

Also DNA-amino-acid braids might be possible in some special cases. The braiding between regions of DNA at which proteins bind could be a completely general phenomenon. In particular, the promoter region of gene could be connected by braids to the transcription factors of the gene and the halting of tqc computation to printing command could induce the reduction of Planck constant for these braids inducing the binding of the transcription factor binds to the promoter region. In a similar manner, the region of DNA at which RNA polymerase binds could be connected by braid strands to the RNA polymerase.

How braid color is represented?

If braid strands carry 4-color (A,T,C,G) then also lipid strands should carry this kind of 4-color. The lipids whose hydrophobic ends can be joined to form longer strand should have same color. This color need not be chemical in TGD Universe.

Only braid strands of the same color can be connected as tqc halts. This poses strong restrictions on the model.

1. Do braid strands appear as patches possessing same color?

Color conservation is achieved if the two lipid layers decompose in a similar manner into regions of fixed color and the 2-D flow is restricted inside this kind of region at both layers. A four-colored map of cell membrane would be in question! Liquid crystal structure [15] applies only up to length scale of $L(151) = 10$ nm and this suggests that lipid layer decomposes into structural units of size $L(151)$ defining also cell membrane thickness. These regions might correspond to minimal regions of fixed color containing $N \sim 10^2$ lipids.

The controversial notion of lipid raft [54] was inspired by the immiscibility of ordered and disordered liquid phases in a liquid model of membrane. The organization to connected regions of particular

phase could be a phenomenon analogous to a separation of phases in percolation. Many cell functions implicate the existence of lipid rafts. The size of lipid rafts has remained open and could be anywhere between 1 and 1000 nm. Also the time scale for the existence of a lipid raft is unknown. A line tension between different regions is predicted in hydrodynamical model but not observed. If the decomposition into ordered and disordered phases is time independent, ordered phases could correspond to those involved with tqc and possess a fixed color. If disordered phases contain no braid strands the mixing of different colors is avoided. The problem with this option is that it restricts dramatically the possible braidings.

If one takes this option seriously, the challenge is to make patches and patch color (A,T,C,G) visible. Perhaps one could try to mark regions of portions of lipid layer by some marker to find whether the lipid layer decomposes to non-mixing regions.

Quantum criticality suggests that that the patches of lipid layer have a fractal structure corresponding to a hierarchy of tqc program modules. The hydrodynamics would be thus fractal: patches containing patches.... moving with respect to each other would correspond to braids containing braids containing ... such that sub-braids behave as braid strands. In principle this is also a testable prediction.

2. Does braid color corresponds to some chemical property?

The conserved braid color is not necessary for the model but would imply genetic coding of the tqc hardware so that sexual reproduction would induce an evolution of tqc hardware. Braid color would also make the coupling of foreign DNA to the tqc performed by the organism difficult and realize an immune system at the level of quantum information processing.

The conservation of braid color poses however considerable problems. The concentration of braid strands of the same color to patches would guarantee the conservation but would restrict the possible braiding dramatically. A more attractive option is that the strands of same color find each other automatically by energy minimization after the halting of tqc. Electromagnetic Coulomb interaction would be the most natural candidate for the interaction in question. Braid color would define a faithful genetic code at the level of nucleotides. It would induce long range correlation between properties of DNA strand and the dynamics of cell immediately after the halting of tqc.

The idea that color could be a chemical property of phospholipids does not seem plausible. The lipid asymmetry of the inner and outer monolayers excludes the assignment of color to the hydrophilic groups PS, PI, PE, PCh. Fatty acids have $N = 14, ..., 24$ carbon atoms and $N = 16$ and 18 are the most common cases so that one could consider the possibility that the 4 most common feet pairs could correspond to the resulting combinations. It is however extremely difficult to understand how long range correlation between DNA nucleotide and fatty acid pair could be created.

3. Does braid color correspond to neutral quark pairs?

It seems that the color should be a property of the braid strand. In TGD inspired model of high T_c super-conductivity [12] wormhole contacts having u and $\overline{d}$ and d and $\overline{u}$ quarks at the two wormhole throats feed electron's gauge flux to larger space-time sheet. The long range correlation between electrons of Cooper pairs is created by color confinement for an appropriate scaled up variant of chromo-dynamics which are allowed by TGD. Hence the neutral pairs of colored quarks whose members are located the ends of braid strand acting like color flux tube connecting the nucleotide to the lipid could code DNA color to QCD color.

For the pairs $u\overline{d}$ with net em charge the quark and anti-quark have the same sign of em charge and tend to repel each other. Hence the minimization of electro-magnetic Coulomb energy favors the neutral configurations $u\overline{u}$, $d\overline{d}$ and $u\overline{u}$, and $d\overline{d}$ coding for A,T,C,G in some order.

After the halting of tqc only these pairs would form with a high probability. The reconnection of the strands would mean a formation of a short color flux tube between the strands and the annihilation of quark pair to gluon. Note that single braid strand would connect DNA color and its conjugate rather than identical colors so that braid strands connecting two DNA strands (conjugate strands) should always traverse through an even (odd) number of cell membranes. The only plausible looking option is that nucleotides A,T,G,C are mapped to pairs of quark and anti-quarks at the ends of braid strand. Symmetries pose constraints on this coding.

1. By the basic assumptions charge conjugation must correspond to DNA conjugation so that one A and T would be coded to quark pair, say $q\overline{q}$ and its conjugate $\overline{q}q$. Same for C and G.

2. An additional aesthetically appealing working hypothesis is that *both* A and G with the same number of aromatic cycles (three) correspond to $q\overline{q}$ (or its conjugate).

   This would leave four options:

$$\begin{array}{ll} (A,G) \to (u\overline{u}, d\overline{d}) \ , & (T,C) \to (\overline{u}u, \overline{d}d) \ , \\ (A,G) \to (d\overline{d}, u\overline{u}) \ , & (T,C) \to (\overline{d}d), \overline{u}u) \ , \\ (T,C) \to (u\overline{u}, d\overline{d}) \ , & (A,G) \to (\overline{u}u, \overline{d}d) \ , \\ (T,C) \to (d\overline{d}, u\overline{u}) \ , & (A,G) \to (\overline{d}d), \overline{u}u) \ . \end{array} \tag{6.4.1}$$

   It is an experimental problem to deduce which of these correspondences - if any - is realized.

Some general predictions

During tqc the lipids of the two lipid layers should define independent units of lipid hydrodynamics whereas after halting of tqc they should behave as single dynamical unit. Later it will be found that these two phases should correspond to high T_c superconductivity for electrons (Cooper pairs would bind the lipid pair to form single unit) and its absence. This prediction is testable.

The differentiation of cells should directly correspond to the formation of a mapping of a particular part of genome to cell membrane. For neurons the gene expression is maximal which conforms with the fact that neurons can have very large size. Axon might be also part of the map. Stem cells represent the opposite extreme and in this case minimum amount of genome should be mapped to cell membrane. The prediction is that the evolution of cell should be reflected in the evolution of the genome-membrane map.

Quantitative test for the proposal

There is a simple quantitative test for the proposal. A hierarchy of tqc programs is predicted, which means that the number of lipids in the nuclear inner membrane should be larger or at least of the same order of magnitude that the number of nucleotides. For definiteness take the radius of the lipid molecule to be about 5 Angstroms (probably somewhat too large) and the radius of the nuclear membrane about 2.5 μm.

For our own species the total length of DNA strand is about one meter and there are 30 nucleotides per 10 nm. This gives 6.3×10^7 nucleotides: the number of intronic nucleotides is only by few per cent smaller. The total number of lipids in the nuclear inner membrane is roughly 10^8. The number of lipids is roughly twice the number nucleotides. The number of lipids in the membrane of a large neuron of radius of order 10^{-4} meters is about 10^{11}. The fact that the cell membrane is highly convoluted increases the number of lipids available. Folding would make possible to combine several modules in sequence by the proposed connections between hydrophobic surfaces.

6.4.2 How quantum states are realized?

Quantum states should be assigned to the ends of the braid strands and therefore to the nucleotides of DNA and conjugate DNA. The states should correspond to many-particle states of anyons and fractional electrons and quarks and anti-quarks are the basic candidates.

Anyons represent quantum states

The multi-sheeted character of space-time surface as a 4-surface in a book like structure having as pages covering spaces of the imbedding space (very roughly, see the appendix) would imply additional degrees of freedom corresponding to the group algebra of the group $G \supset Z_n$ defining the covering. Especially interesting groups are tedra-hedral, octahedral, and icosahedral groups whose action does not map any plane to itself. Group algebra would give rise to $n(G)$ quantum states. If electrons are labeled by elements of group algebra this gives $2^{n(G)}$-fold additional degeneracy corresponding to many-electron states at sheets of covering. The vacuum state would be excluded so that $2^{n(G)} - 1$ states would result. If only Cooper pairs are allowed one would have $m_n = 2^{n(G)-1} - 1$ states.

This picture suggests the fractionization of some fermionic charges such as em charge, spin, and fermion number. This aspect is discussed in detail in the Appendix. Single fermion state would be replaced by a set of states with fractional quantum numbers and one would have an analogy with the full electronic shell of atom in the sense that a state containing maximum number of anyonic fermions with the same spin direction would have the quantum numbers of the ordinary fermion.

One can consider two alternative options.

1. The fractionization of charges inspired the idea that catalytic hot spots correspond to "half" hydrogen bonds containing dark fractionally charged electron meaning that the Fermi sea for electronic anyons is not completely filled [6] . The formation of hydrogen bond would mean a fusion of "half hydrogen bond" and its conjugate having by definition a compensating fractional charges guaranteing that the net em charge and electron number of the resulting state are those of the ordinary electron pair and the state is stable as an analog of the full electron shell. Half hydrogen bonds would assign to bio-molecules "names" as sequences of half hydrogen bonds and only molecules whose "names" are conjugates of each other would form stable hydrogen bonded pairs. Therefore symbolic dynamics would enter the biology via bio-catalysis. Concerning quantum computation the problem is that the full shell assigned to hydrogen bond corresponds to only single state and cannot carry information.

2. The assignment of braids and fractionally charged anyonic quarks and anti-quarks would realize very similar symbolic dynamics. One cannot exclude the possibility that leptonic charges fractionize to same values as quark charges.

This suggest the following picture.

1. One could assign the fractional quantum numbers to the quarks and anti-quarks at the ends of the flux tubes defining the braid strands. This hypothesis is consistent with the correspondence between nucleotides and quarks and assigns anyonic quantum states to the ends of the braid. Wormhole magnetic fields would distinguish between matter in vivo and in vitro. This option is certainly favored by Occam's razor in TGD Universe.

2. Hydrogen bonds connect the DNA strands which suggests that fractionally charged quantum states at the ends of braids might be assignable to the ends of hydrogen bonds. The model for plasma electrolysis of Kanarev [1] , [1] leads to a proposal that new physics is involved with hydrogen bonds. The presence of fractionally charged particles at the ends of bond might provide alternative explanation for the electrostatic properties of hydrogen bonds usually explained in terms of a modification electronic charge distribution by donor-acceptor mechanism. There would exists entire hierarchy of hydrogen bonds corresponding to the increasing values of Planck constant. DNA and even hydrogen bonds associated with water might correspond to a larger value of Planck constant for mammals than for bacteria.

3. The model for protein folding code [3] leads to a cautious conclusion that flux tubes are prerequisites for the formation of hydrogen bonds although not identifiable with them. The model predicts also the existence of long flux tubes between acceptors of hydrogen bonds (such as $O=$, and aromatic rings assignable to DNA nucleotides, amino-acid backbone, phosphates, XYP, $X = A, T, G, C$, $Y = M, D, T$). This hypothesis would allow detailed identification of places to which quantum states are assigned.

Hierarchy of genetic codes defined by Mersenne primes

The model for the hierarchy of genetic codes inspires the question whether the favored values of $n(G) - 1$ correspond to Mersenne primes [4] . The table below lists the lowest hierarchies. Most of them are short.

$\{M_n\}$	$\{n(G)\}$ $\{n_b\}$	
$\{2, 7, 127, 2^{127}-1, ?\}$	$\{4, 8, 128, 2^{127}, ?\}$	$\{2, 6, 126, 2^{126}, ?\}$
$\{5, 31, 2^{31}-1\}$	$\{6, 32, 2^{31}\}$	$\{4, 30, 2^{30}\}$
$\{13, 2^{13}-1\}$	$\{14, 2^{13}\}$	$\{12, 2^{12}\}$
$\{17, 2^{17}-1\}$	$\{18, 2^{17}\}$	$\{16, 2^{16}\}$
$\{19, 2^{19}-1\}$	$\{20, 2^{19}\}$	$\{18, 2^{18}\}$
$\{61, 2^{61}-1\}$	$\{62, 2^{61}\}$	$\{60, 2^{60}\}$
$\{89, 2^{89}-1\}$	$\{90, 2^{89}\}$	$\{88, 2^{88}\}$
$\{107, 2^{107}-1\}$	$\{108, 2^{107}\}$	$\{106, 2^{106}\}$

(6.4.2)

The number of states assignable to M_n is $M_n = 2^n - 1$ which does not correspond to full n bits: the reason is that one of the states is not physically realizable. 2^{n-1} states have interpretation as maximal number of mutually consistent statements and to $n_b = n - 1$ bits. The table above lists the values of n_b for Mersenne primes.

Notice that micro-tubules decompose into 13 parallel helices consisting of 13 tubulin dimers. Could these helices with the conformation of the last tubulin dimer serving as a kind of parity bit realize M_{13} code?

There would be a nice connection with the basic phenomenology of ordinary computers. The value of the integer $n-1$ associated with Mersenne primes would be analogous to the number of bits of the basic information unit of processor. During the evolution of PCs it has evolved from 8 to 32 and is also power of 2.

6.4.3 The role of high T_c superconductivity in tqc

A simple model for braid strands leads to the understanding of how high T_c super conductivity assigned with cell membrane [23] could relate to tqc. The most plausible identification of braid strands is as magnetic or wormhole magnetic flux tubes consisting of pairs of flux tubes connected by wormhole contacts whose throats carry fermion and anti-fermion such that their rotational motion at least partially generates the antiparallel magnetic fluxes at the two sheets of flux tube. The latter option is favored by the model of tqc but one must of course keep mind open for variants of the model involving only ordinary flux tubes. Both kinds of flux tubes can carry charged particles such as protons, electrons, and biologically important ions as dark matter with large Planck constant and the model for nerve pulse and EEG indeed relies on this assumption [57] .

Currents at space-like braid strands

If space-like braid strands are identified as idealized structures obtained from 3-D tube like structures by replacing them with 1-D strands, one can regard the braiding as a purely geometrical knotting of braid strands.

The simplest realization of the braid strand as magnetic flux tube would be as a hollow cylindrical surface connecting conjugate DNA nucleotide to cell membrane and going through 5- and/or 6- cycles associated with the sugar backbone of conjugate DNA nucleotides. The free electron pairs associated with the aromatic cycles would carry the current creating the magnetic field needed.

For wormhole magnetic flux one would have pair of this kind of hollow cylinders connected by wormhole contacts and carrying opposite magnetic fluxes. In this case the currents created by wormhole contacts would give rise to the antiparallel magnetic fluxes at the space-time sheets of wormhole contact and could serve as controllers of tqc. I have indeed proposed long time ago that so called wormhole Bose-Einstein condensates might be fundamental for the quantum control in living matter [84] . In this case the presence of supra currents at either sheet would generate asymmetry between the magnetic fluxes.

There are two extreme options for both kinds of magnetic fields. For B-option magnetic field is parallel to the strand and vector potential rotates around it. For A-option vector potential is parallel to the strand and magnetic field rotates around it. The general case corresponds to the hybrid of these options and involves helical magnetic field, vector potential, and current.

1. For B-option current flowing around the cylindrical tube in the transversal direction would generate the magnetic field. The splitting of the flux tube would require that magnetic flux vanishes requiring that the current should go to zero in the process. This would make possible selection of a part of DNA strand participating to tqc.

2. For A-option the magnetic field lines of the braid would rotate around the cylinder. This kind of field is created by a current in the direction of cylinder. In the beginning of tqc the strand would split and the current of electron pairs would stop flowing and the magnetic field would disappear. Also now the initiation of computation would require stopping of the current and should be made selectively at DNA.

   The control of the tqc should rely on currents of electron pairs (perhaps Cooper pairs) associated with the braid strands. Supra currents would have quantized values and they are therefore very attractive candidates. The (supra) currents could also bind lipids to pairs so that they would define single dynamical unit in 2-D hydrodynamical flow. One can also think that Cooper pairs with electrons assignable to different members of lipid pair bind it to a single dynamical unit.

Do supra currents generate magnetic fields?

Energetic considerations favor the possibility that supra currents create the magnetic fields associated with the braid strands defined by magnetic flux tubes. In the case of wormhole magnetic flux tubes supra currents could generate additional magnetic fields present only at the second sheet of the flux tube.

Supra current would be created by a voltage pulse ΔV, which gives rise to a constant supra current after it has ceased. Supra current would be destroyed by a voltage pulse of opposite sign. Therefore voltage pulses could define an elegant fundamental control mechanism allowing to select the parts of genome participating to tqc. This kind of voltage pulse could be collectively initiated at cell membrane or at DNA. Note that constant voltage gives rise to an oscillating supra current.

Josephson current through the cell membrane would be also responsible for dark Josephson radiation determining that part of EEG which corresponds to the correlate of neuronal activity [23] . Note that TGD predicts a fractal hierarchy of EEGs and that ordinary EEG is only one level in this hierarchy. The pulse initiating or stopping tqc would correspond in EEG to a phase shift by a constant amount

$$\Delta\Phi = Ze\Delta VT/\hbar \ ,$$

where T is the duration of pulse and ΔV its magnitude.

The contribution of Josephson current to EEG responsible for beta and theta bands interpreted as satellites of alpha band should be absent during tqc and only EEG rhythm would be present. The periods dominated by EEG rhythm should be observed as EEG correlates for problem solving situations (say mouse in a maze) presumably involving tqc. The dominance of slow EEG rhythms during sleep and meditation would have interpretation in terms of tqc.

Topological considerations

The existence of supra current requires that the flow allows for a complex phase $exp(i\Psi)$ such that supra current is proportional to $\nabla\Psi$. This requires integrability in the sense that one can assign to the flow lines of A or B (combination of them in the case of A-B braid) a coordinate variable Ψ varying along the flow lines. In the case of a general vector field X this requires $\nabla\Psi = \Phi X$ giving $\nabla \times X = -\nabla\Phi/\Phi$ as an integrability condition. This condition defines what is known as Beltrami flow [8] .

The perturbation of the flux tube, which spoils integrability in a region covering the entire cross section of flux tube means either the loss of super-conductivity or the disappearance of the net supra current. In the case of the A-braid, the topological mechanism causing this is the increase in the dimension of the CP_2 projection of the flux tube so that it becomes 3-D [8] , where I have also considered the possibility that 3-D character of CP_2 projection is what transforms the living matter to a spin glass type phase in which very complex self-organization patterns emerge. This would conform with the idea that in tqc takes place in this phase.

Fractal memory storage and tqc

If Josephson current through cell membrane ceases during tqc, tqc manifests itself as the presence of only EEG rhythm characterized by an appropriate cyclotron frequency. Synchronous neuron firing might therefore relate to tqc. The original idea that a phase shift of EEG is induced by the voltage initiating tqc - although wrong - was however useful in that it inspired the question whether the initiation of tqc could have something to do with what is known as a place coding by phase shifts performed by hippocampal pyramidal cells [30, 45] . The playing with this idea provides important insights about the construction of quantum memories and demonstrates the amazing explanatory power of the paradigm once again.

The model also makes explicit important conceptual differences between tqc a la TGD and in the ordinary sense of wordin particular those related to different view about the relation between subjective and geometric time.

1. In TGD tqc corresponds to the unitary process U taking place following by a state function reduction and preparation. It replaces configuration space ("world of classical worlds") spinor field with a new one. Configuration space spinor field represent generalization of time evolution of Schrödinger equation so that a quantum jump occurs between entire time evolutions. Ordinary tqc corresponds to Hamiltonian time development starting at time $t = 0$ and halting at $t = T$ to a state function reduction.

2. In TGD the expression of the result of tqc is essentially 4-D pattern of gene expression (spiking pattern in the recent case). In usual tqc it would be 3-D pattern emerging as the computation halts at time t. Each moment of consciousness can be seen as a process in which a kind of 4-D statue is carved by starting from a rough sketch and proceeding to shorter details and building fractally scaled down variants of the basic pattern. Our life cycle would be a particular example of this process and would be repeated again and again but of course not as an exact copy of the previous one.

1. Empirical findings

The place coding by phase shifts was discovered by O'Reefe and Recce [30] . In [45] Y. Yamaguchi describes the vision in which memory formation by so called theta phase coding is essential for the emergence of intelligence. It is known that hippocampal pyramidal cells have "place property" being activated at specific "place field" position defined by an environment consisting of recognizable objects serving as landmarks. The temporal change of the percept is accompanied by a sequence of place unit activities. The theta cells exhibit change in firing phase distributions relative to the theta rhythm and the relative phase with respect to theta phase gradually increases as the rat traverses the place field. In a cell population the temporal sequence is transformed into a phase shift sequence of firing spikes of individual cells within each theta cycle.

Thus a temporal sequence of percepts is transformed into a phase shift sequence of individual spikes of neurons within each theta cycle along linear array of neurons effectively representing time axis. Essentially a time compressed representation of the original events is created bringing in mind temporal hologram. Each event (object or activity in perceptive field) is represented by a firing of one particular neuron at time τ_n measured from the beginning of the theta cycle. τ_n is obtained by scaling down the real time value t_n of the event. Note that there is some upper bound for the total duration of memory if scaling factor is constant.

This scaling down - story telling - seems to be a fundamental aspect of memory. Our memories can even abstract the entire life history to a handful of important events represented as a story lasting only few seconds. This scaling down is thought to be important not only for the representation of the contextual information but also for the memory storage in the hippocampus. Yamaguchi and collaborators have also found that the gradual phase shift occurs at half theta cycle whereas firings at the other half cycle show no correlation [45] . One should also find an interpretation for this.

2. TGD based interpretation of findings

How this picture relates to TGD based 4-D view about memory in which primary memories are stored in the brain of the geometric past?

1. The simplest option is the initiation of tqc like process in the beginning of each theta cycle of period T and having geometric duration $T/2$. The transition $T \to T/2$ conforms nicely with the fundamental hierarchy of time scales comings as powers defining the hierarchy of measurement resolutions and associated with inclusions of hyperfinite factors of type II_1 [83] . That firing is random at second half of cycle could simply mean that no tqc is performed and that the second half is used to code the actual events of "geometric now".

2. In accordance with the vision about the hierarchy of Planck constants defining a hierarchy of time scales of long term memories and of planned action, the scaled down variants of memories would be obtained by down-wards scaling of Planck constant for the dark space-time sheet representing the original memory. In principle a scaling by any factor $1/n$ (actually by any rational) is possible and would imply the scaling down of the geometric time span of tqc and of light-like braids. One would have tqc's inside tqc's and braids within braids (flux quanta within flux quanta). The coding of the memories to braidings would be an automatic process as almost so also the formation of their zoomed down variants.

3. A mapping of the time evolution defining memory to a linear array of neurons would take place. This can be understood if the scaled down variant (scaled down value of $\hbar$) of the space-time sheet representing original memory is parallel to the linear neuron array and contains at scaled down time value t_n a stimulus forcing n^{th} neuron to fire. The 4-D character of the expression of the outcome of tqc allows to achieve this automatically without complex program structure.

To sum up, it seems that the scaling of Planck constant of time like braids provides a further fundamental mechanism not present in standard tqc allowing to build fractally scaled down variants of not only memories but tqc's in general. The ability to simulate in shorter time scale is a certainly very important prerequisite of intelligent and planned behavior. This ability has also a space-like counterpart: it will be found that the scaling of Planck constant associated with space-like braids connecting bio-molecules might play a fundamental role in DNA replication, control of transcription by proteins, and translation of mRNA to proteins. A further suggestive conclusion is that the period T associated with a given EEG rhythm defines a sequence of tqc's having geometric span $T/2$ each: the rest of the period would be used to perceive the environment of the geometric now. The fractal hierarchy of EEGs would mean that there are tqc's within tqc's in a very wide range of time scales.

6.4.4 Codes and tqc

TGD suggests the existence of several (genetic) codes besides 3-codon code [33, 29] . The experience from ordinary computers and the fact that genes in general do not correspond to $3n$ nucleotides encourages to take this idea more seriously. The use of different codes would allow to tell what kind of information a given piece of DNA strand represents. DNA strand would be like a drawing of building containing figures (3-code) and various kinds of text (other codes). A simple drawing for the building would become a complex manual containing mostly text as the evolution proceeds: for humans 96 per cent of code would corresponds to introns perhaps obeying some other code.

The hierarchy of genetic codes is obtained by starting from n basic statements and going to the meta level by forming all possible statements about them (higher order logics) and throwing away one which is not physically realizable (it would correspond to empty set in the set theoretic realization). This allows $2^n - 1$ statements and one can select 2^{n-1} mutually consistent statements (half of the full set of statements) and say that these are true and give kind of axiomatics about world. The remaining statements are false. DNA would realize only the true statements.

The hierarchy of Mersenne primes $M_n = 2^n - 1$ with $M_{n(next)} = M_{M_n}$ starting from $n = 2$ with $M_2 = 3$ gives rise to 1-code with 4 codons, 3-code with 64 codons, and $3 \times 21 = 63$-code with 2^{126} codons [33] realized as sequences of 63 nucleotides (the length of 63-codon is about $2L(151)$, roughly twice the cell membrane thickness. It is not known whether this Combinatorial Hierarchy continues ad infinitum. Hilbert conjectured that this is the case.

In the model of pre-biotic evolution also 2-codons appear and 3-code is formed as the fusion of 1- and 2-codes. The problem is that 2-code is not predicted by the basic Combinatorial Hierarchy associated with $n = 2$.

There are however also other Mersenne hierarchies and the next hierarchy allows the realization of the 2-code. This Combinatorial Hierarchy begins from Fermat prime $n = 2^k + 1 = 5$ with $M_5 =$

$2^5 - 1 = 31$ gives rise to a code with 16 codons realized as 2-codons (2 nucleotides). Second level corresponds to Mersenne prime $M_{31} = 2^{31} - 1$ and a code with $2^{30=15\times 2}$ codons realized by sequences of 15 3-codons containing 45 nucleotides. This corresponds to DNA length of 15 nm, or length scale $3L(149)$, where $L(149) = 5$ nm defines the thickness of the lipid layer of cell membrane. $L(151) = 10$ nm corresponds to 3 full 2π twists for DNA double strand. The model for 3-code as fusion of 1- and 2-codes suggests that also this hierarchy - which probably does not continue further - is realized.

There are also further short Combinatorial hierarchies corresponding to Mersenne primes [4] .

1. $n = 13$ defines Mersenne prime M_{13}. The code would have $2^{12=6\times 2}$ codons representable as sequences of 6 nucleotides or 2 3-codons. This code might be associated with microtubuli.

2. The Fermat prime $17 = 2^4 + 1$ defines Mersenne prime M_{17} and the code would have $2^{16=8\times 2}$ codons representable as sequences of 8 nucleotides.

3. $n = 19$ defines Mersenne prime M_{19} and code would have $2^{18=9\times 2}$ codons representable as sequences of 9 nucleotides or three DNA codons.

4. The next Mersennes are M_{31} belonging to $n = 5$ hierarchy, M_{61} with $2^{60=30\times 2}$ codons represented by 30-codons. This corresponds to DNA length $L(151) = 10$ nm (cell membrane thickness). M_{89} (44-codons), M_{107} (53-codons) and M_{127} (belonging to the basic hierarchy) are the next Mersennes. Next Mersenne corresponds to M_{521} (260-codon) and to completely super-astrophysical p-adic length scale and might not be present in the hierarchy.

   This hierarchy is realized at the level of elementary particle physics and might appear also at the level of DNA. The 1-, 2-, 3-, 6-, 8-, and 9-codons would define lowest Combinatorial Hierarchies.

6.5 How to realize the basic gates?

In order to have a more concrete view about realization of tqc, one must understand how quantum computation can be reduced to a construction of braidings from fundamental unitary operations. The article "Braiding Operators are Universal Quantum Gates" by Kaufmann and Lomonaco [16] contains a very lucid summary of how braids can be used in topological quantum computation.

1. The identification of the braiding operator R - a unitary solution of Yang-Baxter equation - as a universal 2-gate is discussed. In the following I sum up only those points which are most relevant for the recent discussion.

2. One can assign to braids both knots and links and the assignment is not unique without additional conditions. The so called braid closure assigns a unique knot to a given braid by connecting n^{th} incoming strand to n^{th} outgoing strand without generating additional knotting. All braids related by so called Markov moves yield the same knot. The Markov trace (q-trace actually) of the unitary braiding S-matrix U is a knot invariant characterizing the braid closure.

3. Braid closure can be mimicked by a topological quantum computation for the original n-braid plus trivial n-braid and this leads to a quantum computation of the modulus of the Markov trace of U. The probability for the diagonal transition for one particular element of Bell basis (whose states are maximally entangled) gives the modulus squared of the trace. The closure can be mimicked quantum computationally.

6.5.1 Universality of tqc

Quantum computer is universal if all unitary transformations of n^{th} tensor power of a finite-dimensional state space V can be realized. Universality is achieved by using only two kinds of gates. The gates of first type are single particle gates realizing arbitrary unitary transformation of $U(2)$ in the case of qubits. Only single 2-particle gate is necessary and universality is guaranteed if the corresponding unitary transformation is entangling for some state pair. The standard choice for the 2-gate is CNOT acting on bit pair (t, c). The value of the control bit c remains of course unchanged and the value of the target bit changes for $c = 1$ and remains unchanged for $c = 0$.

6.5.2 The fundamental braiding operation as a universal 2-gate

The realization of CNOT or gate equivalent to it is the key problem in topological quantum computation. For instance, the slow de-coherence of photons makes quantum optics a promising approach but the realization of CNOT requires strongly nonlinear optics. The interaction of control and target photon should be such that for second polarization of the control photon target photon changes its direction but keeps it for the second polarization direction.

For braids CNOT can be be expressed in terms of the fundamental braiding operation e_n representing the exchange of the strands n and $n+1$ of the braid represented as a unitary matrix R acting on $V_n \otimes V_{n+1}$.

The basic condition on R is Yang-Baxter equation expressing the defining condition $e_n e_{n+1} e_n = e_{n+1} e_n e_{n+1}$ for braid group generators. The solutions of Yang-Baxter equation for spinors are well-known and CNOT can be expressed in the general case as a transformation of form $A_1 \otimes A_2 R A_3 \otimes A_4$ in which single particle operators A_i act on incoming and outgoing lines. 3-braid is the simplest possible braid able to perform interesting tqc, which suggests that genetic codons are associated with 3-braids.

The dance of lipids on chessboard defined by the lipid layer would reduce R to an exchange of neighboring lipids. For instance, the matrix $R = DS$, $D = diag(1,1,1,-1)$ and $S = e_{11}+e_{23}+e_{32}+e_{44}$ the swap matrix permuting the neighboring spins satisfies Yang-Baxter equation and is entangling.

6.5.3 What the replacement of linear braid with planar braid could mean?

Standard braids are essentially linear objects in plane. The possibility to perform the basic braiding operation for the nearest neighbors in two different directions must affect the situation somehow.

1. Classically it would seem that the tensor product defined by a linear array must be replaced by a tensor product defined by the lattice defined by lipids. Braid strands would be labelled by two indices and the relations for braid group would be affected in an obvious manner.

2. The fact that DNA is a linear structure would suggests that the situation is actually effectively one-dimensional, and that the points of the lipid layer inherit the linear ordering of nucleotides of DNA strand. One can however ask whether the genuine 2-dimensionality could provide a mathematical realization for possible long range correlations between distant nucleotides n and $n+N$ for some N. p-Adic effective topology for DNA might become manifest via this kind of correlations and would predict that N is power of some prime p which might depend on organism's evolutionary level.

3. Quantum conformal invariance would suggest effective one-dimensionality in the sense that only the observables associated with a suitably chosen linear braid commute. One might also speak about topological quantum computation in a direction transversal to the braid strands giving a slicing of the cell membrane to parallel braid strands. This might mean an additional computational power.

4. Partonic picture would suggest a generalization of the linear braid to a structure consisting of curves defining the decomposition of membrane surface regions such that conformal invariance applies separately in each region: this would mean breaking of conformal invariance and 2-dimensionality in discrete sense. Each region would define a one parameter set of topological quantum computations. These regions might corresponds to genes. If each lipid defines its own conformal patch one would have a planar braid.

6.5.4 Single particle gates

The realization of single particle gates as $U(2)$ transformations leads naturally to the extension of the braid group by assigning to the strands sequences of group elements satisfying the group multiplication rules. The group elements associated with a n^{th} strand commute with the generators of braid group which do not act on n^{th} strand. G would be naturally subgroup of the covering group of rotation group acting in spin degrees of spin 1/2 object. Since $U(1)$ transformations generate only an overall phase to the state, the presence of this factor might not be necessary. A possible candidate for $U(1)$

factor is as a rotation induced by a time-like parallel translation defined by the electromagnetic scalar potential $\Phi = A_t$.

One of the challenges is the realization of single particle gates representing $U(2)$ rotation of the qubit. The first thing to come mind was that $U(2)$ corresponds to $U(2)$ rotation induced by magnetic field and electric fields. A more elegant realization is in terms of $SU(3)$ rotation, where $SU(3)$ is color group associated with strong interactions. This looks rather weird but there is direct evidence for the prediction that color $SU(3)$ is associated with tqc and thus cognition: something that does not come first in mind! I have myself written text about the strange finding of topologist Barbara Shipman suggesting that quarks are in some mysterious manner involved with honeybee dance and proposed an interpretation.

The realization of qubit as ordinary spin

A possible realization for single particle gate $s \subset SU(2)$ would be as $SU(2)$ rotation induced by a magnetic pulse. This transformation is fixed by the rotation axis and rotation angle around this axes. This kind of transformation would result by applying to the strand a magnetic pulse with magnetic field in the direction of rotation axes. The duration of the pulse determines the rotation angle. Pulse could be created by bringing a magnetic flux tube to the system, letting it act for the required time, and moving it away. $U(1)$ phase factor could result from the electromagnetic gauge potential as a non-integrable phase factor $exp(ie \int A_t dt/\hbar)$ coming from the presence of scale potential $\Phi = A_t$ in the Hamiltonian.

Conrete model for realization of 1-gates in terms of ordinary rotations

What could be the simplest realization of the $U(2)$ transformation in the case of cell membrane assuming that it corresponds to ordinary rotation?

1. There should be a dark spin 1/2 particle associated with each lipid, electron or proton most plausibly. TGD based model for high T_c superconductivity [12] predicts that Cooper pairs correspond to pairs of cylindrical space-time sheets with electrons at the two space-time sheets. The size scale of the entire Cooper corresponds to p-adic length scale $L(151)$ defining the thickness of the cell membrane and cylindrical structure to $L(149)$, the thickness of lipid layer so that electrons are the natural candidates for tqc. The Cooper pair BE condensate would fuse the lipid pairs to form particles of lipid liquid.

2. Starting of tqc requires the splitting of electron Cooper pairs and its halting the formation of Cooper pairs again. The initiation of tqc could involve increase of temperature or an introduction of magnetic field destroying the Cooper pairs. Tqc could be also controlled by supra currents flowing along cylindrical flux tubes connecting 5- and/or aromatic cycles of conjugate DNA nucleotides to the cell membrane. The cutting of the current flow would make it possible for braid strand to split and tqc to begin.

3. By shifting a magnetic flux tube or sheet parallel to the cell membrane to the position of the portion of membrane participating to tqc is the simplest manner to achieve this. Halting could be achieved by removing the flux tube. The unitary rotation induced by the constant background magnetic field would not represent gate and it should be possible to eliminate its effect from tqc proper.

4. The gate would mean the application of a magnetic pulse much stronger than background magnetic field on the braid strands ending at the lipid layer. The model for the communication of sensory data to the magnetic body requires that magnetic flux tubes go through the cell membrane. This would suggest that the direction of the magnetic flux tube is temporarily altered and that the flux tube then covers part of the lipid for the required period of time.

   The realization of the single particle gates requires electromagnetic interactions. That single particle gates are not purely topological transformations could bring in the problems caused by a de-coherence due to electromagnetic perturbations. The large values of Planck constant playing a key role in the TGD based model of living matter could save the situation. The large value of $\hbar$ would be also required by the anyonic character of the system necessary to obtain R-matrix defining a universal 2-gate.

The minimum time needed to inducing full 2π rotation around the magnetic axes would be essentially the inverse of cyclotron frequency for the particle in question in the magnetic field considered$T = 1/f_c = 2\pi m/ZeB$. For electrons in the dark magnetic field of $B = .2$ Gauss assigned to living matter in the quantum model of EEG this frequency would be about $f_c = .6$ MHz. For protons one would have $f_c = 300$ Hz. For a magnetic field of Tesla the time scales would be reduced by a factor 2×10^{-5}.

The realization of 1-gate in terms of color rotations

One can criticize the model of 1-gates based on ordinary spin. The introduction of magnetic pulses does not look an attractive idea and seems to require additional structures besides magnetic flux tubes (MEs?). It would be much nicer to assign the magnetic field with the flux tubes defining the braid strands. The rotation of magnetic field would however require changing the direction of braid strands. This does not look natural. Could one do without this rotation by identifying spin like degree of freedom in some other manner? This is indeed possible.

TGD predicts a hierarchy of copies of scaled up variants of both weak and color interactions and these play a key role in TGD inspired model of living matter. Both weak isospin and color isospin could be considered as alternatives for the ordinary spin as a realization of qubit in TGD framework. Below color isospin is discussed but one could consider also a realization in terms of nuclei and their exotic counterparts [1] , [1] differing only by the replacement of neutral color bond between nuclei of nuclear string with a charged one. Charge entanglement between nuclei would guarantee overall charge conservation.

1. Each space-time sheet of braid strands contains quark and antiquark at its ends. Color isospin and hypercharge label their states. Two of the quarks of the color triplet form doublet with respect to color isospin and the third is singlet and has different hyper charge Y. Hence qubit could be realized in terms of color isospin I_3 instead of ordinary spin but third quark would be inert in the Boolean sense. Qubit could be also replaced with qutrit and isospin singlet could be identified as a statement with ill-defined truth value. Trits are used also in ordinary computers. In TGD framework finite measurement resolution implies fuzzy qubits and the third state might relate to this fuzziness. Also Gödelian interpretation can be consideredthe quark state with vanishing isospin would be associated with counterparts of undecidable propositions to which one cannot assign truth value (consider sensory input which is so ambiguous that one cannot tell what is there or a situation in which one cannot decide whether to do something or not). Note that hyper-charge would induce naturally the U(1) factor affecting the over all phase of qubit but affecting differently to the third quark.

2. Magnetic flux tubes are also color magnetic flux tubes carrying non-vanishing classical color gauge field in the case that they are non-vacuum extremals. The holonomy group of classical color field is an Abelian subgroup of the $U(1) \times U(1)$ Cartan subgroup of color group. Classical color magnetic field defines the choice of quantization axes for color quantum numbers. For instance, magnetic moment is replaced with color magnetic moment and this replacement is in key role in simple model for color magnetic spin spin splittings between spin 0 and 1 mesons as well as spin 1/2 and 3/2 baryons.

3. There is a symmetry breaking of color symmetry to subgroup $U(1)_{I_3} \times U(1)_Y$ and color singletness is in TGD framework replaced by a weaker condition stating that physical states have vanishing net color quantum numbers. This makes possible the measurement of color quantum numbers in the manner similar to that for spin. For instance, color singlet formed by quark and antiquark with opposite color quantum numbers can in the measurement of color quantum numbers of quark reduce to a state in which quark has definite color quantum numbers. This state is a superposition of states with vanishing Y and I_3 in color singlet and color octet representations. Strong form of color confinement would not allow this kind of measurement.

4. Color rotation in general changes the directions of quantization axis of I_3 and Y and generates a new state basis. Since $U(1) \times U(1)$ leaves the state basis invariant, the space defined by the choices of quantization axes is 6-dimensional flag manifold $F = SU(3)/U(1) \times U(1)$. In contrast to standard model, color rotations in general do not leave classical electromagnetic field invariant

since classical em field is a superposition of color invariant induced Kähler from and color non-invariant part proportional classical Z^0 field. Hence, although the magnetic flux tube retains its direction and shape in M^4 degrees of freedom, its electromagnetic properties are affected and this is visible at the level of classical electromagnetic interactions.

5. If color isospin defines the qubit or qutrit in topological quantum computation, color quantum numbers and the flag manifold F should have direct relevance for cognition. Amazingly, there is a direct experimental support for this! Years ago topologist Barbara Shipman made the intriguing observation that honeybee dance can be understood in terms of a model involving the flag manifold F [30] . This led her to propose that quarks are in some mysterious manner involved with the honeybee dance. My proposal [31] was that color rotations of the space-time sheets associated with neurons represent geometric information: sensory input would be coded to color rotations defining the directions of quantization axes for I_3 and Y. Subsequent state function reduction would provide conscious representations in terms of trits characterizing for instance sensory input symbolically.

   In [31] I introduced the notions of geometric and sensory qualia corresponding to two choices involved with the quantum measurement: the choice of quantization axes performed by the measurer and the "choice" of final state quantum numbers in state function reduction. In the case of honeybee dance geometric qualia could code information about the position of the food source. The changes of color quantum numbers in quantum jump were identified as visual colors. In state function reduction one cannot speak about change of quantum numbers but about their emergence. Therefore one must distinguish between color qualia and the conscious experience defined by the emergence of color quantum numbers: the latter would have interpretation as qutrit.

Summarizing, this picture suggests that 1-gates of DNA tqc (understood as "dance of lipids") are defined by color rotations of the ends of space-like braid strands and at lipids. The color rotations would be induced by sensory and other inputs to the system. Topological quantum computation would be directly related to conscious experience and sensory and other inputs would fix the directions of the color magnetic fields.

6.6 About realization of braiding

The most plausible identification of braid strands is as magnetic or wormhole magnetic flux tubes. Flux tubes can contain charged particles such as protons, electrons, and biologically important ions as dark matter with large Planck constant and the model for nerve pulse and EEG indeed relies on this assumption [57] .

6.6.1 Could braid strands be split and reconnect all the time?

As far as braiding alone is considered, braid strands could be split all the time. In other words, there would be no continuation of strands through the cell membrane. Computation would halt when lipids lose their unsaturated cis bonds so that they cannot follow the liquid flow. The conservation of strand color would be trivially true but would not have any implications. Supra currents would not be needed to control tqc and there would be no connection with generalized EEG. It is not obvious how the gene expression for the outcome of tqc could take place since the strands would not connect genome to genome. For these reasons this option does not look attractive.

The models for prebiotic evolution [29] and protein folding [3] lead to a conclusion that braids can connect all kind of bio-molecules to each other and also water molecules and bio-molecules Thus DNA tqc would represent only one example of tqc like activities performed by the living matter. The conclusion is that braidings are dynamical with reconnection of flux tubes representing a fundamental transformation changing the braiding and thus also tqc programs.

6.6.2 What do braid strands look like?

In the following the anatomy of braid strands is discussed at general level and then identification in terms of flux tubes of magnetic body is proposed.

Braid strands as nearly vacuum extremals

The braid strands should be nearly quantum critical sub-manifolds of $M^4 \times CP_2$ so that phase transitions changing Planck constant and thus their length can take place easily (DNA replication, binding of mRNA molecules to DNA during transcription, binding of transcription factors to promoters, binding of tRNA-amino-acid complexes to mRNA...).

Depending on whether phase transition takes place in M^4 or CP_2 degrees of freedom, either their M^4 projection belongs to $M^2 \subset M^4$ or their CP_2 projection to the homological trivial geodesic sphere $S^2 \subset CP_2$. In the latter case a vacuum extremal is in question. Maximal quantum criticality means $X^4 \subset M^2 \times S^2$ so that one has straight string with a vanishing string tension. The almost vacuum extremal property guarantees the braid strands can be easily generated from vacuum.

An additional requirement is that the gravitational mass is small. For objects of type $M^2 \times X^2_g$, $X^2_g \subset E^2 \times CP_2$, the gravitational mass vanishes for $g = 1$ (genus) and is of order CP_2 mass otherwise and negative for $g > 1$. Torus topology is the unique choice. A simple model for the braid strand is as a small non-vacuum deformation of $X^4 = M^2 \times X^2_g \subset M^2 \subset E^2 \times S^2$, $g = 1$. As a special case one has $X^4 = M^2 \times S^1 \times S^1 \subset M^2 \subset E^2 \times S^1$, for which M^4 projection is a hollow cylinder, which could connect the aromatic 5- or 6-cycle of sugar backbone to another DNA strand, lipid, or amino-acid.

Braid strands as flux tubes of color magnetic body

One can make this model more detailed by feeding in simple physical inputs. The flux tubes carry magnetic field when the supra current is on. In TGD Universe all classical fields are expressible in terms of the four CP_2 coordinates and their gradients so that em, weak, color and gravitational fields are not independent as in standard model framework. In particular, the ordinary classical em field is necessarily accompanied by a classical color field in the case of non-vacuum extremals. This predicts color and ew fields in arbitrary long scales and quantum classical correspondence forces to conclude that there exists fractal hierarchy of electro-weak and color interactions.

Since the classical color gauge field is proportional to Kähler form, its holonomy group is Abelian so that effectively $U(1) \times U(1) \subset SU(3)$ gauge field is in question. The generation of color flux requires colored particles at the ends of color flux tube so that the presence of pairs of quark and antiquark assignable to the pairs of wormhole throats at the ends of the tube is unavoidable if one accepts quantum classical correspondence.

In the case of cell, a highly idealized model for color magnetic flux tubes is as flux tubes of a dipole field. The preferred axis could be determined by the position of the centrosomes forming a T shaped structure. DNA strands would define the idealized dipole creating this field: DNA is indeed negatively charged and electronic currents along DNA could create the magnetic field. The flux tubes of this field would go through nuclear and cell membrane and return back unless they end up to another cell. This is indeed required by the proposed model of tqc.

It has been assumed that the initiation of tqc means that the supra current ceases and induces the splitting of braid strands. The magnetic flux need not however disappear completely. As a matter fact, its presence forced by the conservation of magnetic flux seems to be crucial for the conservation of braiding. Indeed, during tqc magnetic and color magnetic flux could return from lipid to DNA along another space-time sheet at a distance of order CP_2 radius from it. For long time ago I proposed that this kind of structures -which I christened "wormhole magnetic fields" - might play key role in living matter [84] . The wormhole contacts having quark and antiquark at their opposite throats and coding for A,T,C,G would define the places where the current flows to the "lower" space-time sheet to return back to DNA. Quarks would also generate the remaining magnetic field and supra current could indeed cease.

The fact that classical em fields and thus classical color fields are always present for non-vacuum extremals means that also the motion of any kind of particles (space-time sheets), say water flow, induces a braiding of magnetic flux tubes associated with molecules in water if the temporary splitting of flux tubes is possible. Hence the prerequisites for tqc are met in extremely general situation and tqc involving DNA could have developed from a much simpler form of tqc performed by water giving perhaps rise to what is known as water memory [102, 186, 135, 136] . This would also suggest that the braiding operation is induced by the a controlled flow of cellular water.

6.6.3 How to induce the basic braiding operation?

The basic braiding operation requires the exchange of two neighboring lipids. After some basic facts about phospholipids the simplest model found hitherto is discussed.

Some facts about phospholipids

Phospholipids [78] - which form about 30 per cent of the lipid content of the monolayer - contain phosphate group. The dance of lipids requires metabolic energy and the hydrophilic ends of the phospholipid could provide it. They could also couple the lipids to the flow of water in the vicinity of the lipid monolayer possibly inducing the braiding. Of course, the causal arrow could be also opposite.

The hydrophilic part of the phospholipid is a nitrogen containing alcohol such as serine, inositol or ethanolamine, or an organic compound such as choline. Phospholipids are classified into 3 kinds of phosphoglycerides [77] and sphingomyelin.

1. Phosphoglycerides

In cell membranes, phosphoglycerides are the more common of the two phospholipids, which suggest that they are involved with tqc. One speaks of phosphotidyl X, where X= serine, inositol, ethanolamine is the nitrogen containing alcohol and X=Ch the organic compound. The shorthand notion OS, PI, PE, PCh is used.

The structure of the phospholipid is most easily explained using the dancer metaphor. The two fatty chains define the hydrophobic feet of the dancer, glycerol and phosphate group define the body providing the energy to the dance, and serine, inositol, ethanolamine or choline define the hydrophilic head of the dancer (perhaps "deciding" the dancing pattern).

There is a lipid asymmetry in the cell membrane. PS, PE, PI in cytoplasmic monolayer (alcohols). PC (organic) and sphingomyelin in outer monolayer. Also glycolipids are found only in the outer monolayer. The asymmetry is due to the manner that the phospholipids are manufactured.

[76] [76] in the inner monolayer is negatively charged and its presence is necessary for the normal functioning of the cell membrane. It activates protein kinase C which is associated with memory function. PS slows down cognitive decline in animals models. This encourages to think that the hydrophilic polar end of at least PS is involved with tqc, perhaps to the generation of braiding via the coupling to the hydrodynamic flow of cytoplasm in the vicinity of the inner monolayer.

2. Fatty acids

The fatty acid chains in phospholipids and glycolipids usually contain an even number of carbon atoms, typically between 14 and 24 making 5 possibilities altogether. The 16- and 18-carbon fatty acids are the most common. Fatty acids [34] may be saturated or unsaturated, with the configuration of the double bonds nearly always cis.

The length and the degree of unsaturation of fatty acids chains have a profound effect on membranes fluidity as unsaturated lipids create a kink, preventing the fatty acids from packing together as tightly, thus decreasing the melting point (increasing the fluidity) of the membrane. The number of unsaturaded cis bonds and their positions besides the number of Carbon atoms characterizes the lipid. Quite generally, there are $3n$ Carbons after each bond. The creation of unsatured bond by removing H atom from the fatty acid could be an initiating step in the basic braiding operation creating room for the dancers. The bond should be created on both neighboring lipids simultaneously.

Could hydrodynamic flow induce braiding operations?

One can imagine several models for what might happen during the braiding operation in the lipid bilayer [53] . One such view is following.

1. The creation of unsaturated bond and involving elimination of H atom from fatty acid would lead to cis configuration and create the room needed by dancers. This operation should be performed for both lipids participating in the braiding operation. After the braiding it might be necessary to add H atom back to stabilize the situation. The energy needed to perform either or both of these operations could be provided by the phosphate group.

2. The hydrophilic ends of lipids couple the lipids to the surrounding hydrodynamic flow in the case that the lipids are able to move. This coupling could induce the braiding. The primary

control of tqc would thus be by using the hydrodynamic flow by generating localized vortices. There is considerable evidence for water memory [102] but its mechanism remains to be poorly understood. If also water memory is realized in terms of the braid strands connecting fluid particles, DNA tqc could have evolved from water memory.

3. Sol-gel phase transition is conjectured to be important for the quantum information processing of cell [11] . In the transition which can occur cyclically actin filaments (also at EEG frequencies) are assembled and lead to a gel phase resembling solid. Sol phase could correspond to tqc and gel to the phase following the halting of tqc. Actin filaments might be assignable with braid strands or bundles of them and shield the braiding. Also microtubules might shield bundles of braid strands.

4. Only inner braid strands are directly connected to DNA which also supports the view that only the inner monolayer suffers a braiding operation during tqc and that the outer monolayer should be in a "freezed" state during it. There is a net negative charge associated with the inner monolayer possibly relating to its participation to the braiding. The vigorous hydrodynamical flows known to take place below the cell membrane could induce the braiding.

6.6.4 Some qualitative tests

In life sciences the standard manner to test a model is to look whether the function of the system is affected in the predicted manner if one somehow interferes the system. Now interfering with tqc should affect the gene expression resulting otherwise.

1. Lipid layer hydrodynamics is predicted to allow two fundamental phases. The pairs of lipids should behave like single dynamical unit in super-conducting phase and as independent units in non-super-conducting phase. The application of magnetic field or increase of temperature should induce a transition between these two phases. These phase transitions applied selectively to the regions of cell membrane should affect gene expression. One could prevent halting of tqc by applying an external magnetic field and thus prevent gene expression. One could dream of deducing gene-membrane mapping with endoplasmic reticulum included.

2. The temperature range in which quantum critical high T_c super-conductivity is possible is probably rather narrow and should correspond to the temperature range in which cell membrane is functional. Brain is functional in a very narrow range of temperatures. Selective freezing of cell membrane might provide information about gene map provided by cell membrane.

3. One could do various things to the cell membrane. One could effectively remove part of it, freeze, or heat some part of the lipid liquid and look whether this has effects on gene expression. The known effects of ELF em fields on the behavior and physiology of vertebrates [23] might relate to the fact that these fields interfere with tqc.

4. Artificially induced braiding by inducing a motion of lipids by some kind of stirring during tqc could induce/affect gene expression.

5. The application of external dark magnetic fields could affect gene expression. Tqc could be initiated artificially in some part of cell membrane by the application of dark magnetic field. Running tqc could be halted by an application of dark magnetic field interfering to zero with the background field. The application of magnetic pulses would affect tqc and thus gene expression. The problem is how to create dark magnetic fields in given length scale (range of magnetic field strength). Perhaps one could generate first ordinary magnetic field and then transform it to dark magnetic field by $\hbar$ changing phase transition. This could be achieved by a variation of some macroscopic parameters such as temperature, magnetic field strength, and analog of doping fraction appearing in standard high T_c super-conductivity.

6. Artificially induced scalings of $\hbar$ by varying temperature and parameters such as pH should induce or stop DNA replication, DNA-mRNA transcription and the translation of mRNA to proteins.

6.7 A model for flux tubes

Biochemistry represents extremely complex and refined choreography. It is hard to believe that this reduces to a mere unconscious and actually apparent fight for chemical survival. In TGD Universe consciousness would be involved even at the molecular level and magnetic body would be the choreographer whose dance would induce the molecular activities. This picture combined with the idea of standard plugs and terminals at which flux tubes end, leads to a to a picture allowing to get rather concrete picture about DNA as topological quantum computer. It becomes also possible to formulate a model for protein folding in which DNA codons can be said to code for both amino-acid sequences and their folding. Hence the information loss thought to occur because of the many-to-one character of the code does not really happen. The model is discussed in [3] .

6.7.1 Flux tubes as a correlate for directed attention

Molecular survival is the standard candidate for the fundamental variational principle motivating the molecular intentional actions. There is entire hierarchy of selves and the survival at the higher level of hierarchy would force co-operation and altruistic behavior at the lower levels. One might hope that this hypothesis reduces to Negentropy Maximization Principle [44] , which states that the information contents of conscious experience is maximized. If this picture is accepted, the evolution of molecular system becomes analogous to the evolution of a society.

Directed attention is the basic aspect of consciousness and the natural guess would be that directed attention corresponds to the formation of magnetic flux tubes between subject and target. The directedness property requires some manner to order the subject and target.

1. The ordering by the values of Planck constant is what first comes in mind. The larger space-time sheet characterized by a larger value of Planck constant and thus at a higher level of evolutionary hierarchy would direct its attention to the smaller one.

2. Also the ordering by the value of p-adic prime characterizing the size scale of the space-time sheet could be considered but in this case directedness could be questioned.

3. Attention can be directed also to thoughts. Could this mean that attention is directed from real space-time sheets to p-adic space-time sheets for various values of primes but not vice versa? Or could the direction be just the opposite at least in the intentional action transforming p-adic space-time sheet to real space-time sheet? Perhaps directions are opposite for cognition and intention.

The generation of wormhole magnetic flux tubes could be the correlate for the directed attention, not only at molecular level, but quite generally. Metaphorically, the strands of braid would be the light rays from the eyes of the perceiver to the target and their braiding would code the motions of the target to a topological quantum computation like activity and form a memory representation at least. The additional aspect of directed attention would be the coloring of the braid strands, kind of coloring for the virtual light rays emerging from the eyes of the molecular observer. In the case of DNA this can induce a coloring of braid strands emerging from amino-acids and other molecules so that it would indeed become possible to assign to amino-acid the conjugate of the middle nucleotide of the codon XYZ coding for it.

Attention can be also redirected. For this process there is a very nice topological description as a reconnection of flux tubes. What happens is that flux tubes $A \to B$ and $C \to D$ fuse for a moment and become flux tubes $A \to D$ and $C \to B$. This process is possible only if the strands have the same color so that the values of the quark charges associated with A and B are the same.

This kind of process can modify tqc programs. For instance, in the case of the flux tubes coming from nucleotides X and X_c and ending to the lipid layer this process means that X and X_c and corresponding lipids become connected and genome builds memory representation about this process via similar link. If proteins are connected with mRNA connected to DNA in this manner, this process would allow the formation of flux tubes between amino-acids of two proteins in such a manner that protein would inherit from DNA codon the color of the middle nucleotide and its interactions effectively reduce to base pairing.

DNA would have memory representation about molecular processes via these changing braiding topologies, and one could say that these molecular processes reflect the bodily motions of the magnetic

body. Entire molecular dynamics of the organism could represent an enormous tqc induced by the motor activities of the magnetic body. At the level of sensory experience similar idea has been discussed earlier [74] : out of body experiences (OBEs) and illusions such as train illusion could be understood in terms of motor action of magnetic body inducing virtual sensory percepts.

Attention can be also switched on and off. Here the structure of the lipid ends containing two nearby situated $=O$:s suggests the mechanism: the short flux tube connecting $=O$:s disappears. The minimization of Coulomb interaction energy at each end implies that re-appearance of the flux tubes creates a short flux tube with the original strand color. Note that the conservation of magnetic flux allows this option only for wormhole magnetic flux tubes.

6.7.2 Does directed attention generate memory representations and tqc like processes?

Directed attention induces braiding if the target is moving and changing its shape. This gives rise to a memory representation of the behavior of the object of attention and also to a tqc like process. A considerable generalization of tqc paradigm suggests itself.

Tqc could be induced by the braiding between DNA and lipids, DNA and proteins via folding processes, DNA RNA braiding and braiding between DNA and its conjugate, DNA and protein braiding. The outcome of tqc would be represented as the temporal patterns of biochemical concentrations and rates and there would be hierarchy of p-adic time scales and those associated with the dark matter hierarchy.

For instance, the protein content of lipid membranes is about 50 per cent and varies between 25-75 per cent so that protein folding and lipid flow could define tqc programs as self-organization patterns. The folding of protein is dynamical process: alpha helices are created and disappear in time scale of 10^{-7} seconds and the side chains of protein can rotate.

The details of the tqc like process depend on what one assumes. The minimal scenario is deduced from the transcription and translation processes and from the condition that magnetic body keeps control or at least keeps book about what happens using genome as a tool. The picture would be essentially what one might obtain by applying a rough model for web in terms of nodes and links. The reader is encouraged to use paper and pencil to make the following description more illustrative.

1. Assume that mRNA and DNA remain connected by flux tubes after transcription and that only reconnection process can cut this connection so that mRNA inherits the conjugate colors of DNA. Assume same for mRNA and tRNA. Assume that amino-acid associated with tRNA has similar flux tube connections with the nucleotides of tRNA. Under these assumptions amino-acid inherits the conjugate colors of DNA nucleotides via the connection line DNA-mRNA-tRNA-amino-acid faith-fully if all links are correspond to quark pairs rather than their superpositions. Wobble pairing for Z nucleotide could actually correspond to this kind of superposition.

2. One can consider several options for the amino-acid-acid DNA correspondence but trial-and-error work showed that a realistic folding code is obtained only if X, Y, and Z correspond to $O-H$, $O=$, and NH_2 in the constant part of free amino-acid. During translation the formation of the peptide bond between amino-acids dehydration leads to a loss of $O-H$ and one H from NH_2. The flux tube from tRNA to $O-H$ becomes a flux tube to water molecule inheriting the color of X so that $O=-NH_2$ of the amino-acid inside protein represents the conjugate of YZ.

3. Hydrogen bonding between NH and $O=$ in alpha helices and beta sheets reduces effectively to base pairing taking place only if the condition $Y_1 = Z_2$ (briefly $Y = Z$ in the sequel) is satisfied. This is extremely restrictive condition on the gene coding the amino-acid unless one assumes quantum counterpart of wobble base pairing for mRNA or tRNA-amino-acid pairing in the case of Z nucleotide (as one indeed must do). Note that the $O=$ atom of the amino-acid is in a special role in that it can have hydrogen bond flux tubes to donors and flux tube connections with $O=$:s of other amino-acids, the residues of amino-acids containing acceptors (say $O=$ or aromatic ring), and with the aromatic rings of say ATP.

4. The recombination process for two conjugate DNA-mRNA-tRNA-amino-acid links can transform the flux tubes in such manner that one obtains link between the $=O$:s of amino-acids A_1 and A_2 characterized by Y and Y_c. Besides hydrogen bonding this mechanism could be central in the

enzyme substrate interaction. The process would pair tRNAs corresponding to Y and Y_c together to give DNA-mRNA-tRNA-tRNA-mRNA-DNA link providing a memory representation about amino-acid pairing $A_1 - A_2$. One could say that magnetic body creates with the mediation of the genome dynamical tqc programs to which much of the bio-molecular activity reduces. Not all however, since two amino-acid pairs $A_1 - A_2$ and $A_3 - A_4$ can recombine to $A_1 - A_4$ and $A_3 - A_2$ without DNA knowing anything about it. Magnetic body would however know.

5. The constant part of non-hydrogen bonded amino-acid inside protein would behave like $Y_c Z_c$ if amino-acid is coded by XYZ. The $COOH$ end of protein would behave like $X_c Y_c Z_c$. Also flux tubes connecting the residue groups become possible and protein does not behave like single nucleotide anymore. By color inheritance everything resulting in the reconnection process between $O =$ and NH_2 and residues reduces in a well-defined sense to the genetic code.

6.7.3 Realization of flux tubes

The basic questions about flux are following. Where do they begin, where do they end, and do they have intermediate plugs which allow temporary cutting of the flux tube.

Where do flux tubes begin from?

The view about magnetic body as a controller of biological body using genome as a control tool suggests that DNA is to a high degree responsible for directed attention and other molecules as targets so that flux tubes emanate from DNA nucleotides. The reason would be that the aromatic cycles of DNA correspond to larger value of Planck constant. Some chemical or geometric property of DNA nucleotides or of DNA nucleotides of DNA strand could raise them to the role of subject. Aromatic cycle property correlates with the symmetries associated with large value of Planck constant and is the best candidate for this property.

If this picture is accepted then also some amino-acid residues might act as subjects/objects depending on the option. Phe, His, Trp, Tyr contain aromatic cycle. The derivatives of Trp and Tyr act as neurotransmitters and His is extremely effective nucleophilic catalyst. This would make possible more specific catalytic mechanisms through the pairing of Phe, His, Trp, and Tyr with residues having flux tube terminals.

This raises the question about the physical interaction determining the color of the strand emerging from the aromatic cycle. The interaction energy of quark at the end of flux tube with the classical electromagnetic fields of nuclei and electrons of the ring should determine this. The wormhole contact containing quark/antiquark at the throat at space-time sheet containing nuclei and electrons could also delocalize inside the ring. One of the earliest hypothesis of TGD inspired model for living matter was that wormhole Bose-Einstein condensates could be crucial for understanding of the behavior of biomolecules [84] . Wormhole throats with quark and antiquark at their throats appear also in the model of high T_c superconductivity [12] . As far as couplings are considered, these wormhole contacts are in many respects analogous to the so called axions predicted by some theories of elementary particle physics. The wormhole contact like property is by no means exceptional: all gauge bosons correspond to wormhole contacts in TGD Universe.

The only manner for the electronic space-time sheet to feed its electromagnetic gauge flux to larger space-time sheets using exactly two wormhole contacts is to use wormhole contacts with $\overline{u}$ and d at their "upper" throat (T, G). For proton one would have $\overline{d}$ and u at their "upper" throat (A, C). The presence of electron or proton at nucleotide space-time sheet near the end of flux tube might allow to understand the correlation. The transfer of electrons and protons between space-time sheets with different p-adic length scale is basic element of TGD based model of metabolism so that there might be some relation.

Acceptors as plugs and donors as terminals of flux tubes?

Standardization constraint suggests that flux tubes are attached to standard plugs and terminals. The explicit study of various biological molecules and the role of water in biology gives some hints.

1. An attractive idea is that $= O$ serves as a plug to which flux arrives and from which it can also continue. For the minimal option suggested by hydrogen bonding $O =$ could be connected to

two donors and $O=$ could not be connected to $O=$. The assumption that the flux tube can connect also two $O=$:s represents a hypothesis going outside the framework of standard physics. A stronger assumption is that all acceptors can act as plugs. For instance, the aromatic rings of DNA nucleotides could act as acceptors and be connected to a sequence of $O=$ plugs eventually terminating to a hydrogen bond.

2. Donors such as $O-H$ would in turn correspond to a terminal at which flux tube can end. One might be very naive and say that conscious bio-molecules have learned the fundamental role of oxygen and water in the metabolism and become very attentive to the presence of $=O$ and $O-H$. $=O$ appears in $COOH$ part of each amino-acid so that this part defines the standard plug. $=O$ appears also in the residues of Asp, Glu, Asn, Gln. $O-H$ groups appear inside the residues of Asp,Glu and Ser, Thr.

3. Hydrogen bonds $X-H--Y$ have the basic defining property associated with directed attention, namely the asymmetry between donor X and acceptor Y. Hence there is a great temptation consider the possibility that hydrogen bonds correspond to short flux tubes, that flux tubes could be seen as generalized hydrogen bonds. Quite generally, Y could be seen as the object of directed attention of X characterized by larger value of Planck constant. The assumption that two $O=$:s, or even two acceptors of a hydrogen bond, can be connected by a flux tube means more than a generalization of hydrogen bond the connection with a donor would correspond only to the final step in the sequence of flux tubes and plugs giving rise to a directed attention.

4. This hypothesis makes the model rather predictive. For instance, $N-H$, NH_2, $O-H$ and much less often $C-H$ and $S-H$ are the basic donors in the case of proteins whereas $O=$, $-O-$, $-N=S-S$, $-S^-$ and aromatic rings are the basic acceptors. Reconnection process should be involved with the dynamics of ordinary hydrogen bonding. Reconnection process implies inheritance of the flux tube color and means a realization of the symbol based dynamics. It turns out that this hypothesis leads to a model explaining basic qualitative facts about protein folding.

What about ions like Ca^{++} and Mg_{++}: can flux tubes attach also to these? Could n flux tubes terminate to an n-valent ion? This assumption leads to a model of the gel phase in which Ca^{++} ions serve as cross links between proteins in the sense that Ca^{++} ion is connected by flux tubes to two proteins whereas monovalent ions such as Na^+ cannot perform such a function. Gel-sol phase transition would be induced by a flow of Na^+ ions to the interior of cell inducing a reconnection process so that in the sol phase proteins would be connected to Na^+ ions.

6.7.4 Flux tubes and DNA

The model of DNA as topological quantum computer gives useful guide lines in the attempt to form a vision about flux tubes. It was assumed that braid strands defined by "wormhole magnetic" flux tubes join nucleotides to lipids and can continue through the nuclear or cell membrane but are split during tqc. The hydrophilic ends of lipids attach to water molecules and self-organization patterns for the water flow in gel phase induce a 2-D flow in the lipid layer which is liquid crystal defining tqc programs at the classical level as braidings. The flow indeed induces braiding if one assumes that during topological computation the connection through the cell membrane is split and reconnected after the halting of tqc.

The challenge is to understand microscopically how the flux tube joins DNA nucleotide to the phospholipid [78] . Certainly the points at which the flux tubes attach should be completely standard plugs and the formation of polypeptide bonds is an excellent guide line here. Recall that phospholipid, the tqc dancer, has two hydrophobic legs and head. Each leg has at the hydrophilic end O=C-O-C part joining it to glyceride connected to monophosphate group in turn connected to a hydrophilic residue R. The most often appearing residues are serine, inositol, ethanolamine, and choline. Only three of these appear in large quantities and there is asymmetry between cell exterior and interior.

Let us denote by $=O_1$ and $=O_2$ the two oxygens (maybe analogs of right and left hemispheres!) in question. The proposal is that DNA nucleotide and $=O_1$ are connected by a flux tube: the asymmetry between right and left lipid legs should determine which of the legs is "left leg" and which $O=$ is the "left brain hemisphere". $=O_2$, the "holistic right brain hemisphere", connects in turn to

the flux tube coming from the other symmetrically situated $= O_2$ at the outer surface of the second lipid layer. Besides this $= O_1$ and $= O_2$ are connected by a flux tube serving as switch on both sides of the membrane.

During tqc the short $O = -O =$ flux tube would experience reconnection with a flux tube acting as hydrogen bond between water molecules so that the connection is split and $O =$:s form hydrogen bonds. The reversal of this reconnection creates the connection again and halts the computation. The lipid residue R couples with the flow of the liquid in gel phase. Since $= O$ is in question the quark or antiquark at the end can correspond to the DNA nucleotide in question. The necessary complete correlation between quark and antiquark charges at the ends of flux tubes associated with $= O_1$ and $= O_2$ can be understood as being due to the minimization of Coulomb interaction energy.

If one is ready to accept magnetic flux tubes between all acceptors then the aromatic rings of nucleotides known to be acceptors could be connected by a flux tube to the $O =$ atom of the lipid or to some intermediate $O =$ atom. The phosphate groups associated with nucleotides of DNA strand contain also $= O$, which could act as a plug to which the flux tube from the nucleotide is attached. The detailed charge structure of the aromatic ring(s) should determine the quark-nucleotide correspondence. The connection line to the lipid could involve several intermediate $O =$ plugs and the first plug in the series would be the $O =$ atom of the monophosphate of the nucleotide.

There is a strong temptation to assume that subset of XYP molecules, $X = A, G, T, C$, $Y = M, D, T$ act as standard plugs with X and phosphates connected by flux tubes to a string. This would make it possible to engineer braid strands from standard pieces connected by standard plugs. DNA nucleotide XMP would have flux tube connection to the aromatic ring of X and the $O =$ of last P would be connected to next plug of the communication line. If so, a close connection with metabolism and topological quantum computation would emerge.

1. Phosphorylation [80] would be an absolutely essential for both metabolism and buildup of connection lines acting as braid strands. Phosphorylation is indeed known to be the basic step activating enzymes. In eukaryotes the phosphorylation takes plane amino-acids most often for ser but also thr, and trp with aromatic rings are phosphorylated. Mitochondrions have specialized to produce ATP in oxidative phosphorylation from ADP and photosynthesis produces ATP. All these activities could be seen as a production of standard plugs for braid strands making possible directed attention and quantum information processing at molecular level.

2. As already noticed, $O = -O =$ flux tubes could also act as switches inducing a shortcut of the flux tube connection by reconnecting with a hydrogen bond connecting two water molecules. This is an essential step in the model for how DNA acts as topological quantum computer. De-phosphorylation might be standard manner to realized this process.

3. This picture would fit with the fact that XYP molecules, in particular AMP, ADP, and ATP, appear in bio-molecules involved with varying functions such as signalling, control, and metabolism. $= O$ might act as a universal plug to which flux tubes from electronegative atoms of information molecules can attach their flux tubes. This would also provide a concrete realization of the idea that information molecules (neurotransmitters, hormones) are analogous to links in Internet [57] : they would not represent the information but establish a communication channel. The magnetic flux tube associated with the information molecule would connect it to another cell and by the join to $= O$ plug having flux tube to another cell, say to its nucleus, would create a communication or control channel.

6.8 Some predictions related to the representation of braid color

Even in the rudimentary form discussed above the model makes predictions. In particular, the hypothesis that neutral quark pairs represent braid color is easily testable.

6.8.1 Anomalous em charge of DNA as a basic prediction

The basic prediction is anomalous charge of DNA. Also integer valued anomalous charge for the structural units of genome is highly suggestive.

The selection of the working option - if any such exists - is indeed experimentally possible. The anomalous charge coupling to the *difference* of the gauge potentials at the two space-time sheets defines the signature of the wormhole contact at the DNA end of braid strand. The effective (or anomalous) em charge is given as sum of quark charges associated with DNA space-time sheet:

$$Q_a = [n(A)-n(T)]Q(q_A)+[n(G)-n(C)]Q(q_G) \quad (6.8.1)$$

is predicted. The four possible options for charge are given explicitly in the table below

$$\begin{array}{l} Q_a = [n(A)-n(T)]\frac{2}{3}-[n(G)-n(C)]\frac{1}{3} \ , \\ Q_a = -[n(A)-n(T)]\frac{1}{3}+[n(G)-n(C)]\frac{2}{3} \ , \\ Q_a = -[n(A)-n(T)]\frac{2}{3}+[n(G)-n(C)]\frac{1}{3} \ , \\ Q_a = [n(A)-n(T)]\frac{1}{3}-[n(G)-n(C)]\frac{2}{3} \ . \end{array} \quad (6.8.2)$$

Second option is obtained from the first option $(A,T,G,C) \to (u,\overline{u},d,\overline{d})$ by permuting u and d quark in the correspondence and the last two options by performing charge conjugation for quarks in the first two options.

The anomalous charge is experimentally visible only if the external electromagnetic fields at the two sheets are different. The negative charge of DNA due to the presence of phosphate groups implies that the first sheet carries different em field so that this is indeed the case.

The presence effective em charge depending on the details of DNA sequence means that electromagnetism differentiates between different DNA:s strands and some strands might be more favored dynamically than others. It is interesting to look basic features of DNA from this view point. Vertebral mitochondrial code has full $A \leftrightarrow G$ and $C \leftrightarrow T$ symmetries with respect to the third nucleotide of the codon and for the nuclear code the symmetry is almost exact. In the above scenario A and C *resp.* G and T would have different signs and magnitudes of em charge but they would correspond to different weak isospin states for the third quark so that this symmetry would be mathematically equivalent to the isospin symmetry of strong interactions.

The average gauge potential due to the anomalous charge per length at space-time sheet containing ordinary em field of a straight portion of DNA strand is predicted to be proportional to

$$\frac{dQ_a}{dl} = [p(A)-p(T)]Q(q_A)+[p(G)-p(C)]Q(q_G)\frac{1}{\Delta L} \ ,$$

where ΔL corresponds to the length increment corresponding to single nucleotide and $p(X)$ represents the frequency for nucleotide X to appear in the sequence. Hence the strength of the anomalous scalar potential would depend on DNA and vanish for DNA for which A and T *resp.* G and C appear with the same frequency.

6.8.2 Chargaff's second parity rule and the vanishing of net anomalous charge

Chargaff's second parity rule states that the frequencies of nucleotides for single DNA strand satisfy the conditions $p(A) \simeq p(T)$ and $p(C) \simeq p(G)$ (I am grateful for Faramarz Faghihi for mentioning this rule and the related [2] [209] to me). This rule holds true in a good approximation. In the recent context the interpretation would be as the vanishing of the net anomalous charge of the DNA strand and thus charge conjugation invariance. Stability of DNA might explain the rule and the poly-A tail in the untranslated mRNA could relate stabilization of DNA and mRNA strands.

Together with $p(A)+p(T)+p(G)+p(C)=1$ Chargaff's rule implies the conditions

$$\begin{array}{ll} p(A)+p(C) \simeq 1/2 \ , & p(A)+p(G) \simeq 1/2 \ , \\ p(T)+p(C) \simeq 1/2 \ , & p(T)+p(G) \simeq 1/2 \ . \end{array} \quad (6.8.3)$$

An interesting empirical finding [209] is that only some points at the line $p(A)+p(C) \simeq 1/2$ are realized in the case of human genome and that these points are in a good accuracy expressible in terms of Fibonacci numbers resulting as a prediction of optimization problem in which Fibonacci

numbers are however put in by hand. $p(A) = p(G) = p(C) = p(T) = 1/4$ results as a limiting case. The poly-A tail of mRNA (not coded by DNA) could reflect to the compensation of this asymmetry for translated mRNA.

The physical interpretation would be as a breaking of isospin symmetry in the sense that isospin up and down states for quarks (A and G *resp.* T and C) do not appear with identical probabilities. This need not have any effect on protein distributions if the asymmetry corresponds to asymmetry for the third nucleotide of the codon having $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries as almost exact symmetries. This of course if protein distribution is invariant under this symmetry for the first two codons.

The challenge would be to understand the probabilities $p_3(X)$ for the third codon from a physical model for the breaking of isospin symmetry for the third codon in the sense that u and $\overline{u}$ at DNA space-time sheet are more favored than d and $\overline{d}$ or vice versa. There is an obvious analogy with spontaneous breaking of vacuum symmetry.

6.8.3 Are genes and other genetic sub-structures singlets with respect to QCD color?

Genes are defined usually as transcribed portions of DNA. Genes are however accompanied by promoter regions and other regions affecting the transcription so that the definition of what one really means with gene is far from clear. In the recent case gene would be naturally tqc program module and gene in standard sense would only correspond to its sub-module responsible for the translated mRNA output of tqc.

Whatever the definition of gene is, genes as tqc program modules could be dynamical units with respect to color interaction and thus QCD color singlets (QCD color should not be confused with braid color) or equivalently - possess integer valued anomalous em charge.

One can consider two alternative working hypothesis - in a well-defined sense diametrical opposites of each other.

1. The division of the gene into structural sub-units correlates with the separation into color singlets. Thus various structural sub-units of gene (say transcribed part, translated part, intronic portions, etc...) would be color singlets.

2. Also different genetic codes that I have discussed in [29] could distinguish between different structural sub-units. For this option only gene - understood as tqc unit with un-transcribed regions included - would be color singlet.

Color singletness condition is unavoidable for mRNA and leads to a testable prediction about the length of poly-A tail added to the transcribed mRNA after translation.

The condition of integer valued anomalous charge for coding regions

In the case of coding region of gene the condition for integer charge is replaced by the conditions

$$n(A) + n(G) \ \ mod \ \ 3 = 0 \ , \quad n(C) + n(T) \ \ mod \ \ 3 = 0 \ . \tag{6.8.4}$$

These conditions are not independent and it suffices to check whether either of them is satisfied. The conditions are consistent with $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries of the third nucleotide. Note that the contribution of the stop codon (TAA, TGA or TAG) and initiating codon ATG to the A+G count is one unit.

General condition for integer valued anomalous charge

The anomalous charge of gene or even that of an appropriate sub-unit of gene is integer valued implies in the general case

$$n(A) - n(T) + n(G) - n(C) \ \ mod \ \ 3 = 0 \ . \tag{6.8.5}$$

Note that this condition does not assume that gene corresponds to $3n$ nucleotides (as I had accustomed to think). The surprising (to me) finding was that gene and also mRNA coding region of the gene in

general fails to satisfy $3n$ rule. This rule is of course by no means requiredonly the regions coding for proteins can be thought of as consisting of DNA triplets.

A possible interpretation is in terms of TGD based model for pre-biotic evolution [29] according to which genetic code (or 3-code) was formed as a fusion of 2-code and 1-code. 2-code and 1-code could still be present in genome and be associated with non-translated regions of mRNA preceding and following the translated region. The genes of 2-code and coding for RNA would have $2n$ nucleotides and the genes of 1-code could also consist of odd number of nucleotides.

There might be analogy with drawings for a building. These contain both figures providing information about building and text giving meta-level information about how to interpret figures. Figures could correspond to 3-code coding for proteins and text could be written with other codes and give instructions for the transcription and translation processes. Prokaryotic code would contain mostly figures (CDS). In eukaryotic code intronic portions could carry rich amounts of this kind of metalevel information. In the case of mRNA untranslated region preceding $5'$ end could provide similar information.

1. Repeating sequences consisting of n copies of same repeating unit could obey 1-code or 2-code. The simplest building blocks of repeating sequences are AT and CG having vanishing anomalous em charge. TATATA.... and CGCGCG... indeed appear often. Also combinations of CG and AT could repeat: so called mini-satellites are CG rich repeating sequences. Interpretation in terms of 2-code suggests itself.

2. Triplet of the unit ATTCG with integer charge repeats also often: in this case 3-code suggests itself. Telomeres of vertebrates consist of a repeating unit TTAGGG which does not have integer charge: this unit appears also as 8-nucleotide variant which suggests 2-code. Color singletness would require that this unit appears $3n$ times.

3. I have also proposed that intronic regions could obey memetic code [32] predicting that intronic codon can be represented as a sequence of 21 3-codons (implying 2^{63} 63-codons!). Individual intronic segments need not satisfy this rule, only their union if even that. Direct experimentation with gene bank data show that neither introns nor their union correspond to integer multiples of 63 nor 3 or 2 in general.

Color singletness conditions for gene

Gene is usually defined as the sequence of DNA coding for mRNA. mRNA involves also two untranslated regions (UTRs) [2] .

1. The $5'$ end of mRNA contains $5'$ cap (methylated G) and $5'$ untranslated region (UTR). The latter can be several kb long for eukaryotes. Methylated G is not coded by DNA but added so that it does not contribute to A+G-T-C count at DNA level.

2. mRNA continues after the stop codon as $3'$ UTR. Translation assigns to UTR also a poly-A tail (up to several hundreds A:s) not coded by DNA and not contributing to A+G-T-C count in the case of DNA. This region contains also AAUAAA which does not contribute to A+G-T-C count of mRNA.

   One could argue that any amino-acid sequence must allow coding and that one function of UTRs is to guarantee integer valued charge for the part of gene beginning from the initiating codon. Of course, also the non-transcribed regions of DNA not included in the standard definition of gene could take care of this.

Color singletness conditions for mRNA

Both poly-A tail and G gap are known to relate to the stabilization of mRNA. The mechanism could be addition of an anomalous charge compensating for the anomalous charge of mRNA to guarantee that second Chargaff's rule is satisfied in a good approximation: this hypothesis is testable.

Second function would be to guarantee color-singletness property. Color singletness would mean that transcribed mRNA + cap G + poly-A tail as a separate unit must be QCD color singlet at DNA space-time sheet. mRNA stability requires the condition

$$n(A) - n(T) + n(G) - n(C) + n_{tail}(A) + 1 \ \ mod \ \ 3 = 0 \tag{6.8.6}$$

to be satisfied. The knowledge of gene would thus predict $n_{tail}(A) \ \ mod \ \ 3$. This hypothesis is testable.

Chargaff's rule for mRNA

If Chargaff's rule applies also to mRNA strands one obtains one of the following predictions

$$\begin{aligned}
&2\left[n(A) + n_{tail}(A) - n(T)\right] - \left[n(G) + 1 - n(C)\right] \simeq 0 \ \ , \\
&-\left[n(A) + n_{tail}(A) - n(T)\right] + 2\left[n(G) + 1 - n(C)\right] \simeq 0 \ \ , \\
&-2\left[n(A) + n_{tail}(A) - n(T)\right] + \left[n(G) + 1 - n(C)\right] \simeq 0 \ \ , \\
&\left[n(A) + n_{tail}(A) - n(T)\right] - 2\left[n(G) + 1 - n(C)\right] \simeq 0 \ \ .
\end{aligned} \tag{6.8.7}$$

Here $n_{tail}(A)$ includes also AAUAA contributing 3 units to it plus possible other structures appearing in the tail added to the translated mRNA. The presence of poly-A tail which could also compensate for the ordinary negative charge of translated part of mRNA would suggest that A corresponds to u or $\overline{d}$ corresponding to options 1 and 4.

Moving genes and repeating elements

Transposons [98] , [43] are moving or self-copying genes. Moving genes cut from initial position and past to another position of double strand. Copying genes copy themselves first to RNA and them to a full DNA sequence which is then glued to the double strand by cut and paste procedure. They were earlier regarded as mere parasites but now it is known that their transcription is activated under stress situations so that they help DNA to evolve. In tqc picture their function would be to modify tqc hardware. For copying transposons the cutting of DNA strand occurs usually at different points for DNA and cDNA so that "sticky ends" result ("overhang" and its complement) [92] . Often the overhang has four nucleotides. The copied transposon have ends which are reversed conjugates of each other so that transposons are palindromes as are also DNA hairpins. This is suggestive of the origin of transposons.

In order to avoid boring repetitions let us denote by "satisfy P" for having having integer valued (or even vanishing) Q_a. The predictions are following:

1) The double strand parts associated with the segments of DNA produced by cutting should satisfy P.

2) The cutting of DNA should take place only at positions separated by segments satisfying P.

3) The overhangs should satisfy P.

4) Transposons should satisfy P: their reverse ends certainly satisfy P.

In the example mentioned in [88] the overhang is $CTAG$ and has vanishing Q_a. The cut site $CCTAGG$ has also vanishing Q_a. It is known [43] that transposons - repeating regions themselves - tend to attach to the repeating regions of DNA [30] .

1. There are several kinds of repeating regions. 6-10 base pair long sequences can be repeated in untranslated regions up to 10^5 times and whole genes can repeat themselves $50 - 10^4$ times.

2. Repeats are classified into tandems (say TTAGGG associated with telomeres), interspersed repetitive DNA (nuclear elements), and transposable repeat elements. Interspersed nuclear elements (INEs) are classified LINEs (long), SINEs (short), TLTRs (Transposable elements with Long Terminal Repeats), and DNA transposons themselves.

3. LINEs contain AT rich regions. SINEs known as alus (about 280 bps) contain GC rich regions whereas mariner elements (about 80 bps) are flanked by TA pairs. LTRs have length 300-1000 bps. DNA transposons are flanked with two short inverted repeat sequences flanking the reading frame: "inverted" refers to the palindrome property already mentioned.

AT and CG have vanishing Q_a so that their presence in LINEs and SINEs would make the cutting and pasting easy allowing to understand why transposons favor these regions. Viruses are known to contain long repeating terminal sequences (LTR). One could also check whether DNA decomposes to regions satisfying P and surrounded by repeating sequences which satisfy P separately or as whole as in the case DNA transposons.

Tests

Some checks of the color singletness hypothesis were made for human genome [43] .

1. For the coding sequences (CDSs) the strong prediction in general fails as expected (condition would pose restrictions on possible amino-acid contents).

2. Color singletness condition fails for genes defined in terms of translated part of mRNA (with gap and poly-A tail excluded). The un-transcribed regions of DNA involved with the gene expression (promoter region, etc...) could guarantee the color singletness. They could also stabilize DNA by bringing in compensating anomalous charge to guarantee second Chargaff's rule. Different genetic codes could distinguish between the subunits of gene.

3. To test color singletness conditions for mRNA one should know the length of poly-A tail. Unfortunately, I do not have access to this information.

4. The computation of total anomalous charges for a handful of genes, introns, and repeat units for some gene bank examples in the case of human genome indicates that both of them tend to carry net em charge which is largest for $(a, g) \leftrightarrow (\overline{d}, \overline{u})$ correspondence. The charge is in the range 5-10 per cent from the charge associated with the phosphates (-2 units per nucleotide). For second option giving negative charge (permute u and d) the anomalous charge is few per cent smaller.

   By Chargaff's law the regions outside genes responsible for the control of gene expression must contain a compensating charge of opposite sign. Kind of spontaneous symmetry breaking of charge conjugation symmetry $A \leftrightarrow T, G \leftrightarrow C$ and analogous to matter antimatter symmetry seems to take place. That control regions and translated regions have opposite densities of anomalous charge might also help in the control gene expression.

5. The poly-A tail of mRNA would carry compensating positive anomalous charge: the RNA-quark assignment could be conjugate to the DNA-quark assignment as suggested by what takes place in transcription. For instance, for the option $A \to \overline{d}$, the prediction for the length of polytail for $A \to \overline{d}$ option would be about $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)$ where $N(mRNa)$ is the number of nucleotides in transcribed mRNA and $p_a(mRNA)$ is the per cent of anomalous charge which is typically 5-10 per cent. For $p_a(mRNA) = 10$ per cent this gives as much as 30 per cent. For $A \to \overline{u}$ option one has $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)/2$. In this case also p_a is considerably smaller, typically by a factor of of order 2-3 per cent and even below per cent in some cases. Hence the relative length of tail would around 3-5 per cent. This option is perhaps more since it minimizes anomalous charge and maximizes the effectiveness of charge compensation by poly-A tail.

6. The predictions for transposons and their cut and past process should be easily testable.

6.8.4 Summary of possible symmetries of DNA

The following gives a list of possible symmetries of DNA inspired by the identification of braid color.

Color confinement in strong form

The states of quarks and anti-quarks associated with DNA both wormhole wormhole throats of braided (living) DNA strand can be color singlets and have thus integer valued anomalous em charge. The resulting prediction depends on the assignment of quarks and antiquarks to A,T,C,G which in principle should be determined by the minimization of em interaction energy between quark and nucleotide. For instance $2(A-T)-(G-C) \mod 3 = 0$ for a piece of living DNA which could make possible color

singletness. As a matter fact, color singletness conditions are equivalent for all possible for braid color assignments. This hypothesis might be weakened. For instance, it could hold true only for braided parts of DNA and this braiding are dynamical. It could also hold for entire braid with both ends included only: in this case it does not pose any conditions on DNA.

Questions: Do all living DNA strands satisfy this rule? Are only the double stranded parts of DNA braided and satisfy the rule. What about loops of hairpins?

Matter antimatter asymmetry at quark level

$A \leftrightarrow T$ and $G \leftrightarrow C$ corresponds to charge conjugation at the level of quarks (quark $\leftrightarrow$ antiquark). Chargaff's rules states $A \simeq T$ and $C \simeq G$ for long DNA strands and mean matter-antimatter symmetry in the scale of DNA strand. Double strand as a whole is matter anti-matter symmetric.

Matter-antimatter asymmetry is realized functionally at the level of DNA double strand in the sense that only DNA strand is transcribed. The study of some examples shows that genes defined as transcribed parts of DNA do not satisfy Chargaff's rule. This inspires the hypothesis about the breaking of matter antimatter symmetry. Genes have non-vanishing net $A-T$ and $C-G$ and therefore also net Q_a with sign opposite to that in control regions. Just as the Universe is matter-antimatter asymmetric, also genes would be matter-antimatter asymmetric.

Isospin symmetry at quark level

$A \leftrightarrow G$ and $T \leftrightarrow A$ correspond change of anomalous em charge by 1 unit and these operations respect color confinement condition. Local modifications of DNA inducing these changes should be preferred. The identification for the symmetries $A \leftrightarrow G$ and $T \leftrightarrow A$ for the third nucleotide of code is as isospin symmetries. For the vertebrate mitochondrial code the symmetry exact and for nuclear code slightly broken.

Matter antimatter asymmetry and isospin symmetries for the first two nucleotides

The first two nucleotides of the codon dictate to a high degree which amino-acid is coded. This inspires the idea that 3-code has emerged as fusion of 1- and 2-codes in some sense. There are two kinds of 2-codons. The codons of type A have fractional em charge and net quark number (consisting of either matter or antimatter at quark level) and are not able to form color singlets. The codons of type B have integer em charge and vanishing quark number (consisting of matter and antimatter) and are able to form color singlets. The 2-codons of type A (resp. B) are related by isospin rotations and there should be some property distinguishing between types A and B. There indeed is: if 2-codon is matter-antimatter symmetric, 1-codon is not and vice versa.

1. For almost all type A codons the amino-acid coded by the codon does not depend on the last nucleotide. There are two exceptions in the case of the nuclear code: (leu,leu,phe,phe) and (ile,ile,ile,met). For human mitochondrial code one has (ile,ile,ile,ile) and thus only one exception to the rule. The breaking of matter-antimatter symmetry for the third nucleotide is thus very small.

2. For codons of type B the 4-columns code always for two doublets in the case of vertebrate mitochondrial code so that for codons with vanishing net quark number the breaking of matter-antimatter symmetry for the third nucleotide is always present.

Em stability

Anomalous em charge Q_a vanishes for DNA and perhaps also mRNA strand containing also the G cap and poly-A tail which could compensate for the Q_a of the transcribed region so that

$$2(A-T)-(G-C) \simeq 0$$

or some variant of it holds true. Chargaff's rules for long DNA strands imply the smallness of Q_a.

Summary of testable working hypothesis

Following gives a summary of testable working hypothesis related to the isospin symmetry and color singletness. The property of having integer valued/vanishing Q_a is referred to as property P.

1. Gene plus control region and also DNA repeats should have property P. Transcribed and control regions of gene have Q_a with opposite signs.

2. Transposons, repeating regions, the overhangs associated with the cut and paste of transposon, and the DNA strands resulting in cutting should have property P. This could explain why transposons can paste themselves to AT and GC ($Q_a = 0$) rich repeating regions of DNA. The points at which DNA can be cut should differ by a DNA section having property P. This gives precise predictions for the points at which transposons and pieces of viral DNA can join and could have implications for genetic engineering.

3. If also mRNA is braided, it has property P. This can be only true if the poly-A tail compensates for the non-vanishing Q_a associated with the translated region.

4. Living hairpins should have property P. If only double helix parts of hairpins are braided, the prediction is trivially true by the palindrome property. tRNA or at least parts of it could be braided. Braids could end to the nuclear membrane or mRNA or to the amino-acid attachable to tRNA. For stem regions Q_a is integer valued. The fact that the nucleotide of the anticodon corresponding to the third nucleotide of codon can base pair with several nucleotides of mRNA suggests that $I(nositol)$ can have Q_a opposite to that of A, T, C and U opposite to that of A, G. For 2-anticodon the pairing would be unique. This would give a lot of freedom to achieve property P in weak sense for tRNA. Braid structure for tRNA + amino-acid could be different that for tRNA alone and also in the translation the braid structure could change.

5. Telomeres [94] are of special interests as far as anomalous em charge is considered. Chromosomes are not copied completely in cell replication, and one function of telomeres is to guarantee that the translated part of genome replicates completely for sufficiently many cell divisions. Telomeres consists of 3-20 kilobases long repetitions of TTAGGG, and there is a 100-300 kilobases long repeating sequence between telomere and the rest of the chromosome. Telomeres can form can also 4-stranded structures. Telomere end contains a hair-pin loop as a single stranded part, which prevents the action of DNA repair enzymes on the chromosome end. Telomerase is a reverse transcriptase enzyme involved with the synthesis of telomeres using RNA strand as a template but since its expression is repressed in many types of human cells, telomere length shortens in each cell replication. In the case of germ cells, stem cells and white blood cells telomerase is expressed and telomere length preserved. Telomere shortening is known to relate to ageing related diseases. On the other hand, overactive telomere expression seems to correlate with cancer.

   If telomeres possess braid strands, the compensation of Q_a might provide an additional reason for their presence. If this the case and if telomeres are strict multiples of TTAGGG, the shortening of telomeres generates a non-vanishing Q_a unless something happens for the active part of DNA too. Color singletness condition should however remain true: the disappearance of $3n$ multiples of TTAGGG in each replication is the simplest guess for what might happen. In any case, DNA strands would become unstable in cell replication. Q_a could be reduced by a partial death of DNA in the sense that some portions of braiding disappear. Also this would induce ill functioning of tqc harware perhaps related to ageing related diseases. Perhaps evolution has purposefully developed this ageing mechanism since eternal life would stop evolution.

6. Also aminoacids could be braided. Q_a could vary and correspond to Q_a for one of the codons coding for it. The aminoacid sequences of catalysts attaching to DNA strand should have opposite Q_a for each codon-aminoacid pair so that aminoacid would attach only to the codons coding for it. The TGD based model for nerve pulse [57] inspires the proposal that magnetic flux tubes connecting microtubules to the axonal membrane allow tqc during nerve pulse propagation when axonal membrane makes transition from gel like phase to liquid crystal phase. Aminoacids of tubulin dimers would be connected by 3-braids, smallest interesting braid, to groups of 3-lipids in axonal membrane and tubulin dimers would define fundamental tqc modules.

6.8.5 Empirical rules about DNA and mRNA supporting the symmetry breaking picture

Somewhat surprisingly, basic facts which can be found from Wikipedia, support the proposed vision about symmetry breaking although, the mechanism of matter antimatter symmetry breaking is more complex than the first guess. I am grateful for Dale Trenary for references which made possible to realize this. Before continuing some comments about the physical picture are in order.

1. The vanishing of the induced Kähler field means that the space-time sheet of DNA is a highly unstable vacuum extremal. The non-vanishing of the induced Kähler electric field is thus a natural correlate for both the stability and the non-vanishing quark number density (matter antimatter asymmetry). The generation of matter antimatter asymmetry induces a net density of anomalous em charge, isospin, and quark number in the portion of DNA considered. This in turn generates not only longitudinal electric field but also a longitudinal Kähler electric field along DNA.

2. Weak electric fields play a key role in living matter. There are electric fields associated with embryos, central nervous system, individual neurons, and microtubules and their direction determines the direction of a process involved (head-to-tail direction, direction of propagation of nerve pulse, ...).

3. Same mechanism is expected to be at work also in the case of DNA and RNA. In the case of gene the direction of transcription could be determined by the direction of the electric field created by gene and telomeres at the ends of chromosomes carrying a net anomalous quark number could be partially responsible for the generation of this field. In the case of mRNA the direction of translation would be determined in the similar manner. The net anomalous em charges of poly-A tail and the transcribed part of mRNA would have opposite signs so that a longitudinal electric field would result.

It will be found that this picture is consistent with empirical findings about properties of DNA.

Breaking of matter antimatter symmetry and isospin symmetry for entire genome

Chargaff's rules are not exact and the breaking gives important information about small breakings of isospin and matter-antimatter symmetries at the level of entire genome. The basic parameters are em charge per nucleotide, isospin per nucleotide, the amount of quark number per nucleotide, and the ratio of u and d type matters coded by $(G+C)/(A+T)$ ratio. Recall that there are four options for the map of A,T,C,G to quarks and antiquarks and for option 3) *resp.* 4) the anomalous em charge is opposite to that for 1) *resp.* 2).

The following table gives A,T,C,G contents (these data are from Wikipedia [19]), the amount of quark charge per nucleotide for the options 1) *resp.* 2) given by $dq_1/dn = p[2(A-T)-G-C)]/3$ *resp.* $dq_2/dn = p[A-T-2(G-C)]/3$, the amount $dI_3/dn = p(A-G+C-T]/2$ of isospin per nucleotide, the amount $d(q-\overline{q})/dn = p(A-T+G-C)$ of quark number per nucleotide, and $(A+T)/(C+G)$ ratio for *entire genomes* in some cases. It will be found that so called Szybalski's rules state that for coding regions there is breaking of the approximate matter antimatter asymmetry.

Note that matter antimatter asymmetry in the scale of entire genome has largest positive value for human genome and negative value only for yeast genome: this case the magnitude of the asymmetry is largest.

	Human	*Chicken*	*Grass−hopper*	*Sea Urchin*	*Wheat*	*Yeast*	*E.Coli*
$p(A)$	0.3090	0.2880	0.2930	0.3280	0.2730	0.3130	0.2470
$p(T)$	0.2940	0.2920	0.2930	0.3210	0.2710	0.3290	0.2360
$p(C)$	0.1990	0.2050	0.2050	0.1770	0.2270	0.1870	0.2600
$p(G)$	0.1980	0.2170	0.2070	0.1730	0.2280	0.1710	0.2570
$\frac{dq_1}{dn}$	0.0103	−0.0067	−0.0007	0.0060	0.0010	−0.0053	0.0083
$\frac{dq_2}{dn}$	0.0057	−0.0093	−0.0013	0.0050	−0.0000	0.0053	0.0057
$\frac{dI_3}{dn}$	0.0080	−0.0080	−0.0010	0.0055	0.0005	0.0000	0.0070
$\frac{d(q-\overline{q})}{dn}$	0.0140	0.0080	0.0020	0.0030	0.0030	−0.0320	0.0080
$\frac{p(A+T)}{p(G+C)}$	1.5189	1.3744	1.4223	1.8543	1.1956	1.7933	0.9342

(6.8.8)

For option 2) the amount of anomalous charge is about .0057e per nucleotide and thus about $3\times 10^7 e$ for entire human DNA having length of about 1.8 meters. The inspection of tables of [94] shows that the anomalous em charge for the repeating sequence defining the telomere is always non-vanishing and has always the same sign. Telomeres for human chromosomes consist of TTAGGG repetitions with anomalous em charge with magnitude $5e/3$ for all options and have a length measured in few kbases. Human genome as has 24 chromosomes so that the total anomalous em charge of telomeres is roughly $24 \times (5/18) \times x10^3 e \sim .8 \times 10^3 xe$, $1 < x < 10$. The anomalous em charge of telomeres is three orders of magnitude smaller than that of entire DNA but if DNA is quantum critical system the change the total anomalous em charge and quark number due to the shortening of telomeres could induce instabilities of DNA (due to the approach to vacuum extremal) contributing to ageing. Note that the small net value of quark number in all the cases considered might be necessary for overall stability of DNA. Telomeres are also known to prevent the ends of chromosomes to stick to each other. This could be partially due to the Coulomb repulsion due to the anomalous em charge.

According to [19] Chargaff's rules do not apply to viral organellar genomes (mitochondria [61] , plastids) or single stranded viral DNA and RNA genomes. Thus approximate matter antimatter symmetry fails for DNA:s of organelles involved with metabolism. This might relate to the fact that the coding portion of DNA is very high and repeats are absent. Chargaff's rule applies not only to nucleotides but also for oligonucleotides which corresponds to DNA or RNA sequences with not more than 20 bases. This means that for single strand oligonucleotides and their conjugates appear in pairs. Matter antimatter asymmetry would be realized as presence of matter blobs and their conjugates. This might relate to the mechanism how the sequences of oligonucleotides are generated from DNA and its conjugate.

Breaking of matter antimatter symmetry for coding regions

As noticed, one can consider three type of symmetry breaking parameters for DNA in DNA as tqc model. There are indeed three empirical parameters of this kind. Chargaff' rules have been already discussed and correspond to approximate matter antimatter symmetry. The second asymmetry parameter would measure the asymmetry between $u\overline{u}$ and $d\overline{d}$ type matter. $p(G+C)$ corresponds to the fraction of $d\overline{d}$ type quark matter for option 1) and $u\overline{u}$ matter for option 2). It is known that G+C fraction $p(G+C)$ characterizes genes [155] and the value of $p(G+C)$ is proportional to the length of the coding sequence [50, 155] .

Besides Chargaff' rules holding true for entire genome also Szybalski's rules [19] hold true but only for coding coding regions. The biological basis of neither rules is not understood. The interpretation of Chargaff's rules would be in terms of approximate matter antimatter symmetry and the vanishing of net isospin at the level of quarks whereas Szybalski's rule would state the breaking of these symmetries non-coding regions. Hence all the three basic empirical rules would have a nice interpretation in DNA as tqc picture.

Consider now Szybalski's rules in more detail.

1. In most bacterial genomes (which are generally 80-90 % coding) genes are arranged in such a fashion that approximately 50 % of the coding sequence lies on either strand. Note that either strand can act as a template (this came as a surprise for me). Szybalski, in the 1960s, showed that in bacteriophage coding sequences purines (A and G) exceed pyrimidines (C and T). This rule has since been confirmed in other organisms and known as Szybalski's rule [19, 179] . While Szybalski's rule generally holds, exceptions are known to exist.

   Interpretation. A breaking of matter antimatter symmetry occurs in coding regions such that the net breakings are opposite for regions using different templates and thus different directions of transcription (promoter to the right/left of coding region).

2. One can actually characterize Szybalski's rules more precisely. By Chargaff's rules one has $p(A+T) \simeq 1 - p(G+C)$). In coding regions with low value of $p(G+C)$ $p(A)$ is known to be higher than on the average whereas for high value of $p(G+C)$ $p(G)$ tends to higher than on the average.

   Interpretation. These data do not fix completely the pattern of breaking of the approximate matter antimatter symmetry.

   i) It could take place for both kinds of quark matter ($u\overline{u}$ and $d\overline{d}$): both $p(A)$ and $p(G)$ would increase from its value for entire genome but the dominance of A over G or vice versa would explain the observation.

   ii) The breaking could also occur only for the dominating type of quark matter ($u\overline{u}$ or $d\overline{d}$) in which case only $p(A)$ or $p(G)$ would increase from the value for entire genome.

   Also a net isospin is generated which is of opposite sign for short and long coding sequences so that there must be some critical length of the coding sequences for which isospin per nucleotide vanishes. This length should have biological meaning.

3. For mRNA $A+G$ content is always high. This is possible only because the template part of the DNA which need not be always the same strand varies so that if it is strand it has higher $A+G$ content and if it is conjugate strand it has higher $T+C$ content.

Interpretation. mRNA breaks always matter antimatter symmetry and the sign of matter antimatter asymmetry is always the same. Thus mRNA is analogous to matter in observed universe. The poly-A tail added to the end of mRNA after transcription to stabilize it would reduce the too large values of isospin and anomalous em charge per nucleon due to the fact that mRNA does not contain regions satisfying Chargaff's rules. It would also generate the needed longitudinal electric field determining the direction of translation. In the case of DNA the breaking of matter antimatter symmetry is realized at the functional level by a varying direction of transcription and variation of template strand so that matter antimatter symmetry for the entire DNA is only slightly broken. Direction of transcription would be determined by the direction of the electric field. The stability of long DNA sequences might require approximate matter antimatter symmetry for single DNA strand if it is long. In the case of simple genomes (mitochondrial, plastid, and viral) the small size of the genome, the high fraction of coding regions, and the absence of repeating sequences might make approximate matter antimatter symmetry un-necessary. An interesting working hypothesis is that the direction of transcription is always the same for these genomes.

One can try to use this information to fix the most probable option for nucleotide quark correspondence.

1. In nuclear physics the neutron to proton ratio of nucleus increases as nucleus becomes heavier so that the nuclear isospin becomes negative: $I_3 < 0$. The increase of the nuclear mass corresponds to the increase for the length of the coding region. Since G/A fraction increases with the length of coding region, G should correspond to either d quark ($(Q_a < 0, I_3 = -1/2)$) or its charge conjugate d_c ($Q_a < 0$). Hence option 1) or its charge conjugate would be favored.

2. If one takes very seriously the analogy with cosmic matter antimatter asymmetry then matter should dominate and only $(A, G, T, C) \to (u, d, \overline{u}, \overline{d})$ option would remain.

Szybalski's findings leave open the question whether non-coding regions obey the Chargaff' rules in good approximation or whether also they appear as pairs with opposite matter antimatter asymmetry.

Introns are belong to coding regions in the sense that they are transcribed to mRNA. Splicing however cuts them off from mRNA. It is not clear whether introns break the approximate matter antimatter symmetry or not. If breaking takes place it might mean that introns code for something but not chemically. On the other hand, the absence of asymmetry might serve at least partially as a signal telling that introns must be cut off before translation. Many interesting questions represent itself. For instance, how the symmetry breaking parameters, in particular matter antimatter asymmetry parameter, depend on genes. The correlation with gene length is the most plausible guess.

6.8.6 Genetic codes and tqc

TGD suggests the existence of several genetic codes besides 3-codon code [33, 29] . The experience from ordinary computers and the fact that genes in general do not correspond to $3n$ nucleotides encourages to take this idea more seriously. The use of different codes would allow to tell what kind of information a given piece of DNA strand represents. DNA strand would be like a drawing of building containing figures (3-code) and various kinds of text (other codes). A simple drawing for the building would become a complex manual containing mostly text as the evolution proceeds: for humans 96 per cent of code would corresponds to introns perhaps obeying some other code.

The hierarchy of genetic codes is obtained by starting from n basic statements and going to the meta level by forming all possible statements about them (higher order logics) and throwing away one which is not physically realizable (it would correspond to empty set in the set theoretic realization). This allows $2^n - 1$ statements and one can select 2^{n-1} mutually consistent statements (half of the full set of statements) and say that these are true and give kind of axiomatics about world. The remaining statements are false. DNA would realize only the true statements.

The hierarchy of Mersenne primes $M_n = 2^n - 1$ with $M_{n(next)} = M_{M_n}$ starting from $n = 2$ with $M_2 = 3$ gives rise to 1-code with 4 codons, 3-code with 64 codons, and $3 \times 21 = 63$-code with 2^{126} codons [33] realized as sequences of 63 nucleotides (the length of 63-codon is about $2L(151)$, roughly twice the cell membrane thickness. It is not known whether this Combinatorial Hierarchy continues ad infinitum. Hilbert conjectured that this is the case.

In the model of pre-biotic evolution also 2-codons appear and 3-code is formed as the fusion of 1- and 2-codes. The problem is that 2-code is not predicted by the basic Combinatorial Hierarchy associated with $n = 2$.

There are however also other Mersenne hierarchies and the next hierarchy allows the realization of the 2-code. This Combinatorial Hierarchy begins from Fermat prime $n = 2^k + 1 = 5$ with $M_5 = 2^5 - 1 = 31$ gives rise to a code with 16 codons realized as 2-codons (2 nucleotides). Second level corresponds to Mersenne prime $M_{31} = 2^{31} - 1$ and a code with $2^{30=15\times 2}$ codons realized by sequences of 15 3-codons containing 45 nucleotides. This corresponds to DNA length of 15 nm, or length scale $3L(149)$, where $L(149) = 5$ nm defines the thickness of the lipid layer of cell membrane. $L(151) = 10$ nm corresponds to 3 full 2π twists for DNA double strand. The model for 3-code as fusion of 1- and 2-codes suggests that also this hierarchy - which probably does not continue further - is realized.

There are also further short Combinatorial hierarchies corresponding to Mersenne primes [4] .

1. $n = 13$ defines Mersenne prime M_{13}. The code would have $2^{12=6\times 2}$ codons representable as sequences of 6 nucleotides or 2 3-codons. This code might be associated with microtubuli.

2. The Fermat prime $17 = 2^4 + 1$ defines Mersenne prime M_{17} and the code would have $2^{16=8\times 2}$ codons representable as sequences of 8 nucleotides.

3. $n = 19$ defines Mersenne prime M_{19} and code would have $2^{18=9\times 2}$ codons representable as sequences of 9 nucleotides or three DNA codons.

4. The next Mersennes are M_{31} belonging to $n = 5$ hierarchy, M_{61} with $2^{60=30\times 2}$ codons represented by 30-codons. This corresponds to DNA length $L(151) = 10$ nm (cell membrane thickness). M_{89} (44-codons), M_{107} (53-codons) and M_{127} (belonging to the basic hierarchy) are the next Mersennes. Next Mersenne corresponds to M_{521} (260-codon) and to completely super-astrophysical p-adic length scale and might not be present in the hierarchy.

   This hierarchy is realized at the level of elementary particle physics and might appear also at the level of DNA. The 1-, 2-, 3-, 6-, 8-, and 9-codons would define lowest Combinatorial Hierarchies.

6.9 Cell replication and tqc

DNA as tqc model leads to quite detailed ideas about the evolution of the genetic code and the mechanisms of bio-catalysis and of protein folding [29] . These applications in turn leads to a considerable generalization of DNA as tqc concept [29] . The presence of braiding leads also to a revision of the model of nerve pulse and EEG [57, 23] . Here the discussion is restricted to one particular example. One can look what happens in the cell replication in the hope of developing more concrete ideas about tqc in multicellular system. This process must mean a replication of the braid's strand system and a model for this process gives concrete ideas about how multicellular system performs tqc.

6.9.1 Mitosis and tqc

Mitosis is the form of cell replication yielding soma cells and it is interesting what constraints this process gives on tqc and whether the special features of this process could be understood from computational point of view.

1. During mitosis chromosomes [62] are replicated. During this process the strands connecting chromosomes become visible: the pattern brings in mind flux tubes of magnetic field. For prokaryotes the replication of chromosomes is followed by the fission of the cell membrane. Also plant nuclei separated by cellulose walls suffer fission after the replication of chromosomes. For animals nuclear membranes break down before the replication suggesting that nuclear tqc programs are reset and newly formed nuclei start tqc from a clean table. For eukaryotes cell division is controlled by centrosomes [18] . The presence of centrosomes is not necessary for the survival of the cell or its replication but is necessary for the survival of multicellular. This conforms with the proposed picture.

2. If the conjugate strands are specialized in tqc, the formation of new double strands does not involve braids in an essential manner. The formation of conjugate strand should lead to also to a generation of braid strands unless they already exist as strands connecting DNA and its conjugate and are responsible for "printing". These strands need not be short. The braiding associated with printing would be hardware program which could be genetically determined or at least inherited as such so that the strands should be restricted inside the inner cell membrane or at most traverse the inner nuclear membrane and turn back in the volume between inner membrane and endoplasmic reticulum.

   The return would be most naturally from the opposite side of nuclear membrane which suggest a breaking of rotational symmetry to axial symmetry. The presence of centriole implies this kind of symmetry breaking: in neurons this breaking becomes especially obvious. The outgoing braid strands would be analogous to axon and returning braid strands to dendrites. Inner nuclear membrane would decompose the braiding to three parts: one for strand, second for conjugate strand, and a part in the empty space inside nuclear envelope.

3. The formation of new DNA strands requires recognition relying on "strand color" telling which nucleotide can condense at it. The process would conserve the braidings connecting DNA to the external world. The braidings associated with the daughter nuclei would be generated from the braiding between DNA and its conjugate. As printing software they should be identical so that the braiding connecting DNA double strands should be a product of a braiding and its inverse. This would however mean that the braiding is trivial. The division of the braid to three parts hinders the transformation to a trivial braid if the braids combine to form longer braids only during the "printing" activity.

4. The new conjugate strands are formed from the old strands associated with printing. In the case of plants the nuclear envelope does not disintegrate and splits only after the replication of chromosomes. This would suggest that plant cells separated by cell walls perform only intracellular tqc. Hermits do not need social skills. In the case of animals nuclear envelope disintegrates. This is as it must be since the process splits the braids connecting strand and conjugate strands so that they can connect to the cell membrane. The printing braids are inherited as such which conforms with the interpretation as a fixed software.

5. The braids connecting mother and daughter cells to extranuclear world would be different and tqc braidings would give to the cell a memory about its life-cycle. The age ordering of cells would have the architecture of a tree defined by the sequence of cell replications and the life history of the organism. The 4-D body would contain kind of log file about tqc performed during life time: kind of fundamental body memory.

6. Quite generally, the evolution of tqc programs means giving up the dogma of genetic determinism. The evolution of tqc programs during life cycle and the fact that half of them is inherited means kind of quantum Lamarckism [51] . This inherited wisdom at DNA level might partly explain why we differ so dramatically from our cousins.

6.9.2 Sexual reproduction and tqc

Meiosis [58] produces gametes in which the pair of chromosomes from parents is replaced with single chromosome obtained as chimera of the chromosomes of parents. Meiosis is the basic step of sexual reproduction and it is interesting to study it from tqc point of view.

1. Sexual reproduction of eukaryotes relies on haploid cells differing from diploid cells in that chromatids do not possess sister chromatids. Whereas mitosis produces from single diploid [84] cell two diploid cells, meiosis gives rise to 4 haploid [84] cells. The first stage is very much like mitosis. DNA and chromosomes duplicate but cell remains a diploid in the sense that there is only single centrosome: in mitosis also centrosome duplicates. After this the cell membrane divides into two. At the next step the chromosomes in daughter cells split into two sister chromosomes each going into its own cell. The outcome is four haploid cells.

2. The presence of only single chromatid [20] in haploids means that germ cells would perform only one half of the "social" tqc performed by soma cells [91] who must spend their life cycle as a member of cell community. In some cells the tqc would be performed by chromatids of both father and mother making perhaps possible kind of stereo view about world and a model for couple - the simplest possible social structure.

3. This brings in mind the sensory rivalry between left and right brain: could it be that the two tqc's give competing computational views about world and how to act in it? We would have inside us our parents and their experiences as a pair of chromatids representing chemical chimeras of chromatid pairs possessed by the parents: as a hardware - one might say. Our parents would have the same mixture in software via sharing and fusion of chromatid mental images or via quantum computational rivalry. What is in software becomes hardware in the next generation.¡/p¿¡p¿

4. The ability of sexual reproduction to generate something new relates to meiosis. During meiosis genetic recombination [37] occurs via chromosomal crossover which in string model picture would mean splitting of chromatids and the recombination of pieces in a new manner $(A_1+B_1)+(A_2+B_2) \to (A_1+B_2)+(A_2+B_1)$ takes place in crossover and $(A_1+B_1+C_1)+(A_2+B_2+C_2) \to (A_1+B_2+C_1)+(A_2+B_1+C_2)$ in double crossover. New hardware for tqc would result by combining pieces of existing hardware. What this means in terms of braids should be clarified.

5. Fertilization is in well-define sense the inverse of meiosis. In fertilization the chromatids of spermatozoa and ova combine to form the chromatids of diploid cell. The recombination of genetic programs during meiosis becomes visible in the resulting tqc programs.

6.9.3 What is the role of centrosomes and basal bodies?

Centrosomes [18] and basal bodies [12] form the main part of Microtubule Organizing Center [60] . They are somewhat mysterious objects and at first do not seem to fit to the proposed picture in an obvious manner.

1. Centrosomes consist two centrioles [17] forming a T shaped antenna like structure in the center of cell. Also basal bodies consist of two centrioles but are associated with the cell membrane. Centrioles and basal bodies have cylindrical geometry consisting of nine triplets of microtubules along the wall of cylinder. Centrosome is associated with nuclear membrane during mitosis.

2. The function of basal bodies which have evolved from centrosomes seems to be the motor control (both cilia [22] and flagella [35]) and sensory perception (cilia). Cell uses flagella and cilia to move and perceive. Flagella and cilia are cylindrical structures associated with the basal bodies. The core of both structures is axoneme having $9 \times 2 + 2$ microtubular structure. So called primary cilia do not posses the central doublet and the possible interpretation is that the inner doublet is involved with the motor control of cilia. Microtubules [59] of the pairs are partially fused together.

3. Centrosomes are involved with the control of [62] [62] . Mitosis can take place also without them but the organism consisting of this kind of cells does not survive. Hence the presence of centrosomes might control the proper formation of tqc programs. The polymerization of microtubules [59] is nucleated at microtubule self-organizing center which can be centriole or basal body. One can say that microtubules which are highly dynamical structures whose length is changing all the time have their second end anchored to the self-organizing center. Since this function is essential during mitosis it is natural that centrosome controls it.

4. The key to the understanding of the role of centrosomes and basal bodies comes from a paradox. DNA and corresponding tqc programs cannot be active during mitosis. What does then control mitosis?

   i) Perhaps centrosome and corresponding tqc program represents the analog of the minimum seed program in computer allowing to generate an operating system like Windows 2000 (the files from CD containing operating system must be read!). The braid strands going through the microtubules of centrosome might define the corresponding tqc program. The isolation from environment by the microtubular surface might be essential for keeping the braidings defining these programs strictly unchanged.

   ii) The RNA defining the genome of centrosome (yes: centrosome has its own genome defined by RNA rather than DNA [18] !) would define the hardware for this tqc. The basal bodies could be interpreted as a minimal sensory-motor system needed during mitosis.

   iii) As a matter fact, centrosome and basal bodies could be seen as very important remnants of RNA era believed by many biologists to have preceded DNA era. This assumption is also made in TGD inspired model of prebiotic evolution [29] .

   iv) Also other cellular organelles possessing own DNA and own tqc could remain partly functional during mitosis. In particular, mitochondria are necessary for satisfying energy needs during the period when DNA is unable to control the situation so that they must have some minimum amount of own genome.

5. Neurons [65] do not possess centrosome which explains why they cannot replicate. The centrioles are replaced with long microtubules associated with axons and dendrites. The system consisting of microtubules corresponds to a sensory-motor system controlled by the tqc programs having as a hardware the RNA of centrosomes and basal bodies. Also this system would have a multicellular part.

6. Intermediate filaments [47] , actin filaments [3] , and microtubules [59] are the basic building elements of the eukaryotic cytoskeleton [26] . Microtubules, which are hollow cylinders with outer radius of 24 nm, are especially attractive candidates for structures carrying bundles of braid strands inside them. The microtubular outer-surfaces could be involved with signalling besides other well-established functions. It would seem that microtubules cannot be assigned with tqc associated with nuclear DNA but with RNA of centrosomes and could contain corresponding braid strand bundles. It is easy to make a rough estimate for the number of strands and this would give an estimate for the amount of RNA associated with centrosomes. Also intermediate filaments and actin filaments might relate to cellular organelles having their own DNA.

6.10 Indirect evidence for the DNA as topological quantum computer model

There is a profound revolution taking place in genetics [38] . It is fair to say that genetic determinism is falling down and the revolution that is waiting just around the corner will be more profound that

anything that has taken place before this in biology. The term "genome's dark matter" expresses what has been discovered during last years. The motivation for the term is the strong analogy with the dark matter of physics. In TGD framework this analogy might be much more than analogy.

The basic anomalies discussed in the article are following.

1. Trans-generational inheritance [165, 188] . The stretches of DNA which were present in parent's or grand parents' genome but are not present in the genome of offspring affect the traits of offspring.

2. Context sensitivity of gene's effect: the effect of gene is highly sensitive on its environment in DNA.

3. Genes explain in many cases only 10 percent of the disease's inheritability: this is "missing heritability" problem [127] .

It is interesting to try to interpret these results in the framework provided by the model of DNA as topological quantum computer. It is good to summarize the basic ideas and concepts behind the model.

6.10.1 The notion of magnetic body

The notion of magnetic body as intentional agent using biological body as a motor instrument and sensory receptor with communications taking place in terms of fractal generalization of EEG is the key idea. Each physical system consisting of matter has magnetic body. Magnetic body of given living organism has a fractal onion like structure with layer sizes varying from sub-cellular scales to the scales assignable to EEG frequencies (Earth size) and even above up to the scale of light-life and maybe beyond to scales characterizing the evolution of species.

Immediate implications are the notion of collective DNA expression made possible by the interaction of DNA strands so that they belong to magnetic flux sheets: in this manner not only DNAs of cells and organelles, organs, single organism but also groups of organisms can form coherent structures expressing themselves in synchronous manner. This is a testable prediction.

6.10.2 DNA as topological quantum computer

Topological quantum computation is based on braiding: various braiding patters for braid strands define the tqc programs. There are two types of braids: time-like and space-like.

1. Cell membrane is 2-D liquid and the flow of lipids affected by the flow of cellular liquid and also by nerve pulse patterns in case of neurons induce braiding. This braiding takes place dynamically at the 2-D parquette defined by the cell membrane in time direction and dance metaphor applies to it. Running tqc program can be seen as dancing.

2. The magnetic flux tubes connecting DNA nucleotides to the lipids of nuclear membrane and cell membrane and possibly also to membranes of other cells define the space-like braid strands. Since the flux tubes connected to DNA strands are like threads connecting the feet of dancers to the walls of the dance hall the resulting space-like braiding codes tqc program to memory, which is highly robust as a topological invariant.

There is a kind of duality between time-like and space-like braidings. This is a new element to the conventional quantum computation paradigm. Combined with the idea that memories are stored in geometric past in zero energy ontology this gives an extremely elegant memory storage mechanism.

6.10.3 Implications for genetics

This vision has profound implications for genetics.

1. Genes define only the hardware of tqc. Software is defined by the braidings. Introns whose portion steadily increases as the evolutionary level becomes higher and is more than 95 per cent in humans, have been traditionally interpreted as junk DNA. In this framework introns

correspond naturally to that part of genome specialized in tqc: from the point of view of tqc it does matter much whether the intronic portions correspond to repeating sequences (interpreted as a signal for "junkness") or not.

2. The evolution of topological quantum computation programs would be far more important than the evolution of genome and the huge differences between species with almost the same genome (such as we and our cousins) could be understood in terms ofw hat at our level of hierarchy corresponds to cultural evolution due to the evolution of topological quantum computer programs. The evolution would have been for a long time evolution of tqc programs rather than that of hardware as the fact that the size of genome and details of does not matter much suggests. The appearance of of prokaryotes (and multi-cellulars) meant the emergence of introns and perhaps also the predecessor of cultural evolution as the evolution of quantum software and collective magnetic bodies.

6.10.4 Implications for Mendelian anomalies

This vision also suggests how to understand the origin of the Mendelian anomalies.

1. Trans-generational inheritance might be understood as an inheritance of tqc programs carrying indirectly information also about the genome of parents. If one accepts TGD vision about organisms as 4-D structures, one must of course be ready to even ask whether genetic effects could be also take place via the mediation of the magnetic bodies assignable to structures formed by several generations.

2. The context sensitivity of the effect of particular gene could be understood in this picture since the programs are determined not only by a single gene but longer portions of DNA. Individual genes do not matter much when one tries to understand genetic correlates for autism, schizophrenia, and other complex diseases related to functions rather than mere structure. If one speaks about structure, such as the color of flowers situation is of course very simple and Mendelian approach works well. An interesting question is how closely the structure-function dichotomy, exon-intron dichotomy and hardware-software dichotomy correspond to each other.

3. High level diseases would be much more programming errors than hardware problems. This would solve "missing heritability" problem.

What is amusing, that the physicist's dark matter would be behind 'genome's dark matter': magnetic flux tubes are assumed to be carriers of dark matter- dark quarks in fact. In the proposed model quarks with large Planck constant meaning that their Compton length scales is scaled up and gives them size scale of order cell at least are in key role!

6.11 Appendix: A generalization of the notion of imbedding space

In the following the recent view about structure of imbedding space forced by the quantization of Planck constant is described. This view has developed much before the original version of this chapter was written.

The original idea was that the proposed modification of the imbedding space could explain naturally phenomena like quantum Hall effect involving fractionization of quantum numbers like spin and charge. This does not however seem to be the case. $G_a \times G_b$ implies just the opposite if these quantum numbers are assigned with the symmetries of the imbedding space. For instance, quantization unit for orbital angular momentum becomes n_a where Z_{n_a} is the maximal cyclic subgroup of G_a.

One can however imagine of obtaining fractionization at the level of imbedding space for space-time sheets, which are analogous to multi-sheeted Riemann surfaces (say Riemann surfaces associated with $z^{1/n}$ since the rotation by 2π understood as a homotopy of M^4 lifted to the space-time sheet is a non-closed curve. Continuity requirement indeed allows fractionization of the orbital quantum numbers and color in this kind of situation.

6.11.1 Both covering spaces and factor spaces are possible

The observation above stimulates the question whether it might be possible in some sense to replace H or its factors by their multiple coverings.

1. This is certainly not possible for M^4, CP_2, or H since their fundamental groups are trivial. On the other hand, the fixing of quantization axes implies a selection of the sub-space $H_4 = M^2 \times S^2 \subset M^4 \times CP_2$, where S^2 is a geodesic sphere of CP_2. $\hat{M}^4 = M^4 \backslash M^2$ and $\hat{CP}_2 = CP_2 \backslash S^2$ have fundamental group Z since the codimension of the excluded sub-manifold is equal to two and homotopically the situation is like that for a punctured plane. The exclusion of these sub-manifolds defined by the choice of quantization axes could naturally give rise to the desired situation.

2. Zero energy ontology forces to modify this picture somewhat. In zero energy ontology causal diamonds (CDs) defined as the intersections of future and past directed light-cones are loci for zero energy states containing positive and negative energy parts of state at the two light-cone boundaries. The location of CD in M^4 is arbitrary but p-adic length scale hypothesis suggests that the temporal distances between tips of CD come as powers of 2 using CP_2 size as unit. Thus M^4 is replaces by CD and $\hat{M}^4$ is replaced with $\hat{CD}$ defined in obvious manner.

3. H_4 represents a straight cosmic string inside CD. Quantum field theory phase corresponds to Jones inclusions with Jones index $\mathcal{M} : \mathcal{N} < 4$. Stringy phase would by previous arguments correspond to $\mathcal{M} : \mathcal{N} = 4$. Also these Jones inclusions are labeled by finite subgroups of $SO(3)$ and thus by Z_n identified as a maximal Abelian subgroup.

   One can argue that cosmic strings are not allowed in QFT phase. This would encourage the replacement $\hat{CD} \times \hat{CP}_2$ implying that surfaces in $CD \times S^2$ and $(M^2 \cap CD) \times CP_2$ are not allowed. In particular, cosmic strings and CP_2 type extremals with M^4 projection in M^2 and thus light-like geodesic without zitterwebegung essential for massivation are forbidden. This brings in mind instability of Higgs=0 phase.

4. The covering spaces in question would correspond to the Cartesian products $\hat{CD}_{n_a} \times \hat{CP}_{2n_b}$ of the covering spaces of $\hat{CD}$ and $\hat{CP}_2$ by Z_{n_a} and Z_{n_b} with fundamental group is $Z_{n_a} \times Z_{n_b}$. One can also consider extension by replacing $M^2 \cap CD$ and S^2 with its orbit under G_a (say tedrahedral, octahedral, or icosahedral group). The resulting space will be denoted by $\hat{CD}\hat{\times}G_a$ *resp.* $\hat{CP}_2\hat{\times}G_b$.

5. One expects the discrete subgroups of $SU(2)$ emerge naturally in this framework if one allows the action of these groups on the singular sub-manifolds $M^2 \cap CD$ or S^2. This would replace the singular manifold with a set of its rotated copies in the case that the subgroups have genuinely 3-dimensional action (the subgroups which corresponds to exceptional groups in the ADE correspondence). For instance, in the case of $M^2 \cap CD$ the quantization axes for angular momentum would be replaced by the set of quantization axes going through the vertices of tedrahedron, octahedron, or icosahedron. This would bring non-commutative homotopy groups into the picture in a natural manner.

6. Also the orbifolds $\hat{CD}/G_a \times \hat{CP}_2/G_b$ can be allowed as also the spaces $\hat{CD}/G_a \times (\hat{CP}_2\hat{\times}G_b)$ and $(\hat{CD}\hat{\times}G_a) \times \hat{CP}_2/G_b$. Hence the previous framework would generalize considerably by the allowance of both coset spaces and covering spaces.

There are several non-trivial questions related to the details of the gluing procedure and phase transition as motion of partonic 2-surface from one sector of the imbedding space to another one.

1. How the gluing of copies of imbedding space at $(M^2 \cap CD) \times CP_2$ takes place? It would seem that the covariant metric of M^4 factor proportional to $\hbar^2$ must be discontinuous at the singular manifold since only in this manner the idea about different scaling factor of M^4 metric can make sense. This is consistent with the identical vanishing of Chern-Simons action in $M^2 \times S^2$.

2. One might worry whether the phase transition changing Planck constant means an instantaneous change of the size of partonic 2-surface in CD degrees of freedom. This is not the case. Light-likeness in $(M^2 \cap CD) \times S^2$ makes sense only for surfaces $X^1 \times D^2 \subset (M^2 \cap CD) \times S^2$, where X^1

is light-like geodesic. The requirement that the partonic 2-surface X^2 moving from one sector of H to another one is light-like at $(M^2 \cap CD) \times S^2$ irrespective of the value of Planck constant requires that X^2 has single point of $(M^2 \cap CD)$ as M^2 projection. Hence no sudden change of the size X^2 occurs.

3. A natural question is whether the phase transition changing the value of Planck constant can occur purely classically or whether it is analogous to quantum tunneling. Classical non-vacuum extremals of Chern-Simons action have two-dimensional CP_2 projection to homologically non-trivial geodesic sphere S^2_I. The deformation of the entire S^2_I to homologically trivial geodesic sphere S^2_{II} is not possible so that only combinations of partonic 2-surfaces with vanishing total homology charge (Kähler magnetic charge) can in principle move from sector to another one, and this process involves fusion of these 2-surfaces such that CP_2 projection becomes single homologically trivial 2-surface. A piece of a non-trivial geodesic sphere S^2_I of CP_2 can be deformed to that of S^2_{II} using 2-dimensional homotopy flattening the piece of S^2 to curve. If this homotopy cannot be chosen to be light-like, the phase transitions changing Planck constant take place only via quantum tunnelling. Obviously the notions of light-like homotopies (cobordisms) and classical light-like homotopies (cobordisms) are very relevant for the understanding of phase transitions changing Planck constant.

6.11.2 Do factor spaces and coverings correspond to the two kinds of Jones inclusions?

What could be the interpretation of these two kinds of spaces?

1. Jones inclusions appear in two varieties corresponding to $\mathcal{M} : \mathcal{N} < 4$ and $\mathcal{M} : \mathcal{N} = 4$ and one can assign a hierarchy of subgroups of $SU(2)$ with both of them. In particular, their maximal Abelian subgroups Z_n label these inclusions. The interpretation of Z_n as invariance group is natural for $\mathcal{M} : \mathcal{N} < 4$ and it naturally corresponds to the coset spaces. For $\mathcal{M} : \mathcal{N} = 4$ the interpretation of Z_n has remained open. Obviously the interpretation of Z_n as the homology group defining covering would be natural.

2. $\mathcal{M} : \mathcal{N} = 4$ should correspond to the allowance of cosmic strings and other analogous objects. Does the introduction of the covering spaces bring in cosmic strings in some controlled manner? Formally the subgroup of $SU(2)$ defining the inclusion is $SU(2)$ would mean that states are $SU(2)$ singlets which is something non-physical. For covering spaces one would however obtain the degrees of freedom associated with the discrete fiber and the degrees of freedom in question would not disappear completely and would be characterized by the discrete subgroup of $SU(2)$.

   For anyons the non-trivial homotopy of plane brings in non-trivial connection with a flat curvature and the non-trivial dynamics of topological QFTs. Also now one might expect similar non-trivial contribution to appear in the spinor connection of $\hat{CD}\hat{\times}G_a$ and $\hat{CP}_2\hat{\times}G_b$. In conformal field theory models non-trivial monodromy would correspond to the presence of punctures in plane.

3. For factor spaces the unit for quantum numbers like orbital angular momentum is multiplied by n_a *resp.* n_b and for coverings it is divided by this number. These two kind of spaces are in a well defined sense obtained by multiplying and dividing the factors of $\hat{H}$ by G_a *resp.* G_b and multiplication and division are expected to relate to Jones inclusions with $\mathcal{M} : \mathcal{N} < 4$ and $\mathcal{M} : \mathcal{N} = 4$, which both are labeled by a subset of discrete subgroups of SU(2).

4. The discrete subgroups of $SU(2)$ with fixed quantization axes possess a well defined multiplication with product defined as the group generated by forming all possible products of group elements as elements of $SU(2)$. This product is commutative and all elements are idempotent and thus analogous to projectors. Trivial group G_1, two-element group G_2 consisting of reflection and identity, the cyclic groups Z_p, p prime, and tedrahedral, octahedral, and icosahedral groups are the generators of this algebra.

By commutativity one can regard this algebra as an 11-dimensional module having natural numbers as coefficients ("rig"). The trivial group G_1, two-element group G_2¡ generated by reflection, and

tedrahedral, octahedral, and icosahedral groups define 5 generating elements for this algebra. The products of groups other than trivial group define 10 units for this algebra so that there are 11 units altogether. The groups Z_p generate a structure analogous to natural numbers acting as analog of coefficients of this structure. Clearly, one has effectively 11-dimensional commutative algebra in 1-1 correspondence with the 11-dimensional "half-lattice" N^{11} (N denotes natural numbers). Leaving away reflections, one obtains N^7. The projector representation suggests a connection with Jones inclusions. An interesting question concerns the possible Jones inclusions assignable to the subgroups containing infinitely manner elements. Reader has of course already asked whether dimensions 11, 7 and their difference 4 might relate somehow to the mathematical structures of M-theory with 7 compactified dimensions. One could introduce generalized configuration space spinor fields in the configuration space labelled by sectors of H with given quantization axes. By introducing Fourier transform in N^{11} one would formally obtain an infinite-component field in 11-D space.

The question how do the Planck constants associated with factors and coverings relate is far from trivial and I have considered several options.

1. If one assumes that $\hbar^2(X)$, $X = M^4$, CP_2 corresponds to the scaling of the covariant metric tensor g_{ij} and performs an over-all scaling of metric allowed by Weyl invariance of Kähler action by dividing metric with $\hbar^2(CP_2)$, one obtains $r^2 \equiv \hbar^2/\hbar_0^2\hbar^2(M^4)/\hbar^2(CP_2)$. This puts M^4 and CP_2 in a very symmetric role and allows much more flexibility in the identification of symmetries associated with large Planck constant phases.

2. Algebraist would argue that Planck constant must define a homomorphism respecting multiplication and division (when possible) by G_i. This requires $r(X) = \hbar(X)\hbar_0 = n$ for covering and $r(X) = 1/n$ for factor space or vice versa. This gives two options.

3. Option I: $r(X) = n$ for covering and $r(X) = 1/n$ for factor space gives $r \equiv \hbar/\hbar_0 = r(M^4)/r(CP_2)$. This gives $r = n_a/n_b$ for $\hat{H}/G_a \times G_b$ option and $r = n_b/n_a$ for $\hat{H}\hat{times}(G_a \times G_b)$ option with obvious formulas for hybrid cases.

4. Option II: $r(X) = 1/n$ for covering and $r(X) = n$ for factor space gives $r = r(CP_2)/r(M^4)$. This gives $r = n_b/n_a$ for $\hat{H}/G_a \times G_b$ option and $r = n_a/n_b$ for $\hat{H}\hat{times}(G_a \times G_b)$ option with obvious formulas for the hybrid cases.

5. At quantum level the fractionization would come from the modification of fermionic anticommutation (bosonic commutation) relations involving $\hbar$ at the right hand side so that particle number becomes a multiple of $1/n$ or n. If one postulates that the total number states is invariant in the transition, the increase in the number of sheets is compensated by the increase of the fundamental phase space volume proportional to $\hbar$. This would give $r(X) \to r(X)/n$ for factor space and $r(X) \to nr(X)$ for the covering space to compensate the n-fold reduction/increase of states. This would favor Option II.

6. The second manner to distinguish between these two options is to apply the theory to concrete physical situations. Since G_a and G_b act as symmetries in CD and CP_2 degrees of freedom, one might of being able to distinguish between the two options if it is possible to distinguish between the action of G as symmetry of quantum states associated with covering and factor space. Also the quantization of the orbital spin quantum number at single particle level as multiples of n can be distinguished from that in multiples of $1/n$.

6.11.3 A simple model of fractional quantum Hall effect

The generalization of the imbedding space suggests that it could possible to understand fractional quantum Hall effect [1] at the level of basic quantum TGD. This section represents the first rough model of QHE constructed for a couple of years ago is discussed. Needless to emphasize, the model represents only the basic idea and involves ad hoc assumption about charge fractionization.

Recall that the formula for the quantized Hall conductance is given by

$$\begin{aligned} \sigma &= \nu \times \frac{e^2}{h} \ , \\ \nu &= \frac{n}{m} \ . \end{aligned} \tag{6.11.1}$$

Series of fractions in $\nu = 1/3, 2/5, 3/7, 4/9, 5/11, 6/13, 7/15...$, $2/3, 3/5, 4/7, 5/9, 6/11, 7/13...$, $5/3, 8/5, 11/7, 14/9...4/3, 7/5, 10$ $1/5, 2/9, 3/13...$, $2/7, 3/11...$, $1/7....$ with odd denominator have been observed as are also $\nu = 1/2$ and $\nu = 5/2$ states with even denominator [1] .

The model of Laughlin [15] cannot explain all aspects of FQHE. The best existing model proposed originally by Jain is based on composite fermions resulting as bound states of electron and even number of magnetic flux quanta [13] . Electrons remain integer charged but due to the effective magnetic field electrons appear to have fractional charges. Composite fermion picture predicts all the observed fractions and also their relative intensities and the order in which they appear as the quality of sample improves.

The generalization of the notion of imbedding space suggests the possibility to interpret these states in terms of fractionized charge, spin, and electron number. There are four combinations of covering and factors spaces of CP_2 and three of them can lead to the increase of Planck constant. Besides this there are two options for the formula of Planck constant so that which the very meager theoretical background one can make only guesses. On the following just for fun consideration option I is considered although the conservation of number of states in the phase transition changing $\hbar$ favors option II.

1. The easiest manner to understand the observed fractions is by assuming that both M^4 and CP_2 correspond to covering spaces so that both spin and electric charge and fermion number are fractionized. This means that e in electronic charge density is replaced with fractional charge. Quantized magnetic flux is proportional to e and the question is whether also here fractional charge appears. Assume that this does not occur.

2. With this assumption the expression for the Planck constant becomes for Option II as $r = \hbar/\hbar_0 = n_a/n_b$ and charge and spin units are equal to $1/n_b$ and $1/n_a$ respectively. This gives $\nu = nn_a/n_b$. The values $m = 2, 3, 5, 7, ..$ are observed. Planck constant can have arbitrarily large values. There are general arguments stating that also spin is fractionized in FQHE.

3. The appearance of $\nu = 5/2$ has been observed [9] . The fractionized charge is $e/4$ in this case. Since $n_i > 3$ holds true if coverings are correlates for Jones inclusions, this requires to $n_b = 4$ and $n_a = 10$. n_b predicting a correct fractionization of charge. The alternative option would be $n_b = 2$ that also Z_2 would appear as the fundamental group of the covering space. Filling fraction $1/2$ corresponds in the composite fermion model and also experimentally to the limit of zero magnetic field [13] . $n_b = 2$ is however inconsistent with the observed fractionization of electric charge and with the vision inspired by Jones inclusions.

4. A possible problematic aspect of the TGD based model is the experimental absence of even values of n_b except $n_b = 2$ (Laughlin's model predicts only odd values of n). A possible explanation is that by some symmetry condition possibly related to fermionic statistics (as in Laughlin model) n_a/n_b must reduce to a rational with an odd denominator for $n_b > 2$. In other words, one has $n_a \propto 2^r$, where 2^r the largest power of 2 divisor of n_b.

5. Large values of n_a emerge as B increases. This can be understood from flux quantization. One has $e \int BdS = n\hbar(M^4) = nn_a\hbar_0$. By using actual fractional charge $e_F = e/n_b$ in the flux factor would give $e_F \int BdS = n(n_a/n_b)\hbar_0 = n\hbar$. The interpretation is that each of the n_a sheets contributes one unit to the flux for e. Note that the value of magnetic field in given sheet is not affected so that the build-up of multiple covering seems to keep magnetic field strength below critical value.

6. The understanding of the thermal stability is not trivial. The original FQHE was observed in 80 mK temperature corresponding roughly to a thermal energy of $T \sim 10^{-5}$ eV. For graphene the effect is observed at room temperature. Cyclotron energy for electron is (from $f_e = 6 \times 10^5$ Hz at $B = .2$ Gauss) of order thermal energy at room temperature in a magnetic field varying in the range 1-10 Tesla. This raises the question why the original FQHE requires so low temperature. The magnetic energy of a flux tube of length L is by flux quantization roughly $e^2B^2S \sim E_c(e)m_eL$ ($\hbar_0 = c = 1$) and exceeds cyclotron roughly by a factor L/L_e, L_e electron Compton length so that thermal stability of magnetic flux quanta is not the explanation. A possible explanation is that since FQHE involves several values of Planck constant, it is quantum critical phenomenon and is characterized by a critical temperature. The differences of

the energies associated with the phase with ordinary Planck constant and phases with different Planck constant would characterize the transition temperature.

As already noticed, it is possible to imagine several other options and the identification of charge unit is rather ad hoc. Therefore this model can be taken only as a warm-up exercise.

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Chapter 7

The Notion of Wave-Genome and DNA as Topological Quantum Computer

7.1 Introduction

For about eight years ago - inspired by a representation in CASYS'2000 conference [147] - I developed a model [84, 9] for the fascinating effects of laser light on genome discovered by Peter Gariaev and his collaborators. This model is somewhat obsolete since it does not involve the recent TGD inspired vision about quantum biology and DNA, and the discussions with Peter in the second Unified Theories conference 2008 in Budapest made clear the need to update this model containing also some misinterpretations.

In this article the effects of laser light on living matter are discussed only briefly with a stronger emphasis on the photographs produced by the scattering of ordinary light on DNA reported in [192] . In TGD framework these photographs could be interpreted as photographs of wormhole magnetic flux tubes containing dark matter. This would realize the dream of making directly visible the basic new structure predicted by TGD inspired quantum biology. Of course, a more conventional explanation might be found for the effect, but the proposed qualitative explanation deserves to be discussed since it fits nicely with the general vision about dark matter in TGD Universe.

7.1.1 The findings of Peter Gariaev and collaborators

These findings of Gariaev and collaborators include the rotation of polarization plane of laser light by DNA [147] , phantom DNA effect [193] , the transformation of laser light to radiowave photons having biological effects [149] , the coding of DNA sequences to the modulated polarization plane of laser light and the ability of this kind of light to induce gene expression in another organisms provided the modulated polarization pattern corresponds to an "address" characterizing the organism [147] , and the formation of images of what is believed to be DNA sample itself and of the objects of environment by DNA sample in a cell irradiated by ordinary light in UV-IR range [192] .

Gariaev and collaborators have introduced the notion of wave genome [147] requiring the coding of DNA sequences to temporal patterns of coherent em fields forming a bio-hologram representing geometric information about the organism. Code could mean that nucleotide is represented by a characteristic rotation angle for the polarization plane of linearly polarized laser radiation scattering from it. This kind rotation is known to be induced by chromosomes by a mechanism which to my best knowledge is poorly understood. Other open questions concern the precise identification of the substrate of the bio-hologram, of the reference wave and of information carrying wave, and of the mechanism making possible (quantum) coherence in macroscopic length scales.

The reading of the DNA sequence to a radiation pattern is assumed to rely on the propagation of an acoustic soliton along DNA [147]. Whatever this process is, one should also identify the reverse process inducing the activation of the genome as the target organism receives the radiation coding for the DNA provided the "address" is correct. One should also identify the mechanism transforming

laser radiation to radio-waves at various frequencies as well as the mechanism creating what is believed to be the image of DNA sample and replicated images of some instruments used in experiment.

7.1.2 The relevant aspects of TGD based view about living matter

The called massless extremals (MEs or topological light rays) distinguish between TGD and Maxwell's electrodynamics: they represent classically signals propagating with light velocity in a precisely targeted and dispersion free manner, and are therefore excellent candidates for the communication and control tools in the TGD based model for a living system as a conscious hologram [50, 9, 23] . The notion of magnetic/field body, which can have layers of even astrophysical size, is an essential element of the model. Magnetic body uses biological body as a sensory receptor and motor instrument and MEs mediate sensory input and control signals between the two kinds of bodies [23] . I have already earlier applied MEs and the notion of magnetic body in an attempt to understand Gariaev's findings [9] .

The new element is the model for DNA as topological quantum computer (tqc) [26] based on time-like braidings of so called wormhole magnetic flux tubes connecting nucleotides to the lipids at lipid layers nuclear and cell membranes. The model leads to a wide variety of predictions about DNA itself [26] , to a universal model for a tissue memory in terms of space-like braidings of wormhole magnetic flux tubes [26] , to a more detailed model of nerve pulse explaining also the origin of EEG and its synchrony [57] , to a model for the evolution of the genetic code [29] , to a model of catalyst action involving a phase transition reducing the value of Planck constant inducing the shortening of the flux tubes connecting the reacting molecules and thus forcing them to the vicinity of each other, and to a model of for protein folding [3] in which the presence of wormhole magnetic flux tubes connecting bio-molecules becomes almost a definition for what it is to be living. It is interesting to combine these new ideas with the earlier [147, 149] and more recent [192] findings of Gariaev. Basically the challenge is to fuse the DNA as tqc model with the model of living systems as a conscious hologram [9] .

7.1.3 The basic assumptions of model explaining findings of Gariaev

The basic assumptions of the model to be discussed are following.

1. The hierarchy of Planck constants requires a generalization of the notion of 8-D imbedding space $H = M^4 \times CP_2$ obtained by gluing together almost copies of H like pages of book along common back. The pages of the book carry matter with various values of Planck constant and the particles at different pages of the book are dark relative to each other in the sense that they cannot appear in the same vertex of Feynman diagram. The particles at different pages of the book can however interact via classical fields and via the exchange of (for instance) photons which suffer a phase transition changing Planck constant as they leak between pages of the book. In principle it is therefore possible to photograph the magnetic flux tubes carrying dark matter, and the proposal is that this is what Gariaev and collaborators have actually achieved [192] .

2. Braid strands realized as wormhole magnetic tubes are identified as correlates for a directed attention. DNA connected by strands to (say) experimental instrument directs its attention to the instrument. One could perhaps say that DNA "sees" the surrounding world. Also ordinary attention for vision and other senses could involve flux tubes connecting DNA to the object of perception. This explains the ability of DNA to generate images of objects of external world [192] . The hierarchy of Planck constants explains the transformation of laser light to radio waves [149] as a phase transition increasing Planck constant and thus also wavelength but keeping the energy of photons as such.

3. Wormhole flux tubes carrying super-conducting matter in large $\hbar$ phase are characterized by anomalous em charges characterizing the nucleotides [26] , and thus define an excellent candidate for the substrate of bio-hologram. A coding of DNA nucleotides to the rotation of polarization plane results for photons traversing through these flux tubes if a large parity breaking making possible rotation of the polarization plane (Faraday effect) is assumed. This is possible by the large parity breaking of fractally scaled up variant of weak physics [6] explaining also chiral selection.

4. The model for the nerve pulse [57] leads to the model of EEG waves in which EEG rhythms induce a complete analog of reference waves whereas nerve pulse induces the analog of information carrying wave [23] . The model predicts a fractal hierarchy of EEGs (EXGs) and their counterparts associated with long ranged color and electro-weak gauge fields having MEs as classical correlates. EEG rhythms are associated with propagating soliton sequences and nerve pulse corresponds to a propagating perturbation associated with this soliton sequence rather than soliton. The model predicts automatically the synchrony and spatiotemporal coherence of neural firing. EEG photons correspond to a large value of Planck constant implying that their energies are above thermal energy at physiological temperatures so that their effects on living matter are not masked by thermal noise.

   This model generalizes essentially as such to the recent context: the counterparts of nerve pulses propagate along the complex formed by DNA connected to the nuclear or cell membrane or even to another cell nucleus by flux tubes. The prediction is that gene expression can be coherent in the scale of organ and even that of population. This conforms with the notion of super-genome stating that the sequences of DNA strands in different nuclei organize along magnetic flux sheet like text lines at the page of a book. The notion of hyper-genome means that these books from different organisms in turn organize to a pages of a book at higher level of fractal hierarchy and give rise to a gene expression at the level of population or even biosphere.

7.2 TGD counterpart for wave genetics

The wave genetic model of Gariaev involves the assumption that soliton waves propagating along DNA induce the reading of DNA sequence to a pattern of radiation. DNA is known to rotate the polarization plane but it is unclear how the coding of DNA sequence to a rotation of polarization plane could be achieved.

Second key element is the notion of bio-hologram. It is assumed that fractality is somehow involved. The key questions are following.

1. What is the substrate of the bio-hologram assuming that it is not based on nonlinear action for electromagnetic field (four-wave mechanism)? The substrate should have size larger than wavelength so that chromosomes are too thin to act as substrate.

2. What guarantees coherence or even quantum coherence in macroscopic scales?

3. How reference wave and the wave carrying the information are represented?

7.2.1 The notion of bio-hologram in TGD framework

TGD based model is based on the model of living matter inspired by the model of DNA as topological quantum computer [26] . DNA is connected to other bio-molecules and also to lipid layers of nuclear and cell membrane by wormhole magnetic flux tubes providing a representation of the genetic code. Braids strands defined by the flux tubes make possible topological quantum computation with tqc programs coded by dynamical braidings of the flux tubes induced by the water flow near the vicinity of cell and nuclear membranes inducing the flow of the 2-D liquid crystal defined by the lipids of the membrane. Flux tubes are dynamical, being able to reconnect and in the case of wormhole flux tubes even disappear without breaking conservation of magnetic flux, and they serve as correlates for a directed attention at the molecular and perhaps even at higher levels. Dark matter at the flux tubes has a large value of Planck constant and therefore a slow dissipation rate. Also superconductivity is possible and the predicted exotic nuclear physics allows bosonic chemical equivalents of all biologically important ions. Long range color and electro-weak interactions implying in particular large parity breaking are possible and could explain chirality selection in living matter.

It is easiest to introduce the model through questions and answers.

Q: What is the substrate of the bio-hologram and how coherence is obtained?

A: Magnetic flux tubes with large $\hbar$ define the substrate and make possible macroscopic quantum coherence. Visible photons can suffer a phase transition to large $\hbar$ variants with wavelengths scaled up like $\hbar$. The interpretation would be in terms of bio-photons and their dark variants [132] .

Q: How the Faraday effect results?

A: Flux tubes contain charged particles in super-conducting state so that diamagnetism results. Large parity breaking makes possible different propagation velocities for the two circular polarizations and thus Faraday effect resulting via the splitting of the linearly polarized wave to two circular polarizations fusing back again at the second end of the flux tube. The magnetic field along flux tubes induces Faraday rotation and codes DNA nucleotide to the rotation angle of the polarization plane.

Q: How coding is achieved?

A: Coding is achieved by the different total charges associated with flux tubes implying that the rotation angles for polarization plane depend on nucleotide. This would be made possible by anomalous em charge associated with DNA sheet of wormhole flux tube implying that the rotation of polarization plane is different for each nucleotide [26] .

Q: What is the identification of reference wave and for the wave representing the information?

A: The model for nerve pulse and EEG suggests that reference waves are induced as Josephson radiation from voltage waves propagating along DNA and represent a fractal variant of EEG. The voltages waves generating reference waves correspond to propagating soliton sequences for Sine-Gordon equation describing idealized cylindrical Josephson junction having as an analog series of coupled gravitational penduli. The propagating soliton sequence along DNA with constant phase differences between subsequent penduli would generate the reference wave as Josephson radiation. The analog of nerve pulse would result as one pendulum kicked so that it begins to oscillate instead of rotating and induces an propagating localized oscillation.

Microscopically cylindrical Josephson junction decomposes into junctions defined by the flux tubes and Josephson currents between the ends of the flux tubes generate em radiation as coherent photons. Josephson radiation would therefore give rise to bio-photons and their dark variants with same photon energy but scaled up wavelength. Obviously the transformation of laser photons to radio-wave photons can be understood in terms of this mechanism and the quantization of Planck constant implies quantization of the energies involved.

7.2.2 How to fuse the notion of bio-hologram with the model of DNA as tqc?

In the most economical picture - inspired by what is known about ordinary computers - intronic sequences would represent the names for tqc programs constructed from basic modules and expressing their outcomes chemically. Calling of the name of tqc would activate the tqc. This would allow an extremely rich combinations of basic modules, explain why the intronic portion of DNA increases during evolution, and why organisms with essentially identical genomes can be at widely differing evolutionary levels (say humans and apes). A further nice feature is that the intronic DNA of a given organism can induce gene expression in an organism for which the genes involved are not identical so that mutations would not be fatal. The prediction is that addresses represented by introns and the portions of promoter regions representing the conjugates of these addresses should be highly conserved.

The reading of the name of tqc to a polarization modulation pattern of incoming light would generate a signal which initiates tqc program in another cell in the case that the reverse polarization to the same linear polarization along the entire length of receiving intronic piece - conjugate of the original - takes place. The resulting overall linear polarization should initiate tqc leading to the eventual gene expression. Why the condition that linear polarization is same along entire piece of the "name" is not quite clear.

Introns could be connected by flux tubes to a part of DNA initiating gene expression. One would expect that this portion of gene is conjugate of the intronic portion containing the name of submodule. This would make possible RAM type representation of tqc programs if the link to next activated part of genome is represented by this same mechanism: exactly similar mechanism realizes links electromagnetically in web. A nucleus performing tqc infects large number of nuclei to perform the same tqc. Same could occur even at the level of population since very large values of $\hbar$ are possible.

7.3 The effects of laser light on living matter

The effects of laser light on living matter are discussed in the following briefly from TGD point of view.

7.3.1 Phantom DNA effect

In phantom DNA effect [193] there is an elastic scattering of the coherent laser radiation from irradiated DNA. When one removes the DNA from the chamber containing it, and irradiates it by laser light, a weak pattern of scattered light is still producedas if there were a kind of phantom DNA there. The pattern can last for months.

For years ago I considered an explanation of the effect based on dropping of part of DNA to larger space-time sheets characterized by larger value of p-adic prime and remaining in the vessel as visible DNA is removed [84, 9] . A variant of this explanation inspired by the dark matter hierarchy is that the anomalous scattering takes place on dark DNA at wormhole flux tubes remaining in the vessel.

The most science fictive possibility is that the flux tubes connect the vessel boundaries to the removed DNA by wormhole flux tubes which are very long and correspond to a large value of $\hbar$. In this case the scattering would involve a phase transition increasing the value of Planck constant and a travel of photons to the removed DNA and back followed by a phase transition to ordinary photons.

Similar explanation works also in the case of homeopathy and allows to understand why the classic experiments of Benveniste [135, 136] could not be replicated when experimenters did not know which bottles contained the treated water [34] . In this case the molecules dissolved in water would lose their magnetic bodies as a consequence of the shaking of the homeopathic remedy and one can say that clusters of water molecules would steal their magnetic coats. This would allow them to mimic the behavior of molecules and their presence would allow the immune system would develop a resistance against real molecules. This of course works only if the cyclotron radiation from the magnetic body is responsible for the biological effects. It is known that em radiation at low frequencies is indeed responsible for the ability of molecules to recognize each other. The generation of cyclotron radiation requires metabolic energy and the magnetic flux tubes connecting the experimenter to the treated bottle of water (correlates for directed attention) could have served as bridges along which metabolic energy could be transferred by using topological light rays (MEs serving as TGD counterparts of Alfwen waves). Experimentalists certainly did have strong desire to have successful experiments and this helped to realize the transfer of the metabolic energy.

7.3.2 Effects of the polarization modulated laser light on living matter

Polarized light with a suitable temporal pattern for the modulation of polarization direction induces biological effects. The effects are not caused to arbitrary target and one can say that the part of target genome involved has an address characterized by a temporal pattern of polarization modulation resulting in the propagation of the scaled variant of nerve pulse along chromosome. DNA is known to induce a rotation of polarization plane of incoming linearly polarized light and Gariaev suggests that the address is due to the propagation of a soliton along DNA inducing the modulation [147] .

TGD based model for the rotation of the polarization plane is based on Faraday effect [5] .

1. Usually diamagnetic dielectric causes the Faraday effect. The effect is due to different propagation velocities of left and right circular polarizations and recombination of polarizations to linear polarization. The rotation of the polarization plane would be caused by a Faraday effect at flux tubes. Superconductivity would imply ideal diamagnetism. Dielectric property is probably not present but large parity breaking due to long range weak interactions [6] could explain why circular polarizations propagate with different velocities. Strong parity breaking could be caused by the presence of electro-weak gauge fields behaving like massless fields below the cell length scale and would explain also chiral selection. For large values of $\hbar$ the range of these fields would be scaled up accordingly.

2. The travel of the photon along a transversal flux tube starting from DNA nucleotide induces a rotation of the direction of polarization plane. The reverse rotation of polarization plane takes place as the light propagates in the reverse direction. The reverse propagation restoring the

original overall linear polarization is expected to induce the biological along the portion of DNA in question. Phase conjugate light might be also involved.

3. The coding of DNA sequences to radiation patterns results since the charge Q associated with the nucleotide end of the wormhole magnetic flux tube affects Faraday rotation and is different for each nucleotide. The value of the charge is given by $Q = -2 + Q_a$, where -2 units come from phosphate and Q_a corresponds to the charge of the quark (u, d) or antiquark ($\overline{u}$, $\overline{d}$) at the DNA space-time sheet associated with wormhole magnetic flux tube formed by a pair of space-time sheets connected by wormhole contacts having at its light-like throats quark and antiquark [26] . Hence the rotation of the polarization plane depends on the nucleotide.

7.3.3 PLR spectroscopy

Bio-systems could generate holograms in much more concrete sense than the wetty and hot and noisy character of this environment would suggest: even mechanisms generating laser beams could be there. The findings of Peter Gariaev and collaborators described in the article "The spectroscopy of bio-photons in non-local genetic regulation" [149] led to a concrete model for how bio-photons affect many-sheeted DNA, and in this manner induce a generation of coherent radio waves and ELF waves [9] . The recent picture brings in the hierarchy of Planck constants and suggests a modification of this model.

The effect

In polarizing laser-radio wave spectroscopy (PLR-spectroscopy) laser light scatters from the target substance. In the experiments of Gariaev *et al* red light ($\lambda = 632.8$ nm, 1.9595 eV) generated by He-Ne laser is used. This energy actually corresponds very precisely to one of the fundamental metabolic energy quanta identified as liberated zero point kinetic energy of proton as it drops from certain space-time sheet to much larger space-time sheet. There are two orthogonal polarizations correlated in intensity in such a manner that the total intensity remains constant. After the interaction of one mode with the target substance, the reflected light is returned to the optical resonator, where the re-distribution of the intensity of these modes occurs. One of the laser modes, at a certain mode of generation, is able during the interaction with the target substance to induce polarization modulated radio waves of a wide spectrum correlated with the modulations of the optical modes of the laser radiation. The modulation is assumed to relate to rotational fluctuations of micro-structural components (say, domains of crystals) and of their optical activity. The PLR-spectrum is present also for in-organic materials. For biological targets there is spectral memory effect present, which means that the radio wave radiation continues even when the laser beam is not present anymore.

The frequency interval of the radio emission settles down at the 1 MHz. The PLR-spectrum is depicted in figures 1 and 2 of [149] for apofillit crystal. The frequency spectrum for the radio waves has a modulated fractal structure suggesting that spectrum is superposition of spectra which consist of harmonics $n_1 f_h - n_2 f_l$ of higher frequency f_h modulated by harmonics of scaled down frequency $f_l = x f_h$. Almost identical copies of a piece of length about

$$\Delta f \sim 100\ Hz$$

appear in a sequence as the pictures 1 and 2 of [149] for the spectrum of apofillit crystal in 1560-1860 Hz range demonstrate. This suggests the presence of harmonics of basic frequencies perhaps shifted by a constant amount. Cyclotron and spin flip transitions in magnetic field suggest itself.

There is also gross structure consisting of peaks in scale of kHz suggesting harmonics of frequency of order kHz. For wheat seed (picture 3 of [149]) the strongly expressed frequency ranges are identified as 800-900 Hz (to my personal opinion the band is 300-900 Hz), 1700-1900 Hz, 2400-2600 Hz, 3600-3800 Hz (to my personal opinion a wider frequency range 1700-2200 Hz is strongly expressed). There is also strongly expressed frequency band below 300 Hz. Also the spectrum of high polymerization DNA sample from calf thymus (picture 4 of [149]) shows a clear peak at 2400-2600 Hz and less pronounced peaks at lower frequencies.

The radio wave radiation from DNA samples is accompanied by specific effects on bio-systems such as ab-normally fast germination and re-vitalization of seeds. Thus it seems that the radio wave radiation is able to restore the genetic control apparatus and the vitality of the seeds.

TGD based explanation of the effect

Dark matter hierarchy suggests the interpretation of radio-wave photons as large $\hbar$ photons with energy equal to that of the original photon. Biophotons and their dark variants could form Bose-Einstein condensates at the wormhole magnetic flux tubes. The flux tubes associated with DNA would transform laser photons to radiowave photons by inducing $\hbar$ increasing phase transition. Large value of $\hbar$ would increase the range of interactions so that they would become possible even in the scale of biosphere. In particular, coherent gene expression in the scale of organism and even population. Genetic code could be represented as radiation patterns with the charges assignable to the end of DNA space-time sheet of flux tube providing the coding.

7.4 The scattering of incoherent UV-IR light on DNA

The proposed model for the findings about scattering of incoherent UV-IR light from DNA lead to an amazing conclusion that the experiments make directly visible the magnetic flux tubes containing dark matter.

7.4.1 Basic facts

The figures of the article [192] give valuable information about what is involved. There are two experimental arrangements.

1. In the first experiment dry/dehydrated DNA is contained in a small seal containing a conical cylinder (4 cm long, .9 cm at its upper end) or 3 ml of DNA water solution 1 mg/ml. The rradiation by UV-C lamp lasts for 10 minutes: note that UV-C wavelengths are in the range 280-10 nm.

2. In the second experiment the DNA sample is in open cell and a light source known as Duna-M irradiates red light from 21 LEDS (650 nm) and IR light (920 nm) from 16 LEDs. Also UV-B lamp and Compact electronic CEST26E17 Black lamp are involvedUV-B wavelengths are in the range 315-280 nm. The light sources are turned on and off with intervals of 2-3 seconds. The exposure time is 1 second.

The basic findings are following [192] .

1. The effects occur only if the sample contains DNA.

2. A large number (tens) of closely spaced replica images of nearby objects, in particular the red LED. The replicas for the image of instrument are along strictly horizontal half line (see Fig. 1).

3. The replica sequences of the instruments appear periodically suggesting that the energy of incoming photons is gradually accumulated and liberated in a burst. The interference by an external DNA source (touching by finger of DNA cell) changes the direction of the half line which disappears at the next exposure to white light.

4. Single vertical curved band like image of roughly the same height as the entire image and with more or less the same width as the distance between replicas of the instrument parts appears to the left from the instrument image (see Fig. 1). This image is not replicated in the horizontal direction. The fine structure of the band for one of the reported images (see Fig. 2) however suggests that also the band like structure consists of replicas of same size as the replicas associated with instruments. The band like structure for second method decomposes to 5 red parallel curves (see Fig. 3) for which the interpretation as images of 5 red LEDs is proposed based on the observation that these LEDs irradiate directly the DNA cell. The phantom of DNA image remains intact for some time after the irradiation.

If I have understood correctly, the interpretation proposed in [192] is following.

1. The sequence of the horizontal images of the instrument would result from a motion of single image moving during the exposures: this requires that the motion is fast in the time scale of exposure. The appearance of equally spaced replicas forces to assume that the motion occurs in discrete jumps in horizontal direction.

2. The band like structure is identified as the image of DNA sample. The band is assumed to correspond to a discrete and non-predictable motion of single image.

There are objections against the idea that the motion of single image produces the image. In particular, the discreteness of the motion looks strange. One can also wonder why the motion for the image of the instrument is strictly horizontal whereas the motion of DNA image is not horizontal and is curvilinear. One can also ask whether the an image of DNA sample is actually in question since the position of the band like structure is to left from the cell containing the DNA.

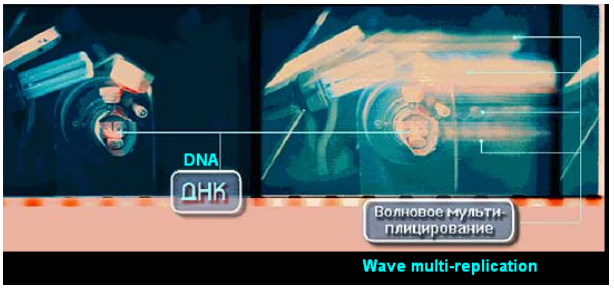

Figure 7.1: The left hand side figure is from [192] and represents the replica images of the instruments and the image interpreted by experimenters as a replica image of DNA sample (second method).

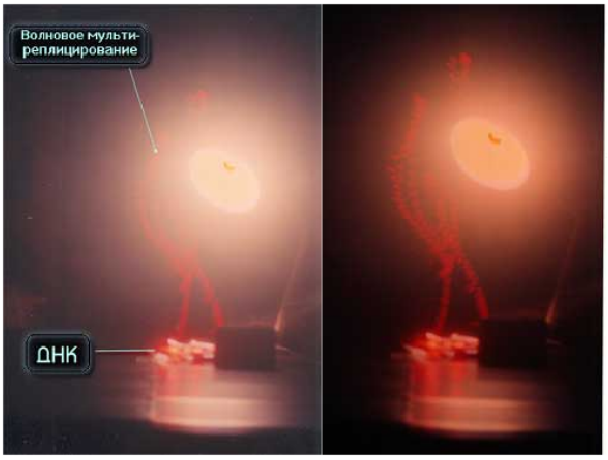

Figure 7.2: The picture shows the discrete replica like structure of the band like image interpreted by experimenters as replica image of DNA sample (first method).

7.4.2 TGD based model for the replicas

One can consider two models for the replicas. The first model assumes that the images are images of dark magnetic flux tubes. Second model assumes that in the case of instrument images diffraction is involved.

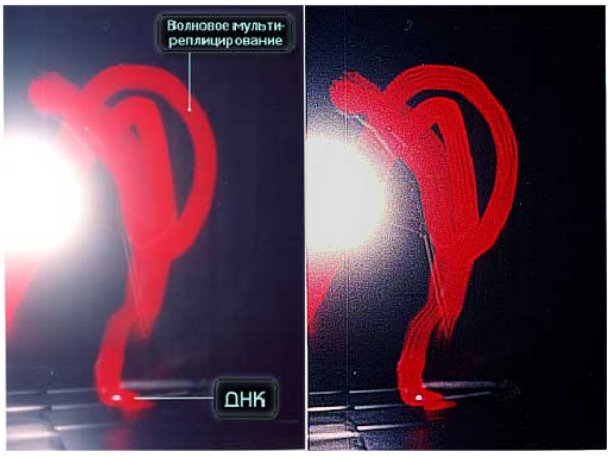

Figure 7.3: The picture reveals the 5-fold fine structure of the band like image interpreted by experimenters as replica image of DNA sample. The 5-fold character probably correspond to five red LEDs above the sample (second method).

Have wormhole magnetic magnetic flux tubes containing dark matter been photographed?

The most elegant model for the effects found hitherto relies on the assumption that both the horizontal replica sequences and the band like structures having also replica structure correspond to real structures, most naturally (wormhole) magnetic flux tubes. In the case of instrument replicas they would emanate directly from the instruments. In the case of DNA image they would emanate from a position to the left from the cell containing DNA. The presence of DNA should somehow generate the flux tubes.

1. In the case of horizontal replications of instruments the replicas would be associated with a magnetic flux tube emanating horizontally from the instruments to the right. Replicas would be obtained if a dipole distribution assignable to the surface of object and representable in terms of Fourier transform restricted to a box containing the object and having discrete momentum spectrum is extended to a periodic Fourier transform along the horizontal flux tube. Flux tube would thus represent a series of images of the geometric object and this would make possible to communicate the data through long distances.

2. Also the DNA image could be the image of a curved flux tube assignable to the cell containing the DNA. The band like structure does not however begin from the cell containing DNA being located left from it. A possible explanation is that there topological light ray connecting the cell containing DNA to a similar sized cell at the end of the flux tube irradiating it with photons emitted from the dipole distribution at its surface. The resulting induced dipole distribution representable in terms of a discrete Fourier transform is then continued along the entire curved flux tube and would generate the replicas.

3. The replication of the dipole distribution along the entire length of the flux tube requires macroscopic quantum coherence suggesting a large value of Planck constant. If the coherence is required at least in the length scale L of the flux tube, one obtains ratio $r = \hbar/\hbar_0 \geq L/\lambda \simeq 10^6$ for $L = .5$m and $\lambda = 500$ nm. This value could correspond to the favored value $r = 2^{20}$ and thus to a favored value of Planck constant [27] . A weaker condition is obtained by replacing L with the size a of the cell giving $r \geq a/\lambda \simeq 2 \times 10^5$ for $a = .1$ m.

4. If the flux tubes correspond to large value of Planck constant, the dark photons emanating from them must transform to ordinary photons since diffractive effects are not involved.

5. The fact that the images of the flux tubes appear periodically suggests that a Bose-Einstein condensate of dark photons is gradually formed at them which bursts out as some critical

number of dark photons are present and leaks to the visible sector of the 8-D imbedding space becoming ordinary photons. One can visualize the sectors of the generalized 8-D imbedding space as pages of a book characterized by different values of Planck constant so that the leakage would occur from page to another one through the back of the book.

6. The effect of touching in the second type experiment involving LEDs can be understood if the touching reverses the direction of the magnetic flux tubes assigned with the instruments. The disappearance of the replicated instrument image 5-8 seconds after the touching could relate to the instability of the right-oriented flux tubes. If the right-directed flux tube is mirror image of the left oriented flux tube, the instability might relate to a parity breaking possible in TGD Universe by the presence of scaled variants of weak interactions. The preferred orientation of the flux tube might be also determined by something in environment, say resources of metabolic energy. If the flux tubes are correlates for attention, one can even imagine that DNA with the mediation of flux tubes directs its attention to something interesting.

There are also some open questions.

1. Why the flux tube assignable to the DNA is curved and why the image of this flux tube does not emanate from the sample?

2. How the presence of DNA induces the generation of the flux tubes? The model for DNA as tqc would suggest that the thin wormhole magnetic flux tubes connecting DNA to the instruments induce the effect, and that the flux tubes explaining the image correspond to higher level structures with larger value of Planck constant and are somehow induced by the presence of DNA. They could also correspond to a larger value of p-adic prime but same value of Planck constant. Perhaps one might say that the magnetic body of DNA makes the instruments in some sense part of its biological body by directing its attention to them.

3. Why the touching chances the orientation of the flux tube?

If this model is on a right track, the findings would mean a direct observation of dark magnetic flux tubes by the em radiation of dark photons transformed to ordinary photons as they leak out from dark sectors of the imbedding space to the sector containing the matter visible to us.

The explanation in terms of diffraction does not work

For the sake of completeness also the interpretation of the replication of the images of the instrument and DNA cell in terms of diffraction is discussed although this explanation forces several ad hoc assumptions unlike the previous model.

1. The appearance of the replicas along horizontal half-line $x > 0$ brings strongly in mind a diffraction through a vertical slit defined by a vertical dark flux sheet attached to the instrument and acting as a window. This requires coherence so that ordinary visible light cannot be responsible for the image whereas dark photons with a large enough value of Planck constant makes the quantum coherence possible.

2. The amplitude for a diffraction through slit behaves as $A = sin(x)/x$, $x = \pi \times (a/\lambda) \times sin(\theta)$, where θ is the angle between the normal of the slit and direction of observation. Hence the maxima of the intensity maxima correspond to the central maximum $\sin(\theta) = 0$ given by geometric optics and $\sin(\theta) = (n + 1/2) \times \lambda/a$ so that for small angles one has $\Delta\theta = \lambda/a$ and the distance between replicas is $x = d\Delta\theta = d\lambda/a$.

3. The distance between the replicas in the image requires a wavelength longer than used in experiments. Thus dark photons with a scaled up wavelength $\lambda = r\lambda_0$, $r = \hbar/\hbar_0$, transforming by Planck constant changing phase transition to ordinary photons in camera could be in question. The value of the Planck constant can be deduced by using the geometric data, the values of wavelength, and the distance between the replicas of instrument images assuming that diffraction effectively takes place through a vertical slit with width of order size of typical replicated instrument, say seal. From $\theta \leq D/d$, where D is the size of camera aperture, and from the number n of horizontal replicas $n < 100$ one obtains the estimate $d\lambda/a \sim D/nd$. This gives

$\lambda/a \sim D/nd^2$. For $D = .01$ m, $d = .5$ m, one would have $\lambda/a \sim 4 \times 10^{-4}$. For $\lambda = 4 \times 10^{-7}$ m this would give $a \sim 10^{-3}$ m. The appearance of details in the replicated image suggest that a is of the same order than the instrument size so that one has $a \geq x > 1$ cm giving $\hbar/\hbar_0 \geq 10x$. The value of λ seems to be too small to allow coherence in the required length scale.

4. The serious problem of this interpretation is that the diffraction pattern for a diffraction through slit corresponds to maxima at an entire transversal line rather than half-line. It is as if the effective vertical flux sheet attached to the left hand side of the object would contain a distribution of horizontal dipoles generating radiation interfering to zero at the left half of the half-space. This distribution should be determined by the radiation coming from the object so that a kind of induced emission process would be in question. One can also imagine is that the dark space-time sheet along which photons arrive is half-space with horizontal coordinate $x \geq 0$. What is intriguing that in p-adic physics for which the values of variables finite in real sense are always positive as real numbers so that half-lines, quadrants, octants,... are very natural objects. One must admit that this assumption looks ad hoc.

5. There is also a second problem. The evidence for the replication of same basic unit with the size of the DNA containing cell suggests that a replication of the image of cell containing the DNA along a curved band is in question with essentially the same distance between replicas as in the previous case. It is impossible to have a curved slit producing this kind of diffraction pattern. One could consider also the possibility that the band corresponds to a real structure, may be magnetic flux tube, and that Planck constant is now larger than in the case of instrument images so that only the central image of the diffraction pattern is visible in the camera. This however forces to ask whether also the replicas of instruments correspond to magnetic flux tubes so that one would end up with the first model.

7.5 Water memory, phantom DNA effect, and development of tqc hardware

This section describes speculative picture in which a connection between homeopathy and water memory [34] with phantom DNA effect is proposed and on basis of this connection a vision about how the tqc hardware represented by the genome is actively developed by subjecting it to evolutionary pressures represented by a virtual world representation of the physical environment.

7.5.1 A possible realization of water memory

The Benveniste's discovery of water memory [135, 136] initiated quite dramatic sequence of events. The original experiment involved the homeopathic treatment of water by human antigene. This meant dilution of the water solution of antigene so that the concentration of antigene became extremely low. In accordance with homeopathic teachings human basophils reacted on this solution.

The discovery was published in Nature and due to the strong polemic raised by the publication of the article, it was decided to test the experimental arrangement. The experimental results were reproduced under the original conditions. Then it was discovered that experimenters knew which bottles contained the treated water. The modified experiment in which experimenters did not possess this information failed to reproduce the results and the conclusion was regarded as obvious and Benveniste lost his laboratory among other things. Obviously any model of the effect taking it as a real effect rather than an astonishingly simplistic attempt of top scientists to cheat should explain also this finding.

The model based on the notion of field body and general mechanism of long term memory allows to explain both the memory of water and why it failed under the conditions described.

1. Also molecules have magnetic field bodies acting as intentional agents controlling the molecules. Nano-motors do not only look co-operating living creatures but are such. The field body of the molecule contains besides the static magnetic and electric parts also dynamical parts characterized by frequencies and temporal patterns of fields. To be precise, one must speak both field and relative field bodies characterizing interactions of molecules. Right brain sings-left brain talks

metaphor might generalize to all scales meaning that representations based on both frequencies and temporal pulse with single frequency could be utilized.

2. The effects of complex bio-molecule to other bio-molecules (say antigene on basofil) in water could be characterized to some degree by the temporal patterns associated with the dynamical part of its field body and bio-molecules could recognize each other via these patterns. This would mean that symbolic level in interactions would be present already in the interactions of bio-molecules. Cyclotron frequencies are most natural candidates for the frequency signatures and the fact that frequencies in 10 kHz range are involved supports this view.

3. The original idea was that water molecule clusters are able to mimic the bio-molecules themselves -say their vibrational and rotational spectra could coincide with those of molecules in reasonable approximation. A more natural idea is that they can mimic their field bodies. Homeopathy could rely on extremely simple effect: water molecule clusters would steal the magnetic bodies of the molecules used to manufacture the homeopathic remedy. The shaking of the bottle containing the solution would enhance the probability for bio-molecule to lose its magnetic body in this manner. For instance, water could produce fake copies of say antigenes recognized by basofils and reacting accordingly if the reaction is based on interaction with the magnetic body of the antigene.

4. The basic objection against this picture is that it does not explain why the repeated dilution works. Rather, it seems that dilution of molecules reduces also the density of mimicking pseudo-molecules. Even more, the potency of the homeopathic remedy is claimed to increase as the the dilution factor increases. Also alcohol is used instead of water so that also alcohol must allow homeopathic mechanism. (I am grateful for Ulla Matfolk for questions which made me to realize these objections).

   (a) The only way out seems to be that the magnetic bodies or water molecule clusters having these magnetic bodies can replicate. The shaking of the remedy could provide the needed metabolic energy so that the population of magnetic bodies grows to a limiting density determined by the metabolic energy feed. In principle it would be possible to infect unlimited amount of water by these pseudo-molecules. When in bottle the population would be in dormant state but in the body of the patient it would wake up and form a population of molecular actors and stimulate the immune system to develop immune response to the real molecule.

   (b) The potency of the homeopathic remedy is claimed to increase with the increased dilution factor. This would suggest that the continued dilution and shaking also increases the density of pseudo molecules, perhaps by feeding to the system metabolic energy or by some other mechanism.

   (c) Also magnetic bodies must replicate in cell replication and their role as intentional agents controlling bio-matter requires that this replication serves as a template for biochemical replication. On can indeed interpret the images about cell replication in terms of replication of dipole type magnetic field. This process is very simple and could have preceded biological replication. The question is therefore whether water is actually a living system in presence of a proper metabolic energy feed. Also the water's ability near critical point for freezing to form nice patterns correlating with sound stimuli might be due to the presence of the molecular actors.

   (d) This picture fits nicely with the vision that evolution of water in this kind of life form might have happened separately and that pre-biotic chemical life forms have formed symbiosis with living water [29] . In the model of DNA as topological quantum computer [26] the asymptotic self organization patterns of water flow in the vicinity of lipid layers indeed define quantum computer programs by inducing the braiding of the magnetic flux tubes connecting DNA nucleotides to lipids so that this symbiosis would have brought in new kind of information processing tool.

5. The magnetic body of the molecule could mimic the vibrational and rotational spectra using harmonics of cyclotron frequencies. Cyclotron transitions could produce dark photons, whose

ordinary counterparts resulting in de-coherence would have large energies due to the large value of $\hbar$ and could thus induce vibrational and rotational transitions. This would provide a mechanism by which molecular magnetic body could control the molecule. Note that also the antigenes possibly dropped to the larger space-time sheets could produce the effect on basofils.

6. There is a considerable experimental support for the Benveniste's discovery that bio-molecules in water environment are represented by frequency patterns, and several laboratories are replicating the experiments of Benveniste as I learned from the lecture of Yolene Thomas in the 7:th European SSE Meeting held in Röros [23] . The scale of the frequencies involved is around 10 kHz and as such does not correspond to any natural molecular frequencies. Cyclotron frequencies associated with electrons or dark ions accompanying these macromolecules would be a natural identification if one accepts the notion of molecular magnetic body. For ions the magnetic fields involved would have a magnitude of order .03 Tesla if 10 kHz corresponds to scaled up alpha band. Also Josephson frequencies would be involved if one believes that EEG has fractally scaled up variants in molecular length scales.

Consider now the argument explaining the failure to replicate the experiments of Benveniste.

1. The magnetic bodies of water molecules need metabolic energy for communications with their "biological body" using the fractally scaled analog of EEG. There is no obvious source for this energy in water. The model for protein folding and DNA as topological quantum computer assumes that magnetic flux tubes connecting subject person and target of directed attention serve as correlates for directed attention at the molecular level [26, 3] . This should be true also in macroscopic scales so that the experimentalist and the bottle containing the treated water should be connected by magnetic flux tubes. If experimenter has directed his attention to the bottle of water, the resulting magnetic flux tubes could allow a transfer of metabolic energy as a radiation along massless extremals parallel to the flux tubes and defining TGD counterparts of Alfwen waves. Experimenter's strong motivation to replicate experiments would help to realize the transfer of the metabolic energy. Experimenters not knowing, which bottles were treated did not have these flux tube bridges to the bottles, and were not able to provide the needed metabolic energy, and the magnetic bodies of antigenes failed to generate the cyclotron radiation making them visible to the basofil.

2. If this interpretation is correct, then Benveniste's experiment would demonstrate besides water memory also psychokinesis and direct action of desires of experimenters on physics at microscopic level. Furthermore, the mere fact that we know something about some object or direct attention to it would mean a concrete interaction of our magnetic body with the object. The so called phenomenon of psi track [32] provides additional support for this conclusion.

7.5.2 Could virtual DNAs allow a controlled development of the genome?

The fundamental question in the evolution biology is the question about the interaction between genome (G), phenotype (P), and environment (E).

1. The standard dogma is that the information transfer from G to P is unidirectional and that environment acts on G by inducing random mutations of G, from which E selects the lucky survivors as those with the best ability to reproduce. Lamarckism [32, 159, 143] represents a deviation from standard dogma by assuming direct information transfer from E to G.

2. Genetic expression is controlled by environment, at least by silencing [32] , which is like selecting only few books to be read from a big library. Cell differentiation represents basic example of selective gene expression. DNA methylation and transposition are accepted to reflect information transfer from E to G, perhaps via P. These modifications are believed to be short lasting and not transferred to the offspring since it is difficult to imagine a mechanism transferring the mutations to the germ cells. There is however also evidence that epigenetic information transfer takes place [195] : this transfer would be selective expression of genes of germ cells rather than that of modified genes.

3. There are findings challenging the dogmas of static genome and random mutations. The cells of the immune system remodel their genes coding for antibodies capable of recognizing large variety of antigens. There is quite recent finding [133] revealing major genetic differences between blood and tissue cells. There are also mutations due to jumping genes - mobile elements of DNA known as LINE-1 elements usually regarded as junk DNA whose portion from genome increases as one climbs up along the evolutionary ladder. In mice jumping genes are limited to brain and germ cells: this is easy to understand since in organs like heart and lungs this kind of mutations would be fatal. Second recent discovery is that there is a high diversity of human brain cells believed to be due to the jumping genes [169] . That brain cells would be producing with a high rate junk DNA is not an idea which would make me shout 'Eureka!'

4. The question however remains whether the $G \to P - E$ actually could complete to a closed loop $G \to P - E - G$ so that genome could directly respond to the changing physical environment and could transfer the successful response to the next generation [159] .

Could genome be developed like computer hardware?

In TGD framework the sequence $G \to P - E$ is replaced with a closed loop $G - P - M - E$ to which E is attached at P by bidirectional arrow (organisms do also modify their environment actively). Magnetic body thus controls genome and receives information from cell membrane (P). The hierarchy of genomes (super-genome, hyper-genome,...) corresponding to the different levels of dark matter hierarchy allows this loop to be realized in different scales rather only at the level of single cell.

The question is whether the magnetic body of organism or higher level magnetic bodies could modify genomes, super-genomes, and hyper-genomes directly, perhaps by generating mutations of the genome in a short time scale; by monitoring how genetically modified organism survives in the environment; and -if the outcome of the experiment is successful - replacing the corresponding portion of DNA with the modified DNA both in ordinary germ cells. One can even ask whether the abstract model of the external environment provided by the internal chemical milieu might be mimicked by water magnetic bodies of water molecule clusters and provide a virtual world testing ground for a search of favorable mutations.

In DNA as a tqc vision essentially the development of a new computer hardware would be in question, and should take place in a controlled manner and involve an experimentation before going to the market rather than by random modifications taking place in computer CPUs. Second basic aspect of DNA as tqc paradigm is that water and bio-molecules live in symbiosis in the sense that self organization patterns of the cellular water flow define the tqc programs. The following first guess for how the development of computer hardware might be achieved is just a first guess but might have something to do with reality.

1. What would be needed is a mechanism generating rapidly modifications of DNA. The mutations should be carried out using a kind of virtual DNA mimicking all the essential aspects of the symbolic dynamics associated with DNA. The magnetic bodies of DNA consisting of flux tubes connecting the nucleotides of DNA strands to cell membrane satisfy these conditions since A,T,G,C is coded to exotic light quarks u, d and anti-quarks $\overline{u}$, $\overline{d}$ at the ends of flux tubes [26] . DNA nucleotides could be replaced with clusters of water molecules but also other options can be imagined. Note that it does not matter when one speaks of mimicry of RNA or DNA molecules.

2. If the proposed model of the phantom DNA and homeopathy has something to do with reality, this kind of virtual DNA exists and is generated in phantom DNA effect as magnetic bodies of DNA, including of course the magnetic flux tubes connecting the nucleotides to the cell membrane or conjugate strand of DNA.

3. The crucial additional assumption would be that also the reversal of phantom DNA effect is possible and corresponds to the analog of DNA replication in which nucleotides attach to the virtual conjugate nucleotides of the virtual DNA strand or RNA strand in turn transformed to DNA strand be reverse transcription. The hypothesis would have rather strong implications for the genetic engineering since homeopathic remedies of genetically engineered DNA sequences could be transferred to cell nuclei just by drinking them.

4. Phantom DNA sequences could form populations and - as far as their properties as a hardware of topological quantum computer are involved - evolve under selection pressures of the virtual world defined by the nuclear, cellular and extracellular water. A competition of components of tqc hardware developed by the higher level magnetic body to realize optimally tqc programs needed for survival would be in question. The simplest mutation of phantom DNA would replace the quark pairs at the ends the (wormhole-) magnetic flux tube with a new one and could occur in very short time scale. Also basic editing operations like cutting and pasting would be possible for these competing phantom DNA sequences. The winners in the competition would be transformed to actual DNA sequences by utilizing the reverse phantom DNA (or RNA -) effect and be inserted to genome. The genetic machinery performing cutting, gluing, and pasting of real DNA in a controlled manner exists. What is needed is the machinery monitoring who is the winner and making the decision to initiate the modification of the real DNA.

5. The transfer of the mutations to germ cells could be achieved by allowing the population of the virtual DNA sequences to infect the water inside germ cells. The genetic program inducing the modification of DNA by using the winner of the tqc hardware competition should run automatically.

6. One open question is whether the nuclear, cellular or perhaps also extracellular water should represent the physical environment and - if answer is affirmative - how it achieves this. As a matter fact, considerable fraction of water inside cells is in gel phase and it might be that the intercellular water, which naturally defines a symbolic representation of environment, is where the virtual evolution takes place. Internal chemical milieu certainly reflects in an abstract manner the physical environment and the ability of the water molecule clusters to mimic bio-molecules would make the representation of the chemical environment possible. Also sudden changes of external milieu would be rapidly coded to the changes in internal milieu which might help to achieve genetic re-organization. The craziest dream is water based simulation of both genes, proteins, and molecules representing external world running at dark space-time sheets.

Dark nuclear strings as analogs of DNA-, RNA- and amino-acid sequences and baryonic realization of genetic code?

The minimal option is that virtual DNA sequences have flux tube connections to the lipids of the cell membrane so that their quality as hardware of tqc can be tested but that there is no virtual variant of transcription and translation machinery. One can however ask whether also virtual amino-acids could be present and whether this could provide deeper insights to the genetic code.

1. Water molecule clusters are not the only candidates for the representatives of linear molecules. An alternative candidate for the virtual variants of linear bio-molecules are dark nuclei consisting of strings of scaled up dark variants of neutral baryons bound together by color bonds having the size scale of atom, which I have introduced in the model of cold fusion and plasma electrolysis both taking place in water environment [1] , [1] . Colored flux tubes defining braidings would generalize this picture by allowing transversal color magnetic flux tube connections between these strings.

2. This seems to work! The states of dark nucleons formed from three quarks can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, and 20 aminoacids and there is natural mapping of DNA and RNA type states to aminoacid type states such that the numbers of DNAs/RNAs mapped to given aminoacid are same as for the vertebrate genetic code.

The basic idea is simple. Since baryons consist of 3 quarks just as DNA codons consist of three nucleotides, one might ask whether codons could correspond to baryons obtained as open strings with quarks connected by two color flux tubes. This representation would be based on entanglement rather than letter sequences. The question is therefore whether the dark baryons constructed as string of 3 quarks using color flux tubes could realize 64 codons and whether 20 aminoacids could be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner.

The following model indeed reproduces the genetic code directly from a model of dark neutral baryons as strings of 3 quarks connected by color flux tubes.

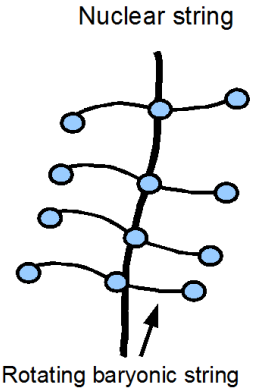

Figure 7.4: Illustration of a possible vision about dark nucleus as a nuclear string consisting of rotating baryonic strings.

1. Dark nuclear baryons are considered as a fundamental realization of DNA codons and constructed as open strings of 3 dark quarks connected by two colored flux tubes, which can be also charged. The baryonic strings cannot combine to form a strictly linear structure since strict rotational invariance would not allow the quark strings to have angular momentum with respect to the quantization axis defined by the nuclear string. The independent rotation of quark strings and breaking of rotational symmetry from SO(3) to SO(2) induced by the direction of the nuclear string is essential for the model.

   (a) Baryonic strings could form a helical nuclear string (stability might require this) locally parallel to DNA, RNA, or aminoacid) helix with rotations acting either along the axis of the DNA or along the local axis of DNA along helix. The rotation of a flux tube portion around an axis parallel to the local axis along DNA helix requires that magnetic flux tube has a kink in this portion. An interesting question is whether this kink has correlate at the level of DNA too. Notice that color bonds appear in two scales corresponding to these two strings. The model of DNA as topological quantum computer [26] allows a modification in which dark nuclear string of this kind is parallel to DNA and each codon has a flux tube connection to the lipid of cell membrane or possibly to some other bio-molecule.

   (b) The analogs of DNA -, RNA -, and of amino-acid sequences could also correspond to sequences of dark baryons in which baryons would be 3-quark strings in the plane transversal to the dark nuclear string and expected to rotate by stringy boundary conditions. In this case all dark baryons would be free to rotate. Thus one would have nuclear string consisting of short baryonic strings not connected along their ends (see Fig. **??**).

2. The new element as compared to the standard quark model is that between both dark quarks and dark baryons can be charged carrying charge $0, \pm 1$. This is assumed also in nuclear string model and there is empirical support for the existence of exotic nuclei containing charged color bonds between nuclei.

3. The net charge of the dark baryons in question is assumed to vanish to minimize Coulomb repulsion:

$$\sum_q Q_{em}(q) = - \sum_{flux\ tubes} Q_{em}(flux\ tube) \quad . \tag{7.5.1}$$

   This kind of selection is natural taking into account the breaking of isospin symmetry. In the recent case the breaking cannot however be as large as for ordinary baryons (implying large mass difference between Δ and nucleon states).

4. One can classify the states of the open 3-quark string by the total charges and spins associated with 3 quarks and to the two color bonds. Total em charges of quarks vary in the range $Z_B \in \{2,1,0,-1\}$ and total color bond charges in the range $Z_b \in \{2,1,0,-1,-2\}$. Only neutral states are allowed. Total quark spin projection varies in the range $J_B = 3/2, 1/2, -1/2, -3/2$ and the total flux tube spin projection in the range $J_b = 2,1,-1,-2$. If one takes for a given total charge assumed to be vanishing one representative from each class (J_B, J_b), one obtains $4 \times 5 = 20$ states which is the number of amino-acids. Thus genetic code might be realized at the level of baryons by mapping the neutral states with a given spin projection to single representative state with the same spin projection. The problem is to find whether one can identify the analogs of DNA, RNA and aminoacids as baryon like states.

1. States in the quark degrees of freedom

One must construct many-particle states both in quark and flux tube degrees of freedom. These states can be constructed as representations of rotation group SU(2) and strong isospin group SU(2) by using the standard tensor product rule $j_1 \times j_2 = j_1 + j_2 \oplus j_1 + j_2 - 1 \oplus ... \oplus |j_1 - j_2|$ for the representation of SU(2) and Fermi statistics and Bose-Einstein statistics are used to deduce correlations between total spin and total isospin (for instance, $J = I$ rule holds true in quark degrees of freedom). Charge neutrality is assumed and the breaking of rotational symmetry in the direction of nuclear string is assumed.

Consider first the states of dark baryons in quark degrees of freedom.

1. The tensor product $2 \otimes 2 \otimes 2$ is involved in both cases. Without any additional constraints this tensor product decomposes as $(3 \oplus 1) \otimes 2 = 4 \oplus 2 \oplus 2$: 8 states altogether. This is what one should have for DNA and RNA candidates. If one has only identical quarks *uuu* or *ddd*, Pauli exclusion rule allows only the 4-D spin 3/2 representation corresponding to completely symmetric representation -just as in standard quark model. These 4 states correspond to a candidate for amino-acids. Thus RNA and DNA should correspond to states of type uud and ddu and aminoacids to states of type *uuu* or ddd. What this means physically will be considered later.

2. Due to spin-statistics constraint only the representations with $(J, I) = (3/2, 3/2)$ (Δ resonance) and the second $(J, I) = (1/2, 1/2)$ (proton and neutron) are realized as free baryons. Now of course a dark -possibly p-adically scaled up - variant of QCD is considered so that more general baryonic states are possible. By the way, the spin statistics problem which forced to introduce quark color strongly suggests that the construction of the codons as sequences of 3 nucleons - which one might also consider - is not a good idea.

3. Second nucleon like spin doublet - call it 2_{odd} - has wrong parity in the sense that it would require $L = 1$ ground state for two identical quarks (*uu* or *dd* pair). Dropping 2_{odd} and using only $4 \oplus 2$ for the rotation group would give degeneracies $(1,2,2,1)$ and 6 states only. All the representations in $4 \oplus 2 \oplus 2_{odd}$ are needed to get 8 states with a given quark charge and one should transform the wrong parity doublet to positive parity doublet somehow. Since open string geometry breaks rotational symmetry to a subgroup SO(2) of rotations acting along the direction of the string and since the boundary conditions on baryonic strings force their ends to rotate with light velocity, the attractive possibility is to add a baryonic stringy excitation with angular momentum projection $L_z = -1$ to the wrong parity doublet so that the parity comes out correctly. $L_z = -1$ orbital angular momentum for the relative motion of *uu* or *dd* quark pair in the open 3-quark string would be in question. The degeneracies for spin projection value $J_z = 3/2, ..., -3/2$ are $(1,2,3,2)$. Genetic code means spin projection mapping the states in $4 \oplus 2 \oplus 2_{odd}$ to 4.

2. States in the flux tube degrees of freedom

Consider next the states in flux tube degrees of freedom.

1. The situation is analogous to a construction of mesons from quarks and antiquarks and one obtains the analogs of π meson (pion) with spin 0 and ρ meson with spin 1 since spin statistics forces $J = I$ condition also now. States of a given charge for a flux tube correspond to the tensor product $2 \otimes 2 = 3 \oplus 1$ for the rotation group.

2. Without any further constraints the tensor product $3 \otimes 3 = 5 \oplus 3 \oplus 1$ for the flux tubes states gives 8+1 states. By dropping the scalar state this gives 8 states required by DNA and RNA analogs. The degeneracies of the states for DNA/RNA type realization with a given spin projection for $5 \oplus 3$ are $(1, 2, 2, 2, 1)$. $8\times$ 8 states result altogether for both *uud* and *udd* for which color bonds have different charges. Also for *ddd* state with quark charge -1 one obtains $5 \oplus 3$ states giving 40 states altogether.

3. If the charges of the color bonds are identical as the are for *uuu* type states serving as candidates for the counterparts of aminoacids bosonic statistics allows only 5 states ($J = 2$ state). Hence 20 counterparts of aminoacids are obtained for *uuu*. Genetic code means the projection of the states of $5 \oplus 3$ to those of 5 with the same spin projection and same total charge.

3. Analogs of DNA,RNA, aminoacids, and of translation and transcription mechanisms

Consider next the identification of analogs of DNA, RNA and aminoacids and the baryonic realization of the genetic code, translation and transcription.

1. The analogs of DNA and RNA can be identified dark baryons with quark content *uud*, *ddu* with color bonds having different charges. There are 3 color bond pairs corresponding to charge pairs $(q_1, q_2) = (-1, 0), (-1, 1), (0, 1)$ (the order of charges does not matter). The condition that the total charge of dark baryon vanishes allows for *uud* only the bond pair $(-1, 0)$ and for *udd* only the pair $(-1, 1)$. These thus only single neutral dark baryon of type *uud resp. udd*: these would be the analogous of DNA and RNA codons. Amino-acids would correspond to *uuu* states with identical color bonds with charges $(-1, -1)$, $(0, 0)$, or $(1, 1)$. *uuu* with color bond charges (-1,-1) is the only neutral state. Hence only the analogs of DNA, RNA, and aminoacids are obtained, which is rather remarkable result.

2. The basic transcription and translation machinery could be realized as processes in which the analog of DNA can replicate, and can be transcribed to the analog of mRNA in turn translated to the analogs of amino-acids. In terms of flux tube connections the realization of genetic code, transcription, and translation, would mean that only dark baryons with same total quark spin and same total color bond spin can be connected by flux tubes. Charges are of course identical since they vanish.

3. Genetic code maps of $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ to the states of 4×5. The most natural map takes the states with a given spin to a state with the same spin so that the code is unique. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1, 2, 3, 2\}$ and $D_b \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of aminoacids coded by D codons would be

$$[N(1), N(2), N(3), N(4), N(6)] = [2, 7, 2, 6, 3] \ .$$

   The correct numbers for vertebrate nuclear code are $(N(1), N(2), N(3), N(4), N(6)) = (2, 9, 1, 5, 3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2, 9, 1, 5, 3)$!

4. Stopping codons would most naturally correspond to the codons, which involve the $L_z = -1$ relative rotational excitation of *uu* or *dd* type quark pair. For the 3-plet the two candidates for the stopping codon state are $|1/2, -1/2\rangle \otimes \{|2, k\rangle\}$, $k = 2, -2$. The total spins are $J_z = 3/2$ and $J_z = -7/2$. The three candidates for the 4-plet from which two states are thrown out are $|1/2, -3/2\rangle \otimes \{|2, k\rangle, |1, k\rangle\}$, $k = 1, 0, -1$. The total spins are now $J_z = -1/2, -3/2, -5/2$. One guess is that the states with smallest value of J_z are dropped which would mean that $J_z = -7/2$ states in 3-plet and $J_z = -5/2$ states 4-plet become stopping codons.

5. One can ask why just vertebrate code? Why not vertebrate mitochondrial code, which has unbroken $A-G$ and $T-C$ symmetries with respect to the third nucleotide. And is it possible to understand the rarely occurring variants of the genetic code in this framework? One explanation

is that the baryonic realization is the fundamental one and biochemical realization has gradually evolved from non-faithful realization to a faithful one as kind of emulation of dark nuclear physics. Also the role of tRNA in the realization of the code is crucial and could explain the fact that the code can be context sensitive for some codons.

4. Understanding the symmetries of the code

Quantum entanglement between quarks and color flux tubes would be essential for the baryonic realization of the genetic code whereas chemical realization could be said to be classical. Quantal aspect means that one cannot decompose to codon to letters anymore. This raises questions concerning the symmetries of the code.

1. What is the counterpart for the conjugation $ZYZ \to X_cY_cZ_c$ for the codons?

2. The conjugation of the second nucleotide Y having chemical interpretation in terms of hydrophobia-hydrophily dichotomy in biology. In DNA as tqc model it corresponds to matter-antimatter conjugation for quarks associated with flux tubes connecting DNA nucleotides to the lipids of the cell membrane. What is the interpretation in now?

3. The A-G, T-C symmetries with respect to the third nucleotide Z allow an interpretation as weak isospin symmetry in DNA as tqc model. Can one identify counterpart of this symmetry when the decomposition into individual nucleotides does not make sense?

Natural candidates for the building blocks of the analogs of these symmetries are the change of the sign of the spin direction for quarks and for flux tubes.

1. For quarks the spin projections are always non-vanishing so that the map has no fixed points. For flux tube spin the states of spin $S_z = 0$ are fixed points. The change of the sign of quark spin projection must therefore be present for both $XYZ \to X_cY_cZ_c$ and $Y \to Y_c$ but also something else might be needed. Note that without the symmetry breaking $(1,3,3,1) \to (1,2,3,2)$ the code table would be symmetric in the permutation of 2 first and 2 last columns of the code table induced by both full conjugation and conjugation of Y.

2. The analogs of the approximate $A-G$ and $T-C$ symmetries cannot involve the change of spin direction in neither quark nor flux tube sector. These symmetries act inside the A-G and T-C sub-2-columns of the 4-columns defining the rows of the code table. Hence this symmetry must permute the states of same spin inside 5 and 3 for flux tubes and 4 and 2 for quarks but leave 2_{odd} invariant. This guarantees that for the two non-degenerate codons coding for only single amino-acid and one of the codons inside triplet the action is trivial. Hence the baryonic analog of the approximate $A-G$ and $T-C$ symmetry would be exact symmetry and be due to the basic definition of the genetic code as a mapping states of same flux tube spin and quark spin to single representative state. The existence of full 4-columns coding for the same aminoacid would be due to the fact that states with same quark spin inside $(2,3,2)$ code for the same amino-acid.

3. A detailed comparison of the code table with the code table in spin representation should allow to fix their correspondence uniquely apart from permutations of n-plets and thus also the representation of the conjugations. What is clear that Y conjugation must involve the change of quark spin direction whereas Z conjugation which maps typically 2-plets to each other must involve the permutation of states with same J_z for the flux tubes. It is not quite clear what X conjugation correspond to.

5. Some comments about the physics behind the code

Consider next some particle physicist's objections against this picture.

1. The realization of the code requires the dark scaled variants of spin 3/2 baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one has a scaled up variant of hadron physics: possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states can be scaled up.

2. Both the absolute and relative mass differences between Δ and N *resp.* ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant 1/137 - so that the mass splittings could be so small as to make decays impossible.

3. Dark hadrons could have lower mass scale than the ordinary ones if scaled up variants of quarks in p-adic sense are in question. Note that the model for cold fusion that inspired the idea about genetic code requires that dark nuclear strings have the same mass scale as ordinary baryons. In any case, the most general option inspired by the vision about hierarchy of conscious entities extended to a hierarchy of life forms is that several dark and p-adic scaled up variants of baryons realizing genetic code are possible.

4. The heaviest objection relates to the addition of $L_z = -1$ excitation to $S_z = |1/2, \pm 1/2\rangle_{odd}$ states which transforms the degeneracies of the quark spin states from $(1, 3, 3, 1)$ to $(1, 2, 3, 2)$. The only reasonable answer is that the breaking of the full rotation symmetry reduces $SO(3)$ to $SO(2)$. Also the fact that the states of massless particles are labeled by the representation of $SO(2)$ might be of some relevance. The deeper level explanation in TGD framework might be as follows. The generalized imbedding space is constructed by gluing almost copies of the 8-D imbedding space with different Planck constants together along a 4-D subspace like pages of book along a common back. The construction involves symmetry breaking in both rotational and color degrees of freedom to Cartan sub-group and the interpretation is as a geometric representation for the selection of the quantization axis. Quantum TGD is indeed meant to be a geometrization of the entire quantum physics as a physics of the classical spinor fields in the "world of classical worlds" so that also the choice of measurement axis must have a geometric description.

The conclusion is that genetic code can be understand as a map of stringy baryonic states induced by the projection of all states with same spin projection to a representative state with the same spin projection. Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin. Charge neutrality is essential for having only the analogs of DNA, RNA and aminoacids and would guarantee the em stability of the states.

Crying and screaming cells and magnetic bodies expressing their emotions

By using nanotechnological methods James Gimzewski [3] , his student Andrew Pelling and collaborators discovered that the cell walls of bacterium Saccharomyces cerevisiae perform periodic motion with amplitude about 3 nm in the frequency range .8-1.6 kHz (one octave) [150] . Or more concretely, bacteria produce sounds audible to humans with average frequency of 1 kHz in a range of one octave. The frequency has strong temperature dependence, which suggests a metabolic mechanism. From the temperature dependence one deduces the activation energy to be 58 kJ/mol, which is consistent with the cell's metabolism involving molecular motors such as kinesin, dynein, and myosin. The magnitude of the forces observed (10 nN) suggests concerted nanomechanical activity is operative in the cell.

From less formal popular articles [160] one can learn that it is difficult to avoid the impression that intelligent communication is in question. Dying cells produce a characteristic screaming sound. One can also distinguish between normal cells and cancel cells on basis of the sound they produces as well as between mammalian and bacterial cells.

What might be the explanation of these findings in TGD framework?

1. It is known that the region of frequencies audible to human ear is from about 20 Hz to 2×10^4 Hz. This is more or less same as the range of frequency range of sferics, the em noise in atmosphere [50] . This suggests a strong coupling between electromagnetic oscillations and sound as also the fact that biological structures are piezo-electrets transforming em oscillations to sounds and vice versa.

2. The activation energy per mole corresponds to .6 eV per molecule which is at the upper range for the variation range the energy associated with the fundamental metabolic energy quantum identified as the change of zero point kinetic as proton is transferred from atomic space-time sheet to much larger space-time sheet or vice versa.That metabolic energy is needed to produce the sounds supports the view that the sounds are produced intentionally.

3. If one takes seriously the notion of magnetic body as intentional agent controlling biological body, one is led to ask which must sound a totally crazy question in reductionistic ears: could magnetic body express its emotions in terms of frequencies of cyclotron transitions transformed to sound via genetic expression using piezo electric mechanism? Could it be that the photons involved are dark photons with large value of Planck constant so that their energy is above thermal energy. Could one propose a materialistic scientist to consider anything more irritating that singing and crying magnetic bodies!

4. Suppose that the homeopathic mechanism is based on replication of pseudomolecules with same magnetic body as that of solvent molecules and that neutral dark nuclear strings realize analogs of DNA, RNA, and aminoacids and realizing genetic code exactly in its vertebrate nuclear form and appearing also in the TGD based model of cold fusion and biological transmutations. If so, then homeopathic mechanism (recognition of molecules) could involve also the transformation of cyclotron radiation to sound at the level of "biological bodies" of molecules.

5. If this picture makes sense then also our speech as a self expression of the magnetic body might involve genetic code mapping sequences of DNA codons to temporal patterns of cyclotron radiation in turn transformed to speech by above mechanism. This would require a realization of genetic code at level of dark matter: could it be that dark nuclear code could define universal quantum level realization of language? The findings of Peter Gariaev and others and structural resemblance of intronic portion of genome with language and their report that DNA sequences are coded to temporal patterns of the rotation angle of the polarization of laser light (in turn inducing genetic expression).

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Chapter 8

Model for the Findings about Hologram Generating Properties of DNA

8.1 Introduction

The findings of Gariaev's group include the rotation of polarization plane of laser light by DNA [147] , phantom DNA effect [193] , the transformation of laser light to radio wave photons having biological effects [149] , the coding of DNA sequences to the modulated polarization plane of laser light and the ability of this kind of light to induce gene expression in another organisms provided the modulated polarization pattern corresponds to an "address" characterizing the organism [147] , and the formation of images of what is believed to be DNA sample itself and of the objects of environment by DNA sample in a cell irradiated by ordinary light in UV-IR range [192] . This chapter represents an article which is an outcome of a collaboration with Peter Gariaev and I want to thank Peter for an enjoyable and instructive co-operation. The article will be published in DNADJ (DNA Decipher Journal) in January 2011 and can be found as preprint in Scireprints archive [43] .

8.1.1 The notion of wave genome

Peter Gariaev and collaborators have introduced the notion of wave genome [147] requiring the coding of DNA sequences to temporal patterns of coherent em fields forming a bio-hologram representing geometric information about the organism. Code could mean that nucleotide is represented by a characteristic rotation angle for the polarization plane of linearly polarized laser radiation scattering from it. The experiments of Peter Gariaev's team [149] suggest that this kind rotation is induced by chromosomes by a mechanism which to my best knowledge is poorly understood. Other open questions concern the precise identification of the substrate of the bio-hologram, of the reference wave and of information carrying wave, and of the mechanism making possible (quantum) coherence in macroscopic length scales.

The reading of the DNA sequence to a radiation pattern is assumed to rely on the propagation of an acoustic soliton along DNA [147] . Whatever this process is, one should also identify the reverse process inducing the activation of the genome as the target organism receives the radiation coding for the DNA provided the genetic "address" is correct. One should also identify the mechanism transforming laser radiation to radio-waves at various frequencies as well as the mechanism creating what is believed to be the image of DNA sample and replicated images of some instruments used in experiment.

8.1.2 Hologram like radiation patterns generated by DNA

In this article one particular experiment, namely the already mentioned experiment involving the formation of two kinds of strange replica structures resulting when DNA sample is radiated by red, IR, and UV light using two methods by Gariaev's group [192] will be discussed. The original interpretation

of the image produce by first method is as a replica image of DNA sample. This interpretation can be challenged. The second image is interpreted as a hologram image of the environment. In the following the interpretation of these images in TGD framework is discussed.

The first method produces what was originally interpreted as replica images of either DNA sample or of five red lamps used to irradiate the sample. Second method produce replica image of environment with replication in horizontal direction but only at the right hand side of the apparatus. Also a white phantom variant of the replica trajectory observed in the first experiment is observed and has in vertical dir

8.1.3 Basic TGD based notions involved with the model

In this article a model explaining the characteristic features of the replica patterns is developed. The model is inspired by Topological Geometrodynamics (TGD), the recent state of which is discussed in Prespacetime Journal [7, 8, 11, 12, 9, 6, 10, 16] . TGD is a proposal for a unified theory of the fundamental interactions based on a generalization of the notion of space-time having perhaps its most important consequences at the level of living systems. TGD inspired theory of consciousness and of quantum biology is discussed in the articles [15, 13, 14] of Journal of Consciousness Research & Exploration. The model differs in many respects from the general model of proposed by Peter Gariaev and collaborators [147] but shares with it the vision about holograms as a basic element of information processing in living systems at DNA level.

The basic notions are magnetic body, massless extremal (topological light ray), the existence of Bose-Einstein condensates of Cooper pairs at magnetic flux tubes, and dark photons with large value of Planck constant for which macroscopic quantum coherence is possible. Also the hypothesis that the differences of zero point kinetic energies for space-time sheets with different p-adic length scales define universal metabolic energy quanta is used in the model for pumping of radiation energy to the system. The hypothesis is that the first method makes part of the magnetic body of DNA sample visible whereas method II would produce replica hologram of environment using dark photons and also the phantom image of the flux tubes becoming visible by method I.

Replicas would result by mirror hall effect in the sense that the dark photons would move back and forth between the part of magnetic body becoming visible by method I and serving as a mirror and the objects of environment serving also as mirrors. What is however required is that not only the outer boundaries of objects visible via ordinary reflection act as mirrors but also the parts of the outer boundary not usually visible perform mirror function so that an essentially 3-D vision providing information about the geometry of the entire object would be in question. Many-sheeted space-time allows this.

The presence of the hologram image for method II requires the self-sustainment of the reference beam only whereas the presence of phantom DNA image for method I requires the self-sustainment of both beams. Non-linear dynamics for the energy feed from DNA to the magnetic body could make possible self-sustainment for both beams simultaneously. Non-linear dynamics for beams themselves could allow for the self-sustainment of reference beam and/or reflected beam. The latter option is favored by data.

8.2 Observations

Two methods are involved to produce images with replica structure in the experiments of Gariaev's team. The detailed experimental arrangement and results of these experiments are described in [192] . Reader can get a concrete idea about the experiments from the figures at the end of this article.

For both methods one uses sources of red and IR photons emitted by diodes as well as sources of UV-B and UV-C photons (for a schematic representation of the experimental apparatus Fig. 8.13). The wave lengths and energies for red and IR photons are given by the following table.

$$\begin{array}{lll} \lambda/nm & 650 & 920 \\ E/eV & 1.91 & 1.35 \end{array} \tag{8.2.1}$$

The wave-length and energy intervals for UV-B and UB-C radiation are given by the following tables.

Energy range	$[\lambda_1, \lambda_2]/nm$	$[E_1, E_2]/eV$
$UV-B$	$[315, 280]$	$[3.94, 4.43]$
$UV-C$	$[280, 100]]$	$[4.43, 12.40]$

(8.2.2)

1. In method I red, IR, and UV-B and UV-C beams are present all the time. During irradiation is one detects what are called DNA replica trajectories (Figs. 8.3 and 8.4) These roughly vertical tubular structures (or less probably, planar structures orthogonal to the preferred horizontal direction) have grainy structure (Fig. 8.3). Replica trajectories decompose to five sub-trajectories which probably correspond to the five red diodes irradiating DNA directly (Fig. 8.4). One could interpret the replica trajectories as images of DNA sample or of red diodes created by the DNA sample.

   Long-lived red DNA replica trajectories called phantom DNA trajectories are present also when the irradiation has ceased (Fig. 8.5). The distributions of brightness for these images in RGB model are represented in Fig. 8.6 representing especially clearly the structure of the trajectories.

2. In method II same beams are present but only periodically. The replicas appear when the beams are not on and are in horizontal direction representing environment (Fig. 15.2.6). The basic feature is that the objects of environment are replicated in horizontal direction with distance defined by the horizontal size of the object so that fractal structure results. There are also phantom DNA replicas which are white and to the left of DNA sample and could correspond to the red replicas seen by method I (Fig. 15.2.6). These structures are thicker than than the red replica trajectoriess of method I.

   What is remarkable that the replicas representing environment carry information about the geometry of the *entire* objects rather than that for the outer surface of these objects seen in reflection: a kind of 3-dimensional vision seems to be in question which cannot be explained in terms of ordinary holograms alone. The vertical region in which replicas are obtained corresponds to the height of the roughly vertical replica structures produced by method I.

   What is equally remarkable is that the replicas appear only at the right hand side of the system but not at the left hand side. Strangely, the touching of the DNA sample however shifts replicas to the left after which they disappear in about 5 to 8 seconds (Fig. s 8.7 and 8.8). The color of the replicas can be white, reddish, red and even blue. It is not quite clear whether the left replicas are mirror images of right replicas or images of the left hand side of the environment.

In both cases the key question is whether the replica trajectories represent real physical objects or whether they are analogous to a sequence of mirror images resulting when one has object between two mirrors and repeated reflections create a sequence of images replicas (mirror hall effect).

8.3 Model for the findings

The model for the findings is based on TGD inspired model of quantum biology. The key physical input of the TGD based model are the notions of magnetic body [38] and of massless extremal (ME) or topological light ray [50] , and the identification of dark matter in terms of a hierarchy of Planck constants [27] assumed to play a key role in living matter. These notions are described briefly in [14] . A more detailed descriptions can be found in online books about TGD: for magnetic body in [38] , for MEs in [50] and for the hierarchy of Planck constants in [27] .

8.3.1 Basic notions and ideas

The key notions and ideas of the TGD inspired model are the same as of the model discussed in [77] as a possible framework for understanding the findings of Gariaev's team. Only the treatment is considerably more detailed.

1. In TGD inspired theory of quantum biology one assigns to all biological structures magnetic bodies which use biological bodies as sensory receptors and motor instruments. This is assumed

to hold true for DNA nucleotides, DNA strands, and even DNA sample itself so that an onion like hierarchy of magnetic bodies results. The basic vision is that magnetic flux sheets traversing through DNA integrate the DNAs of various nuclei to super DNA and that this occurs at level of organs, organisms and even populations and makes possible coherent gene expression responsible for the ability of living organisms to behave as single unit and also co-operate [26, 23] . The magnetic flux quanta and flux sheets can also end to the objects of the environment and this is essential for the model to be proposed.

The matter at flux quanta is identified as dark matter and has Planck constant which is integer multiple of the ordinary one, and can be quite large so that macroscopic quantum coherence becomes possible. This makes possible the formation of holograms and mirror hall effect since the dark counterparts of the ordinary photons can have wave length much longer than the size scale of the experimental apparatus.

Although the DNA preparation in the experiments of Gariaev's team is formed from a cellular structure by a violent chemical process removing proteins and cellular and nuclear membranes, the magnetic body of DNA sample could remain intact so that a natural hypothesis is that magnetic body are involved with the formation of both DNA replica trajectories and hologram like replica trajectories.

2. Topological light rays (MEs) are tubular structures very much analogous to laser beams. They carry radiation moving with light velocity and without dispersion and dissipation in *single* space-time direction that they are ideal for communication and control purposes. This linear superposition of only modes with parallel 4-D wave vectors is a key distinction from Maxwell's electrodynamics and due to non-linearity of the fundamental variational principle. More precisely, if one changes the direction of the 4-D wave vector opposite, both 3-D wave vector and frequency change sign so that the counterpart of phase conjugate laser light is in question. Hence one would have superpositions of beams and their phase conjugates having interpretation as positive and negative energy signals traversing in opposite spatial and temporal directions. At quantum level one might perhaps speak positive and negative energy photons.

   MEs could topologically condense at magnetic flux quanta and would be accompanied by the TGD counterparts of Alfven waves [38] representing transverse geometric oscillations of the magnetic flux quanta (sheets and tubes) regarded as space-time surfaces. It would be very natural to assume that topological light rays serve as correlates for the photons reflected from DNA sample to its magnetic body. In rather precise sense these photons would represent the scaled variant of EEG used by magnetic body to control brain and receive information from brain in TGD based model of brain.

8.3.2 Method I

The details of method I and the absence of the image of the environment (Fig. 8.3) in this case do not encourage hologram interpretation. The interpretation coming first in mind is that the DNA replica trajectory is realized at magnetic flux tubes serving as a screen. Flux sheets orthogonal to the plane of the images cannot be excluded but are less not plausible. The simplest assumption is that the photons of red light travel scattered from DNA sample to the magnetic flux tube like structures defining the screen along MEs topologically condensed at magnetic flux sheets traversing through DNA strands which are partially un-winded and have length of order 1 cm. Red light could transform to dark photons with large Planck constant with wavelength of order 1 cm but at the magnetic body it would transform partially back to visible photons. This is however not necessary. Also UV and IR photons would interact with the DNA sample and could provide the metabolic energy allowing also to amplify the signal. Also UV and IR photons could transform to dark photons and define part of the "EEG" of the DNA sample.

8.3.3 Method II

For method II the interpretation in terms of a hologram like structure resulting when light traveling in horizontal direction is reflected from the objects of the environment is suggestive.

1. For white cable like structures left from DNA sample referred to as phantom DNA replicas the grainy replica structure is actually not present (Fig. 15.2.6) so that phantom DNA replica is perhaps not the proper term. As in the case of method I these structures could be interpreted as images of the magnetic body serving as the hologram substrate. Since red light source is off, only the white light emitted by the DNA substrate is present. These structures are wider than the red DNA replicas and a rough estimate for their thickness is about 1 cm so that the interpretation as a flux tube of magnetic body is suggestive. The interpretation of the signal as counterparts of bio-photons [132] generated when dark photons transform to ordinary visible photons is suggestive.

2. Hologram interpretation for the replica of environment (Fig. 15.2.6) requires the system generates the reference beam prevailing for some time although the irradiations are turned off. The reflected beams due to the irradiation would disappear as the irradiation is turned off so that the reference beam can generate the hologram image.

3. The simplest assumption is that there are horizontal flux tubes or sheet(s) in the plane defined by the vertical and horizontal directions and that the part of the magnetic body corresponding to DNA replica trajectory serves as source of dark photons with large $\hbar$ [27] , which travel to the right in horizontal direction and along flux tubes connected to the outer surfaces of the objects of environment. If the dark photons emanate from the structures visible as phantom DNA replica, one can understand why the image is from the right hand side.

4. Similar connections to other living organisms would explain the original observations of Gurwitsch about mitogenetic radiation at UV frequencies [170]: the UV radiation would represent decay products of dark variants of UV photons. One could also interpret bio-photons [132] at visible wavelengths as decay products of their dark variants with much longer wave lengths. These photons could produce also bunches of EEG photons for large enough value of $\hbar$ [23] . Also the findings of Gariaev's group about the transformation of laser light irradiating DNA to a radiation in a wide range of frequencies extending at least down to 10^4 Hz (corresponds to a wavelength of about 10 km) and having biological effects [149] could be interpreted in terms of long wave length dark photons with energies of visible photons. The role of low frequencies down to 10^4 Hz at least in water memory [135, 136] suggests that the basic mechanism of water memory is based on dark radio wave photons. The recent findings of the group led by HIV nobelist Jean-Luc Montagnier [178] relating to water memory suggest an interaction between DNA samples based on radiation and also a new non-chemical representation of genetic code in terms of electromagnetic radiation patterns proposed also by Gariaev's team [147, 149] . TGD approach suggests besides field representation based on MEs [34], a representation in terms of flux tubes connecting DNA and lipids of cell membrane [26] , and a representation of genetic code in terms of the states of dark nucleons [78] . Computer science inspired view indeed suggests DNA provides only one of the many representations of the genetic code.

5. What differentiates the hologram from the ordinary one is that reflections occur from the entire outer surfaces- not only from the outer surface visible in ordinary sense but also from the "inner side" of the part not usually visible so that information about entire 3-D geometry is obtained (Fig. 15.2.6). Without this assumption it is difficult to understand the replication in the scale of the replicated object. The repeated travel back and forth along these flux tubes or sheets would produce mirror hall effect and the observed replica structure could be understood.

6. A possible reason for why replicas are horizontal is that the magnetic body of DNA sample receives information from the environment and the objects are of environment tend to be in the horizontal direction. Phantom DNA replicas which might relate to phantom DNA effect [193] discovered also by Gariaev's group appear only at the left hand side of the DNA sample and if they represent ordinary images of the hologram substrate and serve as mirrors, the appearance of the hologram replicas at the right hand side only can be understood. These images would result as dark photons emitted by the hologram substrate transforms to visible light.

   What happens in phantom DNA effect is that laser light scatters from the chamber weakly even after the DNA sample has been removed. The simplest explanation could be that some fraction of DNA leaves their magnetic bodies to the sample and that the scattering involves these

magnetic bodies already in the original situation. Also water memory [135, 136, 178] could be due to the fact that for some fraction of the biological molecules originally present in the solution before dilution leaves the magnetic bodies in the sample and generate the radiation responsible for the biological effects as cyclotron radiation [34] .

7. The hologram image would result as the photons of the reflected reference beam transform back to photons of visible (and possibly UV and IR) light. The reflection preserves only the vertical momentum of photon parallel to the flux tube so that reflections occur also in the direction of the camera. The photons in question need not correspond to single wave length. The UV radiation necessary for the experiment might serve as a metabolic energy source allowing to generate dark photons but it could also transform to dark photons defining the hologram. The longitudinal coherence length [194]

$$\xi = \frac{c}{\Delta f} = \frac{\lambda_d^2}{\Delta\lambda_d} = r\frac{\lambda^2}{\Delta\lambda} \quad , \quad r = \frac{\hbar}{\hbar_0}$$

of dark photons must be larger than the size scale $L \sim 20$ cm of the experimental apparatus in order to produce mirror hall effect. From the assumption that the size scale $l \sim 1$ cm of the grains of the replica trajectory is of order $l \sim r\lambda$, one obtains the estimate $r = 15 \times 2^{10}$. This gives $\lambda/\Delta\lambda \sim 20$, which looks rather reasonable value.

The transformation of the right-handed mirror hall image to left handed as the DNA sample is touched should be also understood.

1. The first question is whether the effect of touch (Figs. 8.7 and 8.8) is mechanical or biological. The proposed model encourages to consider the possibility that the magnetic body assignable to the hand or finger touching the sample generates the external irradiation generating dark photons needed to generate a replica hologram from the left hand side of the apparatus. When the finger is removed from the vicinity of the sample, one expects that the hologram disappears as it indeed does within 5-8 seconds. The mechanical instability induced by the direct touch could be the reason for the disappearance of the right sided hologram. Also the intensity of the irradiation from the magnetic body assignable to hand is expected to be stronger than the original reference beam so that the hologram is transformed to left-sided hologram. This explanation could be tested by touching the sample from another side to see whether the hologram remains right sided in this case.

2. One can imagine also alternative but more complex explanation not favored by Occam's razor. What comes in mind that the reference beam needed for the hologram and generated by DNA sample of the magnetic body is transformed to its unstable phase conjugate and thus travels from left to right and produces a left sided replica hologram. An open question is whether this hologram is from left hand side of the system or a mirror image of the hologram from right hand side. Perhaps this could be tested.

   DNA strands and their conjugates should correspond to separate flux sheets and one can wonder whether the double DNA strand maps to a doublet of magnetic bodies (note the analogy with two brain hemispheres and EEG) and whether left-right dichotomy could correspond to DNA-conjugate DNA dichotomy. If so, then touching would lead to the disappearance of DNA reference beam and the generation of its conjugate beam assignable to conjugate strand of DNA and perhaps scattering from the conjugate hologram also formed in the process.

8.4 The realization of the hologram at the level of magnetic body

How the reference beam is generated and how the hologram substrate is realized? These are the basic questions to be answered. Reference beam should be generated by the magnetic body itself and/or by DNA sample since it exists in absence of irradiation. Magnetic body should define the photosensitive substrate and the thickness of the analog of the photographic plate should be of the order of scaled up wavelength in order to achieve this. Note that in the case of EEG photons similar mechanism would mean that the size for the analog of the photographic plate is of order Earth size scale!

8.4.1 How the reference beams and reflected beams are generated?

The explanation for the replica assumes that the reflected beams are horizontal. Reference beams should be such that there exists a mechanism taking care the that they are preserved after the irradiations cease. The mechanism generating the reference beam would be most naturally the coherent decay of the excited state of a Bose-Einstein condensate. This condensate must be however assigned with some other structure than hologram substrate itself.

One can distinguish two DNA replica trajectories near DNA sample and there are even more of them at higher height (Fig. 8.3. The decay of the first replica trajectory could provide reference beam and reflected beam for the second replica trajectory acting as hologram substrate and vice versa. This mechanism works for an arbitary number of hologram substrates and could be at work at red, IR, and UV wave lengths. The mechanism is actually the same as the one generating ordinary laser beams and skeptic can of course ask whether the large value of Planck constant is absolutely necessary.

The replica hologram obtained by method II involves several colors. The figures about the holograms show the presence of red light, reddish or white light, and also blue light and one must understand also this. Holograms are constructed using monochromatic laser light. The reading of the hologram is however possible using even white light if the reference beam is orthogonal to the hologram substrate since in the idealization that hologram is infinitely thin, the information about the wavelength of reference beam is completely lost in this case. The proposed model for the generation of reference is consistent with the orthogonality.

The picture that emerges would be following.

1. At least the incoming red beam is transformed after the passage through the sample to a beam with large value of Planck constant and wavelength of order say .2-.5 m corresponding to the size of the region appearing in the hologram. It is quite possible that also UV and IR photons transform to dark photons. At the magnetic flux tube this beam of dark photons is split to two pieces defining reference bream and the beam reflected from the objects of the environment. All these beams are nearly horizontal. The reflected beam and reference beam recombine and form a hologram substrate defined by magnetic flux tubes assigned to the DNA replica trajectory.

2. The cyclotron Bose-Einstein condensates at magnetic bodies function as analogs of lasers. Instead of the excitations of atomic states one has excitations of cyclotron states of a Bose-Einstein condensate with a large value of Planck constant. The excitation of these states requires pumping of energy. The simplest possibility is that both UV, IR, red, and IR light pump energy to the respective modes so that one would have multi-laser operation. The magnetic body is predicted to have a hierarchical fractal structure with magnetic fields whose strengths correspond to the p-adic length scale in question with p-adic length scales coming as half octaves of basic scale which conveniently can be taken 10 nm defining the thickness of cell membrane (for p-adic length scale hypothesis, which forms one of the corner stones of TGD based particle physics and of quantum biology see [7, 8, 11, 12, 9, 6, 10, 16]. These irradiations would excite different parts of the magnetic body giving rise to a fractal hierarchy of holograms. The camera operating at visible wave lengths would not allow to see UV and IR holograms.

3. It is important to notice that the presence of only say red beam of light is not r enough to generate the hologram so that an interaction between these irradiations must be present. Some of the beams could act as control signals activating the DNA or as sources of metabolic energy (say UV beams).

4. The holograms appear periodically for method II [192] : Figs. 8.9, 8.10, 8.11, 8.12 at the end of the article illustrate what is involved. The periodic irradiation of the sample certainly induces a periodically appearing hologram image: when all irradiating beams are turned on, the conditions for the appearance of hologram are not satisfied and hologram disappears. The period is however considerably longer than the time interval between irradiation periods. This suggests a threshold for the effect.

   When the amount of pumped energy reaches a threshold, the intensity of the reference beam increases dramatically and the hologram becomes visible. This kind of effect requires a non-linear dynamics. The simplest model would be in terms of a potential containing the net value of the pumped energy as a parameter. As this parameter exceeds a threshold value, a phase transition

the equilibrium position of the system would change from that with a vanishing reference beams to that with a large reference beam and the energy stored to the system would be utilized. DNA sample would be the natural storage of the energy.

8.4.2 A simple model for the dynamics of pumping and sustainment of dark photon beams

The basic question is what the pumping of energy could mean at the level of DNA. It seems clear that at least part of the pumped energy is transformed to metabolic energy in turn transformed to dark photons. It is also possible that the chemical energy of stored in DNA molecules is transformed to metabolic energy. The existence of a hierarchy of universal metabolic energy quanta predicted by TGD provides the physical basis of the model.

One should also have a qualitative model for the transformation of the energy of radiation to metabolic energy and to the self sustainment of the dark photon beams.

1. The basic idea is simple. The irradiation kicks particles in DNA to higher energy state and these states decay to the ground state by emission of dark photons making allowing to realize the reference beam for holograms during reading period and both reflected and references beams during irradiation period.

2. For method I both the reference beam and reflected beam remain when irradiation ceases and give rise to the red phantom DNA replica (Fig. 8.5). For method II the presence of hologram image (Fig. 15.2.6) means that only reference beam is sustained. Self-sustainment requires non-linear dynamics. This dynamics could appear either at the level of DNA sample or at the level of the reference beam and reflected beams. For method II the white cable like structures appearing to the left of DNA sample could also correspond phantom DNA replica. They cannot however correspond to hologram like mechanism but ordinary radiation emitted by the hologram substrate.

3. The first possibility (option I) that the non-linear dynamics is realized at the level of DNA. DNA might be able to liberate chemical energy as metabolic energy or store the energy of irradiation and then liberate it. It is however difficult to understand why only the reference beam is sustained in method II. Both beams should be present if they result by a splitting of a beam coming from DNA meaning the absence of replica hologram. Internal consistency would require giving up hologram interpretation.

4. Second possibility (option II) is that non-linear dynamics is realized at the level of reference beam and reflected beams. For method II this dynamics could lead to a self sustainment in the case of reference beam if it is more intense than the reflected beams. For method I the irradiation lasts much longer and both reference beam and reflected beam could be sustained and one would not obtain hologram image but only phantom DNA replica image.

The following qualitative model has same general form for both options.

p-Adic length scale hypothesis and hierarchy of metabolic energy quanta

If one takes seriously the TGD inspired model for metabolic energy quanta, the irradiation would kick charged particles from larger space-time sheets to smaller ones so that the energy would go to the zero point kinetic energy plus surplus. The particles would drop back to the larger space-time sheets emitting the surplus zero point kinetic energy in this process as dark photon going to the magnetic flux tubes to be used to build reference beams and reflected beams for the holograms.

The kicked particles could be electrons or protons but electrons are more plausible candidates.

1. The nominal value of zero point kinetic energy given by

$$E_0 = \frac{3\hbar^2}{2mL^2} , \tag{8.4.1}$$

and corresponds to zero point kinetic energy for a particle in box with side of length L.

2. Possible values of L can be estimated by assuming $L = L(k)$, with $L(k)$ given by the p-adic length scale hypothesis stating

$$L(k) = 2^{(k-151)/2} L(151) \ , \tag{8.4.2}$$

where $L(151) \simeq 10$ nm corresponds to Gaussian Mersenne prime $M_{151,G} = (1+i)^{151} - 1$, which is one of the Gaussian Mersennes $M_{k,G}$, $k = 1151, 157, 163, 167$ between cell membrane thickness 10 nm and length scale 2.5 μm which is roughly one half of the size scale of cell nucleus. For $k = 148$ one obtains $E_0(148) \simeq .5$ eV which is the nominal value of metabolic energy quantum. Other zero point kinetic energies would come as octaves of $E_0(148)$ so that one has has the series (...,.25,.5,1,2, 4,..) eV. Nominal values are in question: the variation can be at least 10 per cent around the nominal value and is due to the fact that in reality space-time sheets do not have the geometry of cube and because the particles inside space-time sheets are not free.

3. Metabolic energy quanta correspond to the zero point kinetic energies liberated as particle drops from space-time sheet characterized by k_1 to $k_1 + \Delta k$ and are given as differences

$$\Delta E_0(k, k+\Delta k) \ = \ \frac{3\hbar^2}{2mL^2(151)} 2^{-k+151}(1 - 2^{-\Delta k}) \ . \tag{8.4.3}$$

This gives a geometric series of metabolic energy quanta for each value of k. Two cases are of special interest: dropping next space-time sheet in the hierarchy ($\Delta k = 1$) and dropping to very large space-time ($\Delta k \to \infty$).

$$\begin{aligned} \Delta E_0(k,1) \ &= \ \frac{3\hbar^2}{2mL^2(151)} 2^{-k+151} \ , \\ \Delta E_0(k,\infty) \ &= \ \Delta E_0(k-1,1) = \frac{3\hbar^2}{4mL^2(151)} 2^{-k+151} \ . \end{aligned} \tag{8.4.4}$$

4. Note that the energy levels form a cascade converging to $\Delta E_0(k,\infty) = \Delta E_0(k-1,1)$. The scaling $\hbar = r\hbar_0$ of Planck constant does not affect the spectrum of metabolic energy quanta if $L(k)$ scales as $L(k) \to rL(k)$.

5. The following table lists the three p-adic length scales, which are possible for the radiation sources used assuming that $\Delta k = 1$ transitions dominate.

k	145	144	143
$\Delta E_0(k,1)/eV$	2	4	8
λ/nm	620	310	155
$L(k)/nm$	1.23	.88	.625

(8.4.5)

The 2 eV metabolic energy is five percent larger than the energy 1.91 eV assignable to 650 nm wavelength of the red light used in irradiation. These wave lengths would be preferred but in principle entire range of metabolic energy quanta is allowed and if one assigns metabolic energy quanta to the transitions $\Delta k \to \infty$ the values of k in the equation are scaled down by one unit: $k \to k-1$. The p-adic length scales correspond to length scales naturally associated with DNA.

In the case of proton the length scales would be obtained by the replacement $k \to k - 11$ and would be considerably below the atomic length scale $L(137)$ for the ordinary value of Planck constant and dark protons would be required.

Linear model for the pumping of energy

If one assumes that the non-linear behavior responsible for self-sustainment is realize at the level of the reference beams and reflected beams the model for pumping of energy to DNA sample can assumed to be linear. The simplest model for the pumping involves only two space-time sheets. The proper variable would be either the number N of charged particles -presumably electrons- and/or net zero point kinetic energy feed to the smaller space-time sheet. One has just population dynamics for the numbers of electrons at the two space-time sheets involved.

1. The equations for the population dynamics have the general form

$$\begin{aligned} \frac{dN_1}{dt} &= k_0(t)N_2 - k_1(t)N \ , \\ \frac{dN_2}{dt} &= -k_0(t)N_2 + k_1(t)N \ , \end{aligned} \tag{8.4.6}$$

   The first term on the right hand side corresponds to the energy feed from irradiation and second term the energy leakage through the dropping of the particles back to the smaller space-time sheet.

2. If the N_2 is very large it can be taken as constant not affected by the process and with an obvious redefinition of $k_0(t)$ one can write

$$\frac{dN_1}{dt} = k_0(t) - k_1(t)N_1 \ . \tag{8.4.7}$$

   The general solution of the equation is

$$N_1(t) = N_0 exp(-\int k_1 dt) + \int_0^t N_1 exp(\int_0^t k_1 dt) k_0(t) dt \ . \tag{8.4.8}$$

As noticed, this model cannot explain self-sustainment in terms of metabolism.

A catastrophe theoretic model for the self-sustainment

The self-sustainment of the beams requires non-linear dynamics. The non-linearity could be assigned with the pumping of energy to DNA by irradiation and would mean the addition of non-linear terms to the population dynamics of electrons (Eq. 8.4.7). This model does not however allow to distinguish between reference beams and reflected beams. The same formal model however applies also to the dark reference beams and reflected beams by re-interpreting number N of electrons as the number of photons in the beam. The following model is only an attempt to characterize the situation qualitatively and does not depend on the interpretation of N. The two alternative interpretations will be referred to as options I and II.

1. The basic equation is

$$\frac{dN}{dt} = P_3(N, k_0) = k_0(t) - k_1(t)N + k_2(t)N^2 - k_3(t)N^3 \ . \tag{8.4.9}$$

   The parameters $k_i(t)$ are assumed to be slowly varying in the time scale of the dynamics for N. In catastrophe theoretic setting [**?**] k_i *resp.* N would be called control parameters *resp.* behavior variable. Depending on option N denotes either the number of electrons kicked to a smaller space-time sheet of photons in the analog of laser beam.

(a) For option I $k_0(t)$ characterizes the rate at which the irradiation kicks electrons to the smaller space-time sheet. For option II the interpretation is as a rate with which photons in the dark analog of laser beam are produced by irradiation. One can assume that $k_0(t)$ is constant during periods of irradiation and is small and vanishes when there is no irradiation.

$$\begin{aligned} k_0(t) &= k_0 \text{ during irradiation } , \\ k_0(t) &= 0 \text{ in absence of irradiation } . \end{aligned} \tag{8.4.10}$$

(b) For option I the term $-k_1 N_1$ corresponds to the dropping of the electrons back to the large space-time sheets. For option II it corresponds to the leakage and absorption of photons from the beam.

(c) For option I the presence of $k_2 N^2$ can make possible self-sustained metabolism and therefore also that of dark photon beams. DNA itself can somehow kick the electrons to smaller space-time sheets. This could be due to the liberation of metabolic energy from DNA, which cannot continue indefinitely so that $k_2(t)$ must go to zero in some time scale of the order of the time period between successive shots (few seconds). For option II this term correspond to non-linear self-amplifying interaction of laser beams and could be due to a resonant interaction of beams associated with different parts of the magnetic body.

(d) The term $-k_3 N^3$ is necessary in order to avoid endlessly increasing N, which is definitely something non-realistic.

2. By construction the system realizes cusp catastrophe [**?**] describing the simplest possible situation in which some parameter region of parameter space allow 3 or only 1 root to the stationarity condition $P_3(N, k_0) = 0$ so that one has a phase transition like behavior. The following considerations show that if $P_3(N, 0)$ allows three non-negative roots and $P_3(N, k_0)$ only one positive root, then sufficiently many and sufficiently long irradiation periods allow to achieve a self-sustaining situation, which lasts as long as $k_2(t)$ characterizing self-sustainment remains large enough. After this a phase transition to a phase characterized by a rapid decrease of N, occurs.

3. One can concretize the situation by imagining that the system climbs to a mountain during the irradiation periods and slides down when the irradiation is off in the case that one has

$$R \equiv \lim_{t \to t_f, +} dN/dt(t) = P_3(N(t_f), 0) < 0 \ . \tag{8.4.11}$$

Here t_f denotes the value of time when irradiation ends. For $R > 0$ the climbing up continues spontaneously but with a slower rate.

4. Quite generally, $P_3(N, k_0)$ can have $n = 0, 1$ or $n = 3$ zeros in the region $N \geq 0$. $P_3(N, 0)$ has always zero at origin and can have two additional zeros of $k_2(t)$ is large enough. Since the polynomials $P_3(N, k_0)$ and $P_3(N, 0)$ differ only by a downwards shift by k_0, one finds the following.

(a) If one has

$$P_3(N, k_0) < k_0 \tag{8.4.12}$$

for $N > 0$, $P_3(N, 0)$ has only one non-negative zero for all positive values of N. The system slides dow towards $N = 0$ as the irradiation ceases.

(b) If the condition

$$P_3(N_f, k_0) \geq k_0 \tag{8.4.13}$$

is satisfied, $P_3(N_f, 0)$ has two positive roots $(N_{2,0}, N_{3,0})$ besides $N_{1,0} = 0$. If R is in the region above $N_{2,0}$, the system slides down to or climbs up to $N_{3,0}$ after the irradiation has ceased. This situation is obviously the interesting one in the recent case. Whether the region $N > N_{2,0}$ can be reached during irradiation depends on the properties of $P_3(N, k_0)$.

5. Consider first what happens during irradiation assuming that $P_3(N_f, 0)$ has two positive roots $(N_{2,0}, N_{3,0})$ besides $N_{1,0} = 0$ (the interesting case). $P_3(N, k_0)$ has certainly one root since $P_3(N, f)$ becomes eventually negative due to the term $-k_3N^3$.

   (a) If k_0 is large enough there is only one root - call it N_3. One has $N_3 > N_{3,0}$ and the energy feed - if allowed to continue long enough or for sufficiently many times- drives the system above $N_{2,0}$ and eventually to N_3, which is stable and is reduced only slowly as $k_2(t)$ decreases. When irradiation ceases, the system goes to $N_{2,0}$, which represents a stable situation and only adiabatically approaches to zero as long as the number of roots remains three. After this N goes rapidly to zero.

   (b) If k_0 is small enough one has one or three roots- let the three roots be $N_1 < N_2 < N_3$. N_1 corresponds to a stable situation in which the linear term has driven dN/dt to zero. One ends up to this situation either from $N \leq N_2$ for three roots and always if one has only one root. Only N_1 is achievable by starting from $N(t = 0) = 0$ or from $N(t_f)$ achievable during irradiation period. Since the graphs of $P_3(N, k_0)$ and $P_3(N, 0)$ differ only by a shift, it is clear that one has $N_1 < N_{2,0}$ so that the system rapidly slides down to $N = 0$.

6. The conclusion is that the desired situation can be achieved only if $k_2(t)$ is so large that $P_3(N, k_0) > k_0$ holds true at the maximum of $P_3(N, k_0)$ (for $N > 0$) and k_0 is so large that $P_3(N, k_0)$ has only single root. This means that the minimum of $P_3(N, k_0)$ is positive. The extrema $N_\pm$ of $P_3(N, k_0)$ correspond to the vanishing of $dP_3(N, k_0)/dN$ so that one has

$$\begin{aligned} N_\pm &= \frac{k_2}{3k_3} \pm \sqrt{(\frac{k_2}{3k_3})^2 - \frac{k_1}{3k_3}} \ , \\ (\frac{k_2}{3k_3})^2 - \frac{k_1}{3k_3} &\geq 0 \ , \end{aligned} \tag{8.4.14}$$

   The conditions for self-sustainment boil down to the equations

$$\begin{aligned} P_3(N_+, 0) &> 0 \ , \\ P_3(N_-, k_0) &> 0 \quad . \end{aligned} \tag{8.4.15}$$

   Self-sustaining situation continues as long as $k_2(t)$ is so large that one has 3 roots for $P_3(N, 0)$. For small enough $k_2(t)$ the two roots disappear and the system slides rapidly to $N = 0$. Fig. 8.1 illustrates these conditions graphically.

8.4.3 A general model for the hologram substrate

The following model for the hologram substrate is based on the earlier vision about the role of Bose-Einstein condensates of Cooper pairs and bosonic ions in TGD inspired quantum biology.

1. DNA replica trajectory should define the analog of the photosensitive substrate so that the scaled up wave length defining its thickness should be of order 1 cm. The TGD inspired model for the effects of ELF em fields on vertebrate brain [23] leads to the proposal that Bose-Einstein condensates of various biologically important ions and of Cooper pairs of electrons in the magnetic field associated with the flux quantum define a key element of biological information processing.

   The natural guess is that this process involves in an essential manner the formation of holograms by a radiation generating cyclotron transitions and in this manner affecting the reflective properties of the hologram substrate determined by the rates of elastic scattering. If the flux quanta are flux tubes, one has photo-sensitive tubes instead of photosensitive plates and only the vertical component of the photon momentum is conserved in the scattering and reflected photons can have any direction in the plane orthogonal to the flux tube so that the reflected

radiation indeed reaches camera. The properties of the hologram seem to be consistent with the prediction that the information carried by it is only about the vertical and preferred horizontal direction.

2. Cyclotron energies E_c are proportional to $\hbar eB/m$ so that they increase with Planck constant and are inversely proportional the mass of the charged particle. This selects the Cooper pairs of electrons as a unique candidate for the Bose-Einstein condensate. TGD assigns to elementary particles macroscopic time scales as fundamental time scales and in the case of electron this time scale is .1 seconds which corresponds to 10 Hz fundamental biorhythm. Also for this reason Bose-Einstein condensate of Cooper pairs of electrons defines a natural candidate for the hologram substrate.

3. Cyclotron transitions induced by the incoming dark photons should in the recent case have frequency of order 30 GHz if $\lambda_d \sim 1$ cm is assumed for the dark variant of red light. In the case of electron the magnetic field .2 Gauss (this is the value of endogenous magnetic field deducible from the effects of ELF em fields on vertebrate brain [23] , [14]) corresponds to frequency of about 6×10^5 Hz so that a magnetic field of order .1 Tesla would give rise to a cyclotron frequency of order 30 GHz. The corresponding magnetic length is $L_B = \sqrt{\hbar/eB}$, which for ordinary value of Planck constant is 4.7×10 nm (note that 10 nm corresponds to cell membrane thickness and thickness of chromosomes). For $r = 15 \times 10^3$ the magnetic length would correspond to 5.8μm length scale to be compared with the size scale 6 μm of cell nucleus. If one requires the quantization of magnetic flux in multiples of $\hbar$ this field corresponds flux tube with thickness of order 6 μm. Therefore there might be a connection with the size of nucleus and the quantization of magnetic flux meaning that the thickness of the DNA replica trajectory reflects the basic cellular length scales.

4. The cyclotron states of Cooper pairs are harmonic oscillator states in the radial direction of flux tube and eigen states of angular momentum and momentum in the direction of the flux tube labelled by (n, m, k). The integer n is harmonic oscillator quantum number. m and k characterize the projections of angular momentum and momentum in the direction of the flux tube. m is integer and also k is quantized from periodic boundary conditions for the flux tube.

5. The hologram would be generated when the incoming dark photons excite Cooper pairs from the lowest energy eigenstate with oscillator quantum number $n = 0$ to the first eigenstate with $n = 1$ and in this manner affect the reflection properties of the system. The life-time of the hologram is determined by the rate at which the system decays back to the ground state so that one would have dynamical rather than static hologram which is of course what biological system needs.

6. The reflection from the hologram corresponds to an elastic scattering in which the Cooper pair condensate receives momentum but its energy is not affected. Elasticity means that the transition does not affect the energy of the Cooper pair which is the sum

$$E_{n,m,k} = n\hbar\omega + \frac{\hbar^2 k^2}{2m}$$

of the cyclotron energy and kinetic energy of free motion in the direction of the flux tube. If the longitudinal momentum k vanishes as the formation mechanism of the hologram strongly suggests, the value of n remains unchanged but the value of angular momentum projection m in the direction of flux tube can change in elastic scattering. The scattering takes place coherently so that the rate is proportional to N^2, N the number of Cooper pairs. The rate of these transitions is affected when a position dependent portion of the Cooper pairs of the Bose-Einstein condensate is in higher energy state. Therefore the transmittance depends on the point of hologram and the change is in the lowest approximation proportional to the intensity $|A + A_R|^2$ of the incoming dark light as in the case of the ordinary hologram.

8.4.4 Is the lifetime of the hologram long enough?

The lower bound for the lifetime of the physical realization of the hologram must be measured in seconds from the results of method II. The lifetime can be also longer since the fading of the physical

hologram after the irradiation has ceased can be due do the decay of the reference bream. This means a killer test for the model since the decay rate of the hologram is easy to estimate. The decay rate of hologram can be estimated from the decay rate of excited cyclotron state and the calculation reduces to standard first order perturbation theory for interacting system of charged particles and electromagnetic field which can be found in text books [5] .

1. The lifetime of the hologram can be estimated as the life-time of the excited state. The excited state decays by a spontaneous emission of photons. The lifetime can be estimated by using standard perturbation theory for the interaction of radiation fields and electrons with a scaled up value of Planck constant. Electrons form cyclotron states at flux tubes characterized by three quantum numbers: the harmonic oscillator quantum number $n = 0, 1, 2..$, the angular momentum projection m in the direction of flux tube, and the momentum of electron in the direction of flux tube.

   The interaction Hamiltonian is obtained by the minimal coupling prescription by adding to the vector potential associated with the static magnetic field of the flux tube time dependent radiation part. This means the replacement

$$\mathbf{A} = \mathbf{A}_{flux} \to \mathbf{A}_{flux} + \mathbf{A}_{rad} \tag{8.4.16}$$

   of the vector potential of the static magnetic field determining cyclotron energy spectrum in the magnetic field parallel to the flux tube with a vector potential containing also the vector potential of the second quantized radiation field.

2. This replacement affects the Hamiltonian of the system in the following manner

$$\begin{aligned} H_0 &= \frac{1}{2m}(\mathbf{p} - Ze\mathbf{A}_{flux}) \cdot (\mathbf{p} - Ze(\mathbf{A}_{flux}) \to H \ , \\ H &\equiv H_0 + H_{int} = \frac{1}{2m}(\mathbf{p} - Ze(\mathbf{A}_{flux} + \mathbf{A}_{rad})) \cdot (\mathbf{p} - Ze(\mathbf{A}_{flux} + \mathbf{A}_{rad})) \ , \\ H_{int} &= -\frac{1}{2m}\left[(Ze\mathbf{p} \cdot \mathbf{A}_{rad} + \mathbf{A}_{rad} \cdot \mathbf{p}) + Z^2e^2\mathbf{A}_{flux} \cdot \mathbf{A}_{rad} + Z^2e^2\mathbf{A}_{rad} \cdot \mathbf{A}_{rad}\right] \end{aligned} \tag{8.4.17}$$

   $Z = 2$ is the charge of the electron Cooper pair and $m = 2m_e$ is its mass. In Coulomb gauge one has

$$\nabla \cdot \mathbf{A}_{rad} = 0$$

   and the the interaction Hamiltonian H_{int} determining the transition rate reduces in the lowest order to

$$\begin{aligned} H_{int} &= -\frac{Ze}{m}\mathbf{A}_{rad} \cdot \mathbf{p} \ , \\ \mathbf{p} &\equiv \frac{\hbar}{i}\nabla \ . \end{aligned} \tag{8.4.18}$$

3. If the radiation generating hologram is in horizontal plane, cyclotron states have vanishing momentum quantum number in the vertical direction. Therefore also the emitted radiation has momentum and polarization in this plane. In principle this could be tested by using polarization sensitive camera.

4. The rate for the return to the ground state is calculable by using standard time dependent perturbation theory the result of which can be expressed as a formula for the total transition rate to the ground state

$$\Gamma = \frac{mE}{(2\pi)^2\hbar^4}\int d\Omega |\langle f,\hbar\mathbf{k}|H_{int}|i\rangle|^2 \ . \quad (8.4.19)$$

Here integration is over the solid angle that is over the momentum directions of the emitted photon. Here m is the mass of Cooper pair (two times electron mass) and E is photon energy (in eV range for visible photons).

5. The matrix element $|\langle f,\hbar\mathbf{k}|H_{int}|i\rangle$ of the interaction Hamiltonian is expressible in the lowest order approximation as

$$\langle f,\hbar\mathbf{k}|H_{int}|i\rangle = -i\frac{\hbar Ze}{m\sqrt{\omega}}\int \overline{\Psi}_{n_f,m_f,k_f}e^{i\mathbf{k}\cdot\mathbf{r}}\mathbf{e}\cdot\nabla\Psi_{n_i,m_i,k_i}dV \ . \quad (8.4.20)$$

e denotes the polarization vector of the photon and **k** its wave vector. The integration is over the flux tube volume.

In dipole approximation one can expand the plane wave to the first non-trivial order. If one assumes that the transitions responsible for the decay of the hologram correspond to the transitions $(n_i,m_i,0)=(1,\pm 1,0)\to(n_f,m_f,0)=(0,0,0)$, one has

$$\langle f,\hbar\mathbf{k}|H_{int}|i\rangle \simeq \frac{\hbar Ze}{m\sqrt{\omega}}\int \overline{\Psi}_{0,0,0}\mathbf{e}\cdot\nabla\Psi_{1,\pm 1,0}dV \ . \quad (8.4.21)$$

The result does not depend on photon energy at all. Angular momentum conservation requires that the angular momentum projection of the state in the direction of the flux tube changes by one unit corresponding to the spin of the photon. This allows to transform the matrix element to

$$\langle f,\hbar\mathbf{k}|H_{int}|i\rangle \simeq \pm i\frac{\hbar Ze}{m\sqrt{\omega}}\int \overline{\Psi}_{0,0,0}\mathbf{e}\times\mathbf{e}_\rho\frac{1}{\rho}\Psi_{1,\pm 1,0}dV \ . \quad (8.4.22)$$

Here $\mathbf{e}_\rho$ denote the unit vector $(x\mathbf{i}+y\mathbf{j})/\rho$ in radial direction. The magnitude of the matrix element is of order

$$\langle H_{int}\rangle \sim (\hbar Ze/m\sqrt{\omega})\times\langle\frac{1}{\rho}\rangle \sim \frac{\hbar e}{mR\sqrt{\omega}} \ , \quad (8.4.23)$$

where R is the radius of the flux tube.

6. The overall rate for the decay of the hologram has the order of magnitude

$$\Gamma \sim \frac{4\pi^2\alpha}{r}\frac{\hbar_0}{R^2m_e}\sim\frac{4\pi^2\alpha}{r^3}\frac{\hbar_0}{\lambda^2m_e} \ , \ r=\frac{\hbar}{\hbar_0} \ . \quad (8.4.24)$$

Here λ denotes the wave length of ordinary visible photon. Formally the rate scales as $1/r$ as the naive dimensional estimate suggests but $R\simeq r\lambda$ brings in an additional $1/r^2$ reduction factor so that $1/r^3$ over-all dependence results. For $r=\hbar/\hbar_0\sim 10^4$ the order of magnitude for the decay rate is for visible light $\Gamma\sim 10^{-5}$ s^{-1}, which is consistent with the observed slow rate of decay. As noticed, the fading of the hologram in experiment two could be due to the decay of the reference beam rather than the decay of hologram. Maybe also this could be tested. In any case, the model survives the first killer test.

8.4.5 The amplitude for the elastic scattering from hologram

The rate for the elastic scattering of photons of the reference beam from the hologram substrate defines the intensity of the hologram image and should be high enough.

1. This process involves two photons. The term

$$H_{int}^{2)} = \frac{e^2}{2m}\mathbf{A}_{rad}\cdot\mathbf{A}_{rad} \tag{8.4.25}$$

   in H_{int} makes this transition possible in the first order of perturbation theory.

2. One can worry about second order perturbation theoretic contribution to the rate which is also of order e^2. The generalization of the Golden Rule is obtained by the replacement

$$\langle f|H_{int}|i\rangle \quad \rightarrow \quad \langle f|H_{int}|i\rangle + \sum_m \frac{\langle f|H_{int}|m\rangle\langle m|H_{int}|i\rangle}{E_n - E_0 + i\eta\hbar} \quad , \quad \eta \rightarrow 0_+ \quad . \tag{8.4.26}$$

   The sum over m denotes sum over intermediate states. In the second order of perturbation theory the scattering can be thought of as taking place via intermediate states of Cooper pairs decaying back to the original state via the emission of photon. In the following rough estimate only the lowest ordinary contribution is taken into account.

3. In this approximation the amplitude for elastic scattering responsible for the hologram formation with $(n_i, m_i, k_i) = (n_f, m_f, k_f)$ and $\omega_i = \omega_f = \omega$ with the amplitude is apart from numerical factor of order unity given by

$$\langle f, \hbar\mathbf{k}|H_{int}|i\rangle \quad = \quad \frac{e^2\hbar^{1/2}\mathbf{e}_i\cdot\mathbf{e}_f\omega_i}{m\sqrt{\omega_f}}\int \overline{\Psi}_{n_i,m_i,0}e^{i(\mathbf{k}_i-\mathbf{k}_f)\cdot\mathbf{r}}\Psi_{n_i,m_i,0}dV \quad . \tag{8.4.27}$$

   In the lowest order approximation plane wave factor can be neglected. The order of magnitude for rate differs by a factor $4\pi\alpha(\omega R)^2$ from the matrix element for the decay of the hologram. For $R \sim \lambda_d$ the rates are of the same order. This rate corresponds to single photon case. In the case of many-photon state defined by the reference beam the rate is amplified by a factor N^2, where N is the number of photons in the reference beam.

8.5 Appendix: Details about methods I and II

Methods two represent the two schemes developed for our experimental purposes. In order to adduce and visualize DNA wave replicas, the following is to be performed: by means of timing relay (Fig. 8.13, position #3) in varied combinations the operator switches on the required emitters BS (UV-B, which is incandescent lamp in blue spectrum, glass type- Fig. 8.13, position #5), a matrix with red and infrared diodes (Fig. 8.13, position #8) and germicidal mercurial lamp/bulb or lamp Compact electronic CEST26E27 Black (UV-C, Fig. 8.13, position #6), or BS (UV-B) and MXT-90 (cold cathode Fig. 8.13, position #4).

1. Method I.
   Dehydrated/dry DNA sample from bull' s spleen - about 100 milligrams in a sealed plastic conical test tube, which is 4 centimeters long and 0.9 cm in its upper end; or 3 milliliters of DNA water solution, 1mg/ml) are placed in the effective zone of the emitters (1mm-50cm from the light emitters) and then the emitters are activated. The progression of the experiment was filmed using Fuji 24-27 DIN film. Oscillograph is in operation during the experiment and is to register and record the electromagnetic fields/frequencies within the zone of the experiment;

averaged normal electromagnetic background noise from within the premises is recorded, defined by the behavior of sinusoid in the oscillograph. Further, by means of the timing relay the emitter UV-C is turned off 10 minutes later. The camera captures an emergence of unique dynamic wave structures multi-replicated DNA replicas and of the surrounding objects invisible to the naked eye, yet perceivable by the camera and fixed on the film. These are directly related to the photonic influences effected by the emitters on the DNA samples. In other words, multiplication of a number of reflection of DNA samples occurs and is redistributed in space on complex trajectory patterns (the first method) and on horizontal patterns (the second method), including mapping of the objects responsible for exciting the DNA samples.

2. Method II
The second method to obtain and visualize DNA wave replicas involves the following: dehydrated/dry DNA sample, 100 milligrams is placed in an open mode into a holder made of aluminum foil. With intervals of 2-3 seconds the BS (UV-B) lamp, Compact Electronic CEST26E27 Black lamp and apparatus Duna-M are turned on and off. Photographs are taken 5 minutes later. By this method the DNA replicas and of close objects are registered and they are propagating strictly to the right hand side. With external mechanical interference (a touch) with the DNA samples the distribution vector alters to the opposite that is the DNA replicas begin propagating to the left hand side and than 5-8 seconds after the mechanical interference the replicas disappear or are not perceived by the present equipment4 or the utilized film, regardless of the equipment still being in an activated state.

Books related to TGD

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8.6 Figures

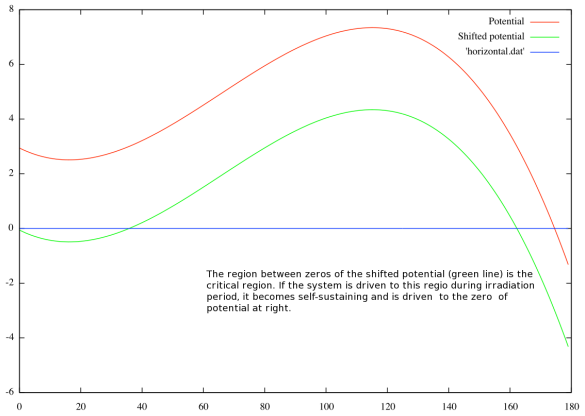

Figure 8.1: Illustrations of a potential $V(x) = P_3(x) = a - bx + cx^2 - dx^3$ and shifted potential $V(x) - a$ allowing self-sustainment. Note that the full potential allows only single zero and shifted potential two zeros. If the system ends up to the region between the two zeros of the shifted potential during irradiation, it ends up to the the rightmost zero after the irradiation period. When the value of the parameter c decreases adiabatically below certain critical value, the value of x (having interpretation as photon number) goes rapidly to zero.

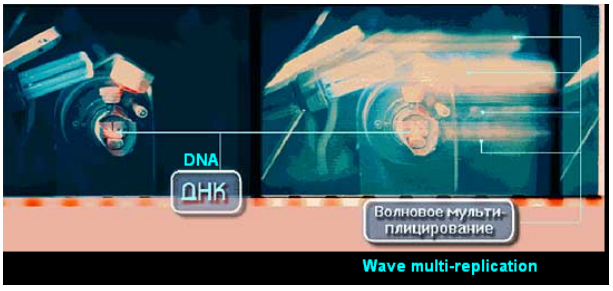

Figure 8.2: The left hand side figure is from [9] and represents the replica images of the instruments and the image interpreted by experimenters as a replica image of DNA sample (method II). The white cable like structures to the left from DNA sample have interpretation as phantom DNA image.

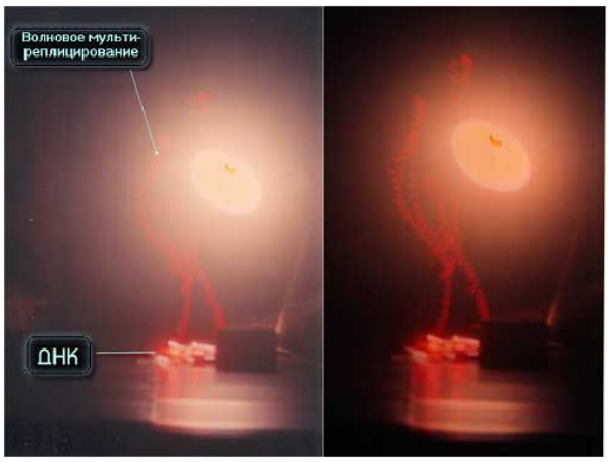

Figure 8.3: The picture shows the discrete replica like structure of the band like image obtained by method I and interpreted by experimenters as replica image of DNA sample.To the left image is the original image and to the right the contrasted one.

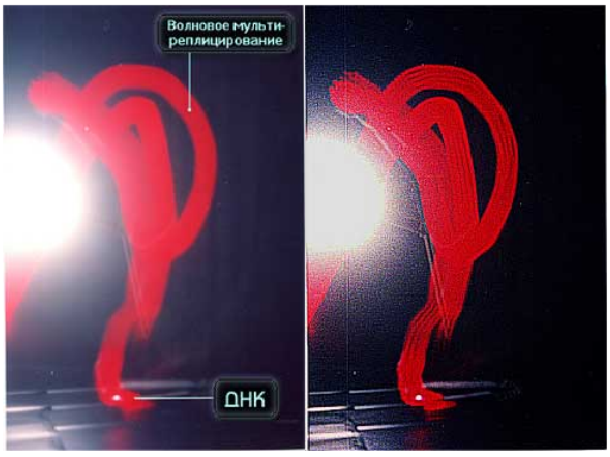

Figure 8.4: Spatial structure of DNA wave replicas obtained by method I. The picture reveals the 5-fold fine structure of the tube like image interpreted by experimenters as replica image of DNA sample. The 5-fold character probably correspond to five red LEDs above the sample. To the left image is the original image and to the right the contrasted one.

Figure 8.5: Long living DNA wave replica from the experiment in Fig. 3 (referred to as phantom image as opposed to the image seen during irradiation) subsequent to switching off of the initiating electromagnetic fields/frequencies sources.

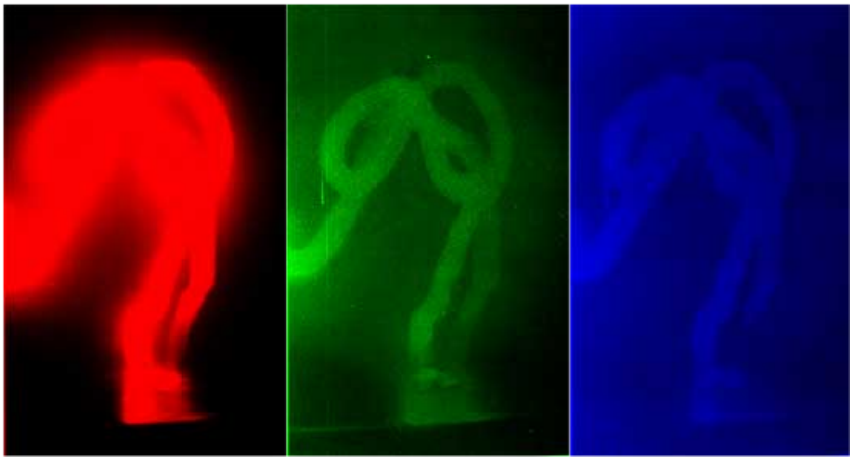

Figure 8.6: Distribution of the brightness values per RGB color model, Red, Green, Blue of the phantom DNA image of previous figure. The green image gives especially clear picture about the structure of phanton DNA image.

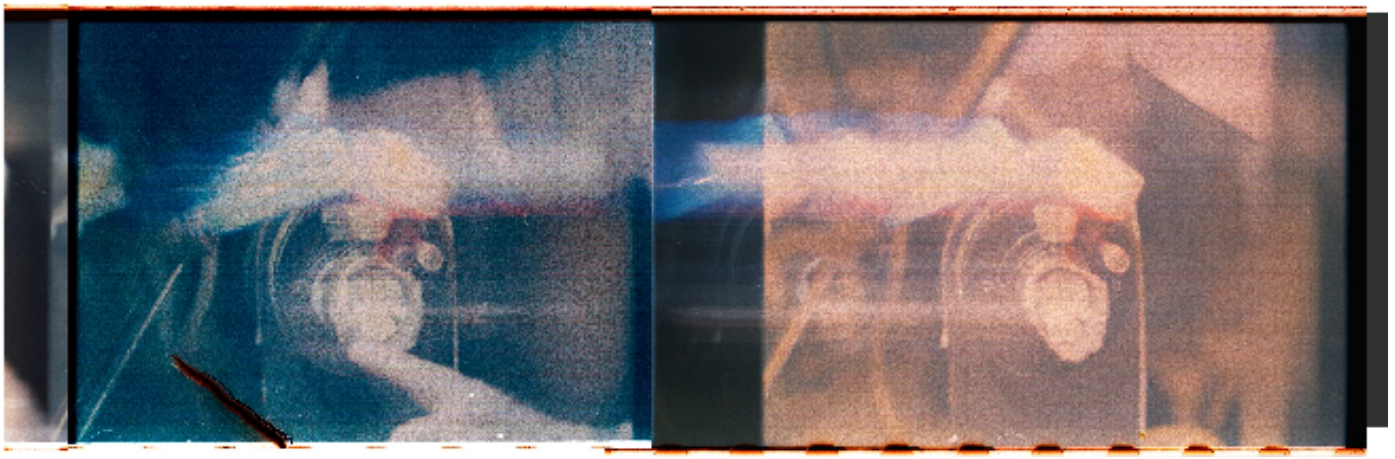

Figure 8.7: a) The moment of mechanical external interference (touch, which could have also biological effect) with DNA sample. The second method of elicitation of DNA wave replicas. b) Shift to the left of the wave replicas immediately after the interference. It is also commonly noticed that there is a sharp distinction of the shot from others by brightness and color scheme, which is unrelated to the working of the camera.

Figure 8.8: Disappearance of DNA wave replica formation effect after 5-8 seconds following the interference with the DNA sample (touch, see previous figure) while the entire equipment initializing the replicas is still on.

Figure 8.9: One of the modified experiments, shown in Fig. 5 (old DNA sample replaced by new). Refer to the shots # 3 and #4 above. The shot #4 reveals replicas of the Duna-M diodes, shifting to the right side. Note the appearance of replicas of perforation and exposed parts of the film close to diodes.

Figure 8.10: Shots #11 and #12 above. It is to be mentioned that from shot #1 until shot #11 the Duna-M diodes wave replicas are absent, however appearing again in the shot #12.

Figure 8.11: Shots #13 and #14 above. In the #13 we can distinguish wave replicas of the Duna-M diodes with the commonly observed intrusion in into the unexpected space between the shots. The shot #14 does not capture the wave replicas of the diodes and they disappear.

Figure 8.12: Shots #23 and #24 above. From shot #14 until #22 replicas disappear, they are dimly captured in the shots #23 and #24.

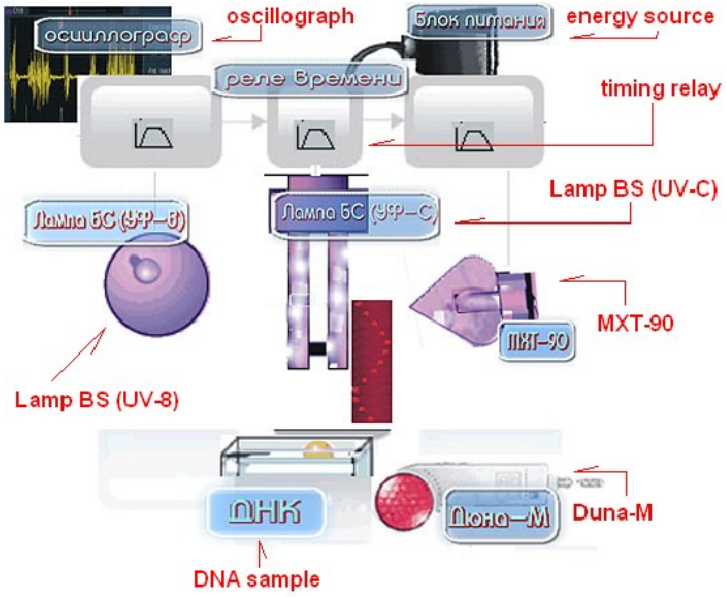

Figure 8.13: Schematic representation of the parts of the experimental apparatus

Chapter 9

Quantum Model for Remote Replication

9.1 Introduction

The idea about remote replication, transcription and translation of genes in terms of electromagnetic field patterns is very attractive and would be in accordance with the wave DNA vision. This requires a coding of DNA nucleotides. I have proposed several codings of this kind.

1. In DNA as topological quantum computer model [**?**]uark and anti-quark at the ends of a flux tube connecting DNA nucleotide to a lipid of the nuclear or cell membrane takes care of the coding. Also sequences of dark nucleons giving rise to dark nuclei realize the analogs of DNA, RNA, tRNA, and amino-acids as well as vertebrate genetic code [**?**] Dark nucleons sequences could correspond to the phantom DNA discovered by Gariaev's group [**?**]

2. Quantum antenna hypothesis represents one of the oldest ideas of TGD inspired quantum biology [**?**] molecules would act like quantum antennas. Frequency coding would be very natural for groups of molecules participating in the same reaction: the flux tubes connecting the molecules would carry the radiation inducing resonant antenna interaction and phase transitions reducing Planck constant would bring the reacting molecules near to each other. Magnetic flux tubes connecting the molecules would be essential element of the mechanism. Remote replication would represent an example about a situation in which $\hbar$ changing phase transition does not take place. If one wants coding of individual molecules -such as DNA nucleotides- by frequency in turned coded by the value of $\hbar$ for given photon energy ($E = hf$), one is forced to make ad hoc assumptions and it is difficult to find any plausible scenario. Quantum antenna mechanism could make possible remote replication for which the findings of Montagnier's group as well as remote transcription for which the work of Gariaev's group gives some evidence.

3. One can consider also a coding by field patterns. In fact, the quark and antiquark at the ends of the flux tube generate a color magnetic field coding for the quark pair since the classical color field depends on the color of the quark and its antiquark. Gariaev's group has proposed that the change of polarization direction could provide a possible mechanism of coding of DNA sequences to radiation patterns [**?**] The proposal is discussed from TGD point of view in [**?**] The mechanism changing the polarization direction should reduce to different propagation velocities for the two circular polarizations. The other polarization should act more strongly with the DNA related structures and this should cause the slowing down of propagation since it would correspond to sequence of absorptions and emissions. The constraint that this occurs coherently for DNAs and codes the DNA sequence is very powerful condition. It is however difficult to imagine how this mechanism alone could give rise to remote replication of DNA or similar processes: the coding from radiation pattern to DNA sequences is the bottle neck. Therefore this mechanism will not be discussed in the following.

In the sequel a model for the coding of DNA in terms of radiation patterns is discussed. There are three experimental guidelines: the phantom DNA [**?**]dentified as dark nucleon sequences in TGD

framework and the evidence for remote activation of DNA transcription [**?**] both discovered by Gariaev's group - are assumed as the first two key elements of the model. The remote replication of DNA suggested by the experimental findings of Montagnier's group serves as a further guideline in the development of the model. Also the results of the latest experiment of Gariaev's group in many respects similar to that of Montagnier's experiment but differing in certain crucial aspects from it are used as input.

Polymerase chain reaction (PCR) is the technique used in the experiments of Montagnier's group [**?**]nd later in somewhat modified experiment by Gariaev's group involving irradiation of the second test tube by laser light. DNA polymerase catalyzes the formation of DNA from existing DNA sequences serving as a template. Since the catalytic interaction of DNA polymerase takes place with already existing DNA sequence, the only possibility is that first some conjugate DNA sequences are generated by remote replication after which DNA polymerase uses these sequences as templates to amplify them to original DNA sequences. Whether the product consists of original DNA or its conjugate can be tested.

The model inspires the proposal that the magnetic body of a polar molecule codes for it using dark nucleon sequences assignable to the hydrogen bonds between the molecule and surrounding ordered water layer. Quantum antenna mechanism would allow the immune system to modify itself by developing ordinary DNA coding for amino-acids attaching to and thus "catching" the polar molecule. The mechanism could be behind water memory and homeopathic healing. Every polar molecule in living matter would have dark nucleon sequence or several of them (as in the case of amino-acids) serving as its name. This would also associate unique dark nucleon sequence also with the magnetic body of DNA so that DNA-dark DNA association would be automatic. Same applies to mRNA and tRNA and amino-acids.

9.2 The findings that one should understand

It is good to start by summarizing the experimental findings that the model should explain.

1. One should be able to identify phantom DNA [**?**] This identification explains the findings about phantom DNA if ordinary and dark DNA have common resonance frequencies and therefore behave like resonantly interacting quantum antennae.

2. The earlier findings of Gariaev's group suggesting remote gene expression [**?**, **?**] which becomes also possible if the DNAs of the sender can activate the DNA of the receiver by radiation. Direct activation could be based on electromagnetic signal between DNA of the sender and ordinary conjugate DNA of the receiver. Scattering from ordinary and possibly also phantom DNA and would generate this kind of signal. The challenge is to explain why the activation obeys genetic code in the sense that a given DNA sequence activates only similar DNA sequence.

3. The claim of Montagnier's team [**?**]s that the radiation generated by DNA affects water in such a manner that it behaves as if it contained the actual DNA. A brief summary of experiment of Montagnier and collaborators is in order.

   (a) Two test tubes containing 100 bases long DNA fragments were studied. Both tubes were subjected to 7 Hz electromagnetic radiation. Earth's magnetic field was eliminated to prevent its possible inteference (the cyclotron frequencies of Earth's magnetic field are in EEG range and one of the family secrets of biology and neuroscience since seventies is that cyclotron frequencies in magnetic fields have biological effects on vertebrate brain). The frequencies around 7 Hz correspond to cyclotron frequencies of some biologically important ions in the endogenous magnetic field of .2 Tesla explaining the findings. This field is 2/5 of the nominal value of the Earth's magnetic field.

   (b) What makes the situation so irritating for skeptics who have been laughing for decades for homepathy and water memory is that the repeated dilution process used for the homeopathic remedies was applied to DNA in the recent case. The solution containing no detectable amounts DNA (dilution factor was 10^{-12}) was placed in second test tube whereas the first test tube contained 100 bases long DNA in the original concentration.

(c) After 16 to 18 hours both tubes were subjected to polymerase chain reaction (PCR), which builds DNA from its basic building bricks using DNA polymerase enzyme. What is so irritating from the point of view of skeptic was that DNA was generated also in the test tube containing the highly diluted water. Water in presence of second test tube seems to be able to cheat the polymerase by mimicking the presence of the actual DNA serving in the usual situation as a template for builing copies of DNA. One could also speak about the analog quantum teleportation. Note that the presence of both test tubes - and therefore some kind of communication between the samples - is absolutely esential for the process to take place: repeated dilution is not enough.

4. Peter Gariaev's team has carried out an analogous experiment recently in which one has two test tubes containing water. Tube A contained DNA fragments and tube B contained only water and DNA nucleotides plus DNA polymerase - just as as in Montagnier's experiment. The analog of the homeopathic procedure was not however applied to tube B. The experiments use a drop of DNA in water in gamma concentration in tube A. This DNA (with length of 600 base pairs) was scanned by laser radiation from helium-neon laser. The scattered radiation having a wide spectrum of frequencies down to kHz frequencies was applied on tube B at distance of 3 m in refrigerator (+4 Celsius) containing distilled water solution of DNA nucleotides and DNA polymerase inducing polymer chain reaction PCR amplifying DNA template if present. The generation of DNA sequences in tube B with the same mass distribution as in tube A by polymer chain reaction (PCR) is observed suggesting that the necessary DNA template is generated as a direct copy or conjugate of the original in test tube A by some unknown mechanism. Nucleotide sequences have not been analyzed to see whether they are identical or conjugates of those in tube A.

9.3 The model of remote replication consistent with DNA as topological quantum computer model

The basic assumptions are that the scattered radiation, the flux tubes of the magnetic body of DNA along which the radiation propagates, and quarks and antiquarks at the ends of the flux tubes from system able to serve as a template for the formation of conjugate of ordinary DNA. To understand how remote remote replication could take place, some further assumptions are necessary.

1. The flux tubes emanating from DNA are parallel and condensed at 2-D flux sheet having DNA at is first boundary so that DNA nucleotides can attach to the flux tubes at the second boundary. The attached nucleotides would be along the same line and would form DNA sequence in remote replication process.

2. Quantum antenna interaction takes place between group of molecules participating a given reaction so that they have common antenna frequency as resonance frequency. The frequencies characterize the radiation propagating along magnetic flux tubes connecting the molecules, and could come as sub-harmonics of the frequency of (in the case considered) visible light from the formula

$$E = h_n f, \quad h_n = nh \quad , \quad n = 1, 2, 3, ... \quad .$$

Here E is the fixed energy of photon. h_n denotes value of Planck constant which in TGD Universe can have infinite number of values coming as multiplies of the ordinary Planck constant h.

For a given photon energy E one obtains harmonics of the basic wavelength

$$\lambda = \frac{c}{f(n)} = n\lambda_0 \quad .$$

Wave length would correspond to the length of the flux tube proportional to n. DNAs with flux tubes characterized by different values of n would correspond to different levels in the evolutionary hierarchy. In TGD inspired theory of consciousness the value of h_n serves as the measure for the time scale of planned action and memory span and neurons of frontal lobe would represent the highest level in the hierarchy,

3. If resonance frequency is same for all nucleotides, frequency cannot distinguish between DNA nucleotides. In the model of DNA as topological quantum computer the quark (u or d) and antiquark ($\overline{u}$ or $\overline{d}$) at the ends of the flux tube code for A, T, C, G. This model is the simplest one and does not require any additional assumptions about frequency coding. It also allows resonant interaction at several frequencies: the scattering of visible light from DNA indeed produces a wide spectrum of frequencies interpreted in terms of dark variants of visible photons.

   One can criticize the assumption that particular quark or antiquark is associated with the flux tube ending at particular nucleotide. At this moment this assumption does not have a convincing dynamical explanation. Presumably this explanation would rely on the minimization of the interaction energy.

4. What is needed is a model explaining why the resonant antenna frequency does not depend on nucleotide: obviously the frequency should relate to something shared by all nucleotides. An energy level associated with sugar-phosphate backbone of DNA is what comes first in mind. A more exotic option is transition involved with quark-antiquark pair. Since electromagnetic field for non-vacuum extremals is accompanied by classical color field, the exchange of gluons between quark and antiquark suggests itself as the quantum antenna interaction distinguishing between nucleotides.

Quantum antenna mechanism is extremely general and flexible and might be a fundamental mechanism of bio-catalysis allowing also communication between visible and dark matter sectors. Antenna mechanism is of course central also in ordinary communications. If the biologically most relevant interactions of biomolecules via quantum antenna mechanism then also water memory and the claimed effects of homeopathically treated water might be understood [**?**] The testing of the dark photon aspect of the hypothesis would require the detection of the dark photons somehow: the decay to a bunch of n ordinary photons with same wavelength is the obvious manner to achieve this.

9.3.1 Identification of phantom DNA

The observed residual coherent scattering from a chamber from which ordinary DNA is removed inspired the notion of phantom DNA [**?**] The questions are what phantom DNA is and is it relevant to remote replication of the ordinary DNA.

Phantom DNA observed in the scattering experiments could correspond to dark nucleon sequences realizing vertebrate genetic code with dark nucleons consisting of three quarks representing both DNA,RNA, tRNA, and aminoacids as particular nucleon states [**?**] The resonant interaction between ordinary and dark DNA would explain why light at same frequencies scatters also from dark DNA in phantom DNA experiments. In Montagnier's experiments it could give rise to a positive feedback amplifying the radiation from second sample containing DNA. Water would be living in the sense that it contains "dark DNA" and dark DNA might allow remote transcription to ordinary DNA sequences in presence of ordinary DNA codons (triplets) and vice versa.

Skeptic can of course ask whether one could explain the experimental findings without assuming phantom DNA.

1. In Gariaev's experiments [**?**, **?**] which inspired the notion of phantom DNA part of DNA could "drop" to parallel space-time sheets and have the same effect on the scattered radiation as the ordinary DNA. This explanation would however require the many-sheeted space-time of TGD - probably equally abominable to skeptic as phantom DNA.

2. In Montagnier's experiment and also in the recent experiment of Gariaev the ordinary DNA contained by water droplet could diffuse to dark space-time sheets and enter from flux tube A to flux tube B along the same magnetic flux tubes as radiation propagates. DNA polymerase would allow to amplify this leaking DNA and produce conjugate DNA. The irradiation of the original DNA would generate the flux sheets serving as a route for the transfer. The killer test is to check whether it is indeed conjugate of the original DNA which is produced. Again many-sheeted space-time is required.

3. For the option based on DNA as topological quantum computer hypothesis discussed above the remote replication would take place via the direct formation of conjugate DNA template and

DNA polymerase produces from this copies of the *original* DNA whereas for "trivial" option conjugate DNA is produced. Phantom DNA would not be absolutely necessary. It is however questionable whether the intensity of the radiation is high enough and the resonant interaction with phantom DNA which could give rise to a positive feedback might be needed to amplify the radiation.

9.3.2 Dark DNA and frequency coding by quantum antenna mechanism

The remote transcription of dark DNA (phantom DNA) to ordinary DNA and vice versa would have quite far reaching implications for evolution since dark DNA/RNA/tRNA/amino-acids could define a virtual world serving as $R\&D$ lab where new DNAs could be developed and if needed translated to ordinary DNA. The dark DNA could be also transferred through cell membranes without difficulty, in particular to germ cells. Also the genetic transfer between different organisms would become possible. Second possibility is that the magnetic flux tubes mediating the dark photons traverse the cell membranes so that even the transfer of dark nucleons through the cell membrane is un-necessary. The implications for genetic engineering would be obvious.

Could one generalize the quantum antenna mechanism to the interaction between dark nucleons representing DNA triplets as entangled states of three quarks and ordinary DNA codons consisting of three unentangled nucleotides? Could similar mechanism realize genetic code assigning to dark DNA dark variants of RNA, tRNA and amino-acids via the analogs of transcription and translation processes? It seems that frequency coding, which - somewhat disappointingly - did not look natural for remote replication of ordinary DNA, is ideal for these processes so that the original idea of wave DNA would be realized at the level of dark-visible and dark-dark interactions.

The flux tubes would be associated with entire codons -DNA triplets - rather than individual nucleotides. Different DNA triplets do not form interacting groups in the sense that they should be connected by flux tubes. Therefore the simplest possibility would be frequency coding with specific resonance frequency for each DNA triplet. No quarks at the ends of the flux tubes connecting codons are needed.

Remark:: A hierarchy of flux quanta is essential and must distinguish between its levels. Flux tubes associated with nucleotides at flux tubes associated with DNA codons at flux sheets traversing DNA strands.

If one assumes that octaves correspond to the same frequency this would require odd multiples

$$\lambda(n) = (2n+1)\lambda_0 \quad , \quad n = 0, ..., 63$$

of λ_0 so that the longest wavelength would be $127\lambda_0$. In the number theoretic model of the genetic code based on the notion of Combinatorial Hierarchy [**?**]odons are indeed labeled by 64 integers in the range $0, ..., 127 = 2^7 - 1$. These integers are however not assumed to be odd. One can also consider the possibility that the frequencies are coded by the value of Planck constant and this option leads to an interpretation of the earlier proposed realization of divisor code [**?**]o be discussed later on.

Support for this option comes from the phenomenon of phantom DNA demonstrating that resonant scattering of light from DNA and dark DNA occurs for the same frequencies.

Can one imagine remote transcription of dark DNA to ordinary DNA using *only nucleotides* as building bricks? This process would require coupling of DNA nucleotides to dark nucleons representing DNA triplets and it is not easy to imagine any simple mechanism making this possible. Already existing DNA triplets seem to be necessary.

9.3.3 Common explanation for the findings of Montagnier and Gariaev

In the experiments of Montagnier's group [**?**]he outcome is remote replication whereas the earlier experiments Gariaev's group [**?**]ive evidence for phantom DNA and remote activation of DNA transcription by scattered laser light able to represented genetic code. There must be interaction between the test tubes in Montagnier's experiments and in the recent experiments of Gariaev's group observing remote replication there is explicit interaction between the test tubes due to the scattered laser radiation. Hence one expects a common underlying mechanism based on radiation between the tubes and phantom DNA.

1. The TGD based explanation [**?**]f Montagnier's findings relies on the assumption that the homeopathic procedure generated a population of dark DNA nucleotides in the diluted system. The sequence of dilutions and shakings was like a series of environmental catastrophes driving the evolution of dark DNA and also feeding metabolic energy to the system. The outcome was dark DNA population mimicking the original DNA in the test tube B. In the presence of DNA polymerase in tube B and second test tube A containing ordinary DNA the dark DNA was somehow able to generate ordinary DNA in tube B. The detailed mechanism for this remained open.

2. Could the scattered laser light have the same effect as the homeopathic procedure? This would require a direct transcription of dark DNA to ordinary DNA in the presence of DNA polymerase and nucleotides (only them!). It is very difficult to understand how this could happen. DNA polymerase very probably does not have the same catalyzing effect on dark DNA sequences as on ordinary DNA sequences. It is also difficult to imagine the build-up of ordinary DNA from nucleotides using dark nucleon sequences as templates: if frequency coded codons would serve as building bricks, situation would be simpler as already found.

3. One must not forget that the presence of the test tube A was essential in the experiment of Montagnier: communications between the test tubes crucial for the outcome must have taken place. The consistency between the two experiments could be achieved if the DNA in test tube A generated the counterpart of the scattered laser signal in Gariaev's experiments but certainly as a much weaker signal.

4. This signal should have been amplified somehow by the presence the dark DNA sequences in tube B so that it would have been able to generate critical amounts of conjugate of the original DNA amplified by DNA polymerase to the copy of the original. What suggests itself is a positive feedback loop ordinary DNA sequences $\rightarrow$ dark DNA sequences $\rightarrow$ ordinary DNA sequences..... causing the amplification of the weak signal so that it is able to induce remote replication by the proposed mechanism. This kind of feedback of signals propagating between magnetic bodies was assumed also in the model for the strange images produced by the irradiation of DNA sample by ordinary light interpreted as photographs of magnetic flux tubes containing dark matter [**?**]

This model explains also the findings of the recent experiment (unpublished) of Gariaev. In this case the amplification by feedback mechanism could be present but might not be needed since the scattered laser radiation could give strong enough signal to produce the needed amount of conjugate DNA serving as a template. What is nice from TGD point of view that the consistency between the two experiments gives support also for the notion of dark DNA and its identification as phantom DNA.

9.3.4 Summing up the basic assumptions of the mechanism

The basic assumptions of the model of remote replication deserve a short summary.

1. Bio-molecules would serve as receiving and sending quantum antennas forming populations with communications between members just like higher organisms. The molecules participating the same reaction would naturally have same antenna frequencies. Quarks and antiquarks at the ends of the flux tubes would code for different nucleotides and the frequencies associated with the nucleotides would be identical. The character of classical electromagnetic field would code for a particular nucleotide.

2. Remote replication and other remote polymerization processes would differ from the ordinary one only in that the phase transition reducing the value of Planck constant for the flux tube would not take place and bring the molecules near each other. Note that the fractal hierarchy of flux quanta: nucleotide flux tubes, codon flux tubes and flux sheets associated with DNA strands is essential.

3. The immediate product of remote replication would be the conjugate of the original DNA sequence and DNA polymerase would amplify it to the copy of the original DNA sequence. This prediction could be tested by using very simple DNAs sequences- say sequences consisting two

nucleotides which are not conjugates. For instance, one could check what happens if conjugate nucleotides are absent from the target (neither conjugate nor original DNA sequence should be produced). If the target contains conjugate nucleotides but no originals, only conjugate DNA sequences would be produced - one might hope in sufficiently large amounts to be detectable.

4. Frequency coding would be natural for quantum antenna interactions between ordinary DNA and its dark variant and also between dark variants of DNA, RNA, tRNA, and amino-acids. The reason is that dark nucleons represent the genetic code by entanglement and it is not possible to reduce the codon to a sequence of letters.

9.4 Possible implications

The proposed realization of remote replication seems to have rather far reaching implications for the understanding of the mechanism of homeopathy and basic mechanisms of immune system as well as to the understanding of how DNA -dark nucleon sequence association. One can also interpret the proposed TGD based realization of the divisor code [**?**]uggested by Khrennikov [**?**]s frequency coding of DNA triplets by the value of Planck constant assignable to flux tubes emerging from DNA triplets.

9.4.1 Possible relevance for homeopathy and immune system

TGD inspired vision about water memory assumes that the magnetic bodies of molecules dis-solved into water represent the molecules in terms of cyclotron frequencies characterizing its magnetic body. Molecules can lose their magnetic bodies as the hydrogen bonds connecting the molecule to the magnetic body are split. The population of these lost magnetic bodies would define a representation for the dissolved substance able to mimic it.

The hitherto unanswered questions concern the detailed structure of the magnetic body of the molecule and how it codes for the molecule. The hydrogen bonds connecting the molecule to the ordered water forming a kind of ice covering the molecule in the inactive state should be crucial aspect of the coding. If dark nucleon sequences are associated with the hydrogen bonds of this "ice layer" or generated in their splitting as I have proposed, one can ask whether dark nucleon sequences could characterize the molecular magnetic body. If so, cyclotron resonance frequencies or more general frequencies associated with the dark DNA sequences could code for the molecule. DNA sequences would define a universal language allowing for the system to name for polar molecules.

Quantum antenna mechanism would in turn associate ordinary DNA sequences with the dark nucleon sequences coding for the molecule. Hence one can imagine a development of a mechanism allowing the organism to modify its DNA by adding to it genes coding for proteins characterized by the same resonance frequencies as the magnetic bodies of the invader molecules. These proteins would couple strongly to the invader molecules via quantum antenna mechanism and the phase transition reducing Planck constant would allow them to catch the invader molecules by attaching to them. The fact that the DNA of immune system evolves very rapidly conforms with this vision.

9.4.2 Frequency coding for DNA sequences by the value of Planck constant as a realization of divisor code

The realization of dark magnetic bodies of polar molecules in terms of dark nucleon sequences allows to understand the association of dark DNA with ordinary DNA, RNA, and tRNA making among other things possible the transcription of dark DNA to DNA and vice versa. Dark nucleon sequences would be associated with the magnetic bodies of DNA, mRNA, and tRNA. This would apply also to amino-acid sequences. Dark DNA would separate from ordinary DNA as it loses its magnetic body in the splitting of hydrogen bonds and suffers denaturation. Similar mechanism would cause denaturation of other biomolecules and would mean that they "lose their names" and thus information content and become mere organic molecules instead of living bio-molecules. This kind of association would make the emergence of the genetic code and its generalization to the naming of molecules by DNA sequences trivial.

Genetic code can be understood from the proposed natural correspondence between dark nucleon sequences and DNA, RNA, tRNA, and acmino-acids). I have however developed also another realizaton based on TGD based realization of so called divisor code first suggested by Khrennikov and

Nilsson [**?**]nd the following argument allows to interpret in terms of frequency for fixed value of photon energy with frequencies coded by the value of Planck constant.

1. The observation of Khrennikov and Nilsson is following. Consider the integers n in the range 1,...,21 and obviously labeling amino-acids and let $k(n)$ the number of divisors of n. Define $B(k)$ as the number of integers n for which the number of divisors is k. It turns out that the numbers $B(k)$ are rather near to the numbers $A(k)$ of amino-acids coded by k codons. This suggests that given amino-acid A is coded by a product of prime $p(A)$, which alone characterizes it, and integer $n(A)$ in the range $1, ..., 21$. The product of integers characterizing the codon coding for A would be characterized by the product of $p(A)$ and some factor $r(A)$ of $n(A)$. With these assumptions given codon would code for only single amino-acid and the number of DNAs coding for amino-acid A is the number of the factors $r(A)$ of $n(A)$. The codons coding for A would be coded by integers $p(A)r(A)$ such that $r(A)$ divides $n(A)$. The safest assumption would be that the primes $p(A)$ satisfy $p(A) > 19$ so that $p(A)$ does not divide $n(A)$ for any A. If $p(A)$ is as small as possible the value spectrum of $p(A)$ is

$$\{23, 29, 31, 37, 41, 43, 47, 53, 59, 61, 67, 71, 73, 79, 83, 89, 97, 101, 103, 107, 109\} \ .$$

   If one assumes that the two additional aminoacids coded in some cases by non-vertebrate genetic code correspond to primes also the primes $113, 127$ are included.

   What is interesting is that Mersenne prime $M_7 = 2^7 - 1 = 127$ appears in the model of genetic code based on the notion of Combinatorial Hierarchy [**?**] This model assumes that DNA codons correspond to 64 integers in the range $1, ..., 127$. This realization of the genetic code cannot however be consistent with the divisor code realized in the proposed manner since it would require that the integers $n(A)p(A)$ belong to the range $1, .., 127$. The prime factors of these integers can however belong to this range.

2. The TGD inspired proposal [**?**]as that the flux tube assignable to amino-acid A corresponds to $\hbar = p(A) \times n(A)\hbar_0$ whereas the DNA triplet (for quark-antiquark coding nucleotide rather than triplet) coding for it is characterized by $\hbar = p(A) \times r(A)\hbar_0$ such that $r(A)$ divides $n(A)$.

3. This proposal could be interpreted in terms of frequency coding by quantum antenna mechanism. For a given photon energy E wave length would be coded by the value of $\hbar$ and one would have $\lambda_n = n\lambda_0$, $n = p(A)n(A)$ for amino-acids and $n = p(A)r(A)$ for codons. The condition that flux tube lengths are same for different DNA triplets would be satisfied if the common length of the flux tubes is an integer multiple of λ_0 proportional to the product of all integers appearing as factors in the integers coding for amino-acids. The common length of the flux tubes would be therefore proportional to the product $\prod_A p(A) \prod_A r_A$.

Books related to TGD

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Chapter 10

Evolution in Many-Sheeted Space-Time

10.1 Introduction

This chapter was originally about prebiotic evolution but gradually extended so that it became natural to drop the attribute "prebiotic" away. Of course, a collection of ideas rather than detailed history of life is in question.

If was already early that the notion of many-sheeted space-time could allow to understand many puzzles related to the pre-biotic evolution [174, 184] . There are many constraints on the models for pre-biotic evolution. The models have also many difficulties [125, 172] .

TGD replaces materialistic view about universe with a continual re-creation in which classical universe in 4-dimensional sense is replaced by a new one in each quantum jump. p-Adic length scale hypothesis allows to formulate the notion of evolution precisely as a generation of increasingly larger space-time sheets characterized by preferred p-adic primes. A second aspect is the emergence of new levels in dark matter hierarchy making possible macroscopic quantum coherence and inducing great leaps in evolution. Also a hierarchy of dark weak bosons and gluons becomes an essential part of the physics of living matter. The notion of field/magnetic body carrying dark matter is a further key element in the model and has become increasingly important during years, and the vision about DNA-cell membrane system as a topological quantum computer utilizing braids defined by magnetic flux tubes connecting nucleotides to lipids meant a breakthrough in the understanding of the real function of DNA in information processing.

10.1.1 Questions and answers about evolution

A good manner to introduce the essentials of the TGD inspired model for the prebiotic evolution is by a sequence of questions and answers relating to evolution.

Q: Is life as we know it result of an accident?.

A: Quantum TGD predicts a genuine cosmic evolution occurring by quantum jumps for which dynamics is characterized by Negentropy Maximization Principle [44] . The generalization of the notion of space-time implies dark matter hierarchy with levels characterized by arbitrarily large values of Planck constant so that macroscopic quantum coherence is possible even in astrophysical length scales. Even astrophysical systems are analogous to atomic systems which implies a strong standardization of planetary system so that Earth like planets are abundant. There are also other good reasons for why the evolution of life would not have been accident in TGD Universe and life should appear everywhere in TGD Universe.

Q: What were the most primitive living systems?

A: The notion of magnetic body brings to biology several completely new elements. Magnetic flux quanta containing dark charged matter and quantum controlling ordinary matter in plasma phase is perhaps the simplest system which can develop characteristics of a living system. The braiding of magnetic flux tubes makes possible topological quantum computation and a fundamental representation of memories and its presence could be even taken as a definition for what it is to be

living. Tqc programs correspond to asymptotic self organization patterns for liquid flows inducing braidings and are non-trivial in presence of external energy feed.

Q: How metabolic machinery emerged?

A: Many-sheeted space-time concept predicts a hierarchy of universal metabolic energy quanta as differences of zero point kinetic energies for space-time sheets characterized by different p-adic length scales. What remains is to understand how chemical energy storage and utilization mechanisms developed.

Q: What is behind biocatalytic machinery?

A: The magnetic flux tubes connecting bio-molecules imply long range correlations between molecules. The reduction of Planck constant for magnetic flux tubes implying their shortening provides a mechanism making possible for bio-molecules to "find" each other in a very selective manner, and explains also why molecules end up to precisely defined conformations necessary for a selective bio-catalysis.

Q: How symbolic dynamics emerged?

A: The notion of fractional atom suggested by the fractionization of electron and nucleon quantum numbers for dark matter hierarchy brings in a candidate for a symbolic dynamics assigning to molecules "names" which need not correlate very strongly with the chemical properties of the molecule but would dictate to a high degree its biochemical behavior. Molecular "sex" emerges in the sense that molecules labeled with "names" and "co-names" tend to pair. The model of DNA as tqc assumes a 4-coloring of braid strands realized by an assignment of DNA nucleotides to quarks and anti-quarks. Also this means symbolic dynamics since only molecules connected by colored braids have high probability to participate in same biochemical reaction and do it in a very specific manner. Since the quarks involved with braid strands can have fractional charges, molecular sex can be realized also in this manner.

Q: What selected the bio-molecules during chemical evolution?

A: The proposed symbolic dynamics based on the notions of colored braids and fractional atom poses very strong constraints on the subsets of bio-molecules that can react with considerable rates.

Q: How biochemical pathways emerged?

A: It is now possible to realize in practice sequences of arbitrarily complex self-catalyzing biochemical reactions utilizing DNA hairpins. The mechanism generalizes to more complex molecules. At a given step of the reaction sequence the structure formed during the previous steps acts as a key fitting to a lock represented by some hairpin in the solution, and opens it to a linear molecule and in this manner makes it a key. The braids between reactants make it possible for the key and lock to find each other.

Q: How genetic code evolved?

A: The symmetries of the third codon of the genetic code allow in DNA as tqc model an interpretation as isospin and matter antimatter symmetries for quarks and antiquarks assigned with DNA nucleotides and representing 4-color of braid strands. These symmetries together with the study of the detailed structure of tRNA lead to a model for the evolution of the genetic code as a fusion of a non-deterministic 1-code and one-to-one 2-code corresponding to the conjugation of mRNA molecules. During RNA era two kinds of RNAs, call them RNA_1 and RNA_2, were present and played the roles of mRNA and aminoacid sequences. 2-code *resp.* 1-code mediated the analog of replication *resp.* translation using hairpin like molecules $tRNA_1$ and $tRNA_2$ to bring in RNA nucleotides and RNA doublets to the growing RNA_i sequence. Amino-acids attached to the stem of $tRNA_2$ acted as catalysts. The transition to RNA-aminoacid era took place via a fusion of the $tRNA_1$ and $tRNA_2$ to the ordinary tRNA and instead of sequences of two kinds of RNAs were replaced by aminoacid sequences were formed. After a period of symbiosis involving all these three tRNAs a transition to DNA-RNA-aminoacid world took place as an aminoacid sequence acting like reverse transcriptase emerged.

Q: Did RNA world precede the life as we know it?

A: The model for the evolution of the genetic code forces to conclude tha RNA world [158] preceded the recent biology and allows also to deduce that the nucleotides involved with second form of RNA where A,T,U,I(nositol). The exotic RNA in question could have been $2', 5'$ form of RNA rather than $3', 5'$ RNA produced also in the classical experiments of Leslie Orgel [55] .

Q: Does the notion of protocell make sense?

A: The model of DNA as tqc involves essentially the magnetic flux tubes connecting DNA nucleotides and cell membrane. Since topological quantum computation should have taken place also during the RNA era, some kind of cell membrane consisting of exotic RNA should have been present.

It has been found that DNA indeed forms membrane like structures which are liquid crystals consisting of sequences of DNA nucleotides with length up to 20 nucleotides [146] and same might be true in the case of exotic RNA.

Q: How life could evolve in the harsh primordial environment? Does the notion of primordial ocean make sense?

A: Evolving life had to cope with the grave difficulties due to the irradiation by UV light and meteoric bombardment. A simple solution of these problems is to evolve in the interior of Earth, say in underground lakes. This idea conforms nicely with the observation that continents would have formed a single super continent at time of Cambrian explosion provided the radius of Earth at that time was by a factor 1/2 smaller than now. TGD predicts that cosmic evolution does not occur continuously but by quantum jumps in which the Planck constant of appropriate space-time sheet increases. A phase transition of this kind increasing the radius of Earth during a relatively short time interval would have led to a burst of life from underground lakes to the surface of Earth. This would also explain the sudden emergence of a huge variety of highly developed life forms during Cambrian explosion.

10.1.2 Topics of the chapter

The topics of the chapter has been restricted to those, which seem to represent the most well-established ideas. The topics of the article have been restricted to those, which seem to represent the most well-established ideas about evolution in TGD Universe. There are many other, more speculative, ideas such as the notion of fractional atom [24] based on fractalization of electron charge and strong form of the hypothesis that some life forms has evolved in "Mother Gaia's womb", maybe even in the hot environment defined by the boundary of mantle and core.

1. Basic facts about and TGD based model for pre-biotic evolution are discussed.

2. A model for the evolution of the recent genetic code (3-codons) as a fusion of codes for which codons are nucleotides (1-codons) and di-nucleotides (2-codons) is discussed. The symmetries of the genetic code, the observation that tRNA can be seen as a fusion of two hairpin like DNA molecules, and the finding that the first nucleotides of 3-codon code for the reaction path leading from a precursors of the aminoacid to aminoacids for hydrophobic/hydrohilic dichotomy, serve as motivations of the model. 1- and 2-codes corresponding to the two forms of RNA (the exotic $2'-5'$ RNA and the usual $3'-5'$ RNA) would have prevailed in RNA world. Aminoacids would have served as catalysts for the copying of RNA on one hand, and RNA molecules would have catalyzed the formation of aminoacids from their precursors on one hand, meaning the presence of a positive feedback loop. In the transition to DNA-aminoacid era RNA began to be translated to aminoacid sequences.

3. Cambrian explosion represents a rather mysterious period in biology: new highly developed phylas emerged out of nowhere. A second strange finding is that continents would fit together to form single super-continent covering entire Earth's surface at time of Cambrian explosion if the radius of Earth would have been one half of its recent value. This finding has inspired Expanding Earth theories but it has not been possible to identify the mechanism causing the expansion. The success of the standard tectonic plate theory requires that possible expansion must have occurred in relatively short geological time scale. The hierarchy of Planck constants implies that cosmic expansion has occurred in quantum leaps increasing the value of $\hbar$ and thus of quantum scales by factors which tend to be powers of 2. Cosmic expansion would have occurred as jerks even in the case of planets. In the proposed model Cambrian explosion would have accompanied the expansion of the Earth's radius by a factor of 2: during this period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place.

4. TGD based view about the evolution of genetic code is compared to the views of McFadden [185] . This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding [3] .

5. A vision about biological evolution and evolution of brain is discussed on basis of the wisdom gained from the construction of the models of sensory receptor and generalized EEG [31, 56, 23] .

10.2 What is known about pre-biotic evolution?

In the following the basic facts and ideas about pre-biotic are summarized.

10.2.1 Some believed-to-be facts about the early history of life

The following basic facts allow to get rough view about the time scales of the pre-biotic evolution.

1. The origin of Earth occurs roughly 4.5 Ga (Ga=billion years ago). Bombardment phase, that is the period of large scale impacts, ended roughly 4-3.8 Ga.

2. ^{12}C enrichment is seen as a signature of photosynthesis. By this criterion the oldest known micro-fossils date back to 3.5 Ga and are found in volcanoes. There is a hot debate going on about whether these micro-fossils are really genuine micro-fossils. For instance, they are accompanied by complex quartz structures and this does not conform with what one might expect.

3. Levels of atmospheric oxygen began to increase during second half of precambrian era (2 Ga) and reached 10 per cent level at the eon's end at 1 Ga.

4. There are not many fossils or fossil bearing rocks from the precambrian eon. The simplest explanation is that the precambrian fossils have been soft bodied. Abundant fossils appear at Cambrian period which started .55 Ga. Cambrian explosion meant emergence of extremely rich spectrum of various life-forms.

5. The time interval between bombardment phase and the emergence of the first micro-fossils is only .3 billion years. This means that the time window for the life to develop on the surface of Earth is surprisingly narrow, and one can ask whether the primordial life could really have developed spontaneously in the environement provide by the surface of young Earth.

10.2.2 Standard approaches are mechanistic

Various hard science approaches to the pre-biotic evolution share a common philosophy dating to the beginning of the previous century. This philosophy is reductionistic materialism according to which life can be explained as a purely mechanistic phenomenon which just happened to occur by change ("change and necessity" using the phrase in the title of the classic of Monod). This view is highly questionable and certainly in dramatic conflict with more modern views relying on macroscopic and even astrophysical quantum coherence as basic elements.

At the experimental level the failure of mechanistic approach is easy to see. The components of cell inside test tube do not form a living system. The numerical simulations using computer models have demonstrated convincingly that spontaneous emergence of life is not possible. Empirical facts support completely different conclusion: the emergence of life is unavoidable and occurs everywhere in the universe, and there are good reasons that it has some universal characteristics. The challenge is to develop the conceptual framework so that it can explain this naturally.

10.2.3 The notion of primordial ocean

The following discussion uses basic facts which I have learned from articles of Chris King [174] representing updated view about facts and theories about pre-biotic evolution as well as articles criticing the existing theories [125, 172] .

The generation of biomonomers requires the presence of C, H and O. During 1920′s Oparin and Haldane independently proposed that life, or its chemical precursors including amino-acids, formed spontaneously under the conditions associated with primordial atmosphere. Genetic code was not yet known, and both Oparin and Haldane believed that life evolved from proteins, and that life's

precursors including amino-acids were formed spontaneously in a reducing atmosphere whose principal components where CH_4 and/or CO_2, NH_3, and H_2O.

Oparin suggested that methane served as the source of carbon whereas Haldane believed that the source was CO_2. Oparin also suggested that what he called coacervatives were precessors of the cell. Haldade thought that the gradual increase in the complexity of pre-biotic molecules in the presence of UV radiation led automatically to the generation of a protocell.

The assumption that the atmosphere is reducing is essential: the presence of oxygen would be fatal for the biomonomers. This assumption can be however questioned. The primordial atmosphere was due to the outgassing associated with volcanic eruptions but aund volcanic fumes the atmosphere is oxidizing which means that biomonomers would have been rapidly destroyed by oxidation. Interestingly, the photographs of Earth taken during the Apollo 16 mission allow to conclude that a gigantic cloud of hydrogen, extending 40,000 miles into space surrounds the Earth. The only source of hydrogen can be water vapour, bombarded by high energy UV light rays above ozone layer [115] . If this water has been there during the primordial period, the atmosphere must have contained oxygen so that the basic assumption would be wrong.

Even if the atmosphere was reducing, one encounters a problem. There would have been no shield against UV radiation which according to [125] would have dissociated COOH whereas CH_4 and heavier hydrocarbons would have polymerized forming an oil slick 1-10 deep over the surface of the Earth. Ammonium would have photo-dissociated into nitrogen and hydrogen so that the conditions of the experiments of Miller [34] and others to be discussed below would not been satisfied.

10.2.4 Urey-Miller experiment

Urey-Miller experiment [34] meant a dramatic step of progress on the experimental side, and for a along time it was believed to be conform the vision of Oparin and Haldane. The experiment involved a reducing atmosphere and electric sparks simulating the effect of lightnings. In the later experiments 19 of 20 amino-acids were identified. Also nucleosides A, G were produced. Cyanoacetaldehyde together with urea believed to be accumulated to primordial ponds, allowed to generate U and C as was discovered by Miller 40 years after his classical experiment. These impressive results were interpreted as a support for the view about primordial ocean as a "dilute soup" of organic molecules which precipitated out of the atmosphere.

For a long time it was believed that the synthesis of ribose necessary for the generation of RNA was impossible in these circumstances. It turn out that ribose was generated from glyseralhehyde phosphate in presence of COOH [128] . Glyseraldehyde phosphate was generated also in Miller's experiments. In case of deoxiribose necessary for DNA no plausible synthesis mechanism has been identified.

Organic compounds (in particular A, U, C, G) and even membrane forming products are present in carbonaceous chondrites (meteorites). Chondrites are essentially what the Earth is made of. Galactic gas clouds contain sugars, amino-acids, nucleic acids. In an experiment of Dworkin and his colleagues [138] thin ice at temperature of 10 K containing H_2O, ammonia, CO, CO_2 methanol was located in vacuum and bombarded by UV radiation to mimick the situation prevaling in the interstellar space. Contrary to expectations, hundreds of different complex organic molecules appearing also in meteorites were generated. Thus it seems that the molecules generated by pre-biotic evolution appear everywhere in cosmos but ironically, the environment provided by the surface of young Earth's does not seem to favor the pre-biotic evolution.

10.2.5 RNA world

One of the basic questions in theorizing about pre-biotic evolution is which came first: proteins, nucleic acids or both or possibly something else. The vision known as RNA world [168, 158] is dominating the stage at this moment. It is assumed that RNA polymers serve all the basic functions associated with DNA, RNA and amino-acids. These functions are based on genetic and catalytic capacity of RNA. Later a genetic takeover occurred involving the emergence of DNA and genetic code in which amino-acids replaced RNA somehow.

One can represent good experimental justifications for the RNA world vision (for the summary and for references the article of Chris King [174] is recommended warmly).

1. Ribose can be synthetized in the same circumstances as amino-acids and nucleosides. The presence of kaolinite clays and volcanic magmas stabilizes RNA polymerization. When montmorillonite, a positively charged clay believed to exist copiously in young Earth, was added to a solution of negatively charged amino-acids, a solution of RNA nucleotides gave rise to RNA 10-15 nucleotides long [171] . These chains attached to the surface of the clay, and when more nucleotides were feeded by washing them with the solution, they grew up to 55 nucleotides long. It seems that reversible dehydration in a medium containing phosphates, bases and sugars provides the routes to polynucleotide formations. Besides water, Mg_{++} plays a key role in stabilizing mono- and oligonucleotides by compensating the negative charges of the phosphates.

2. RNA can form double helices and has 3-dimensional tertiary structures analogous to that of proteins so that one might expect the ability to act as catalyst. The discovery of spontaneous splicing of RNAs in living systems is possible meant a breakthrough in this respect [119] . Second crucial finding was that these RNAs could act as catalysts in transesterifications crucial for the protein synthesis [168] . Even high fidelity complementary replication of arbitrary short RNA sequences has been demonstrated [152] . Simple biological RNAs have shown to have autocatalytic self-assembling capacity. The catalytic activity hinges on various forms of proton transfer (perhaps the leakage of protons between space-time sheets is involved). RNA appears to be the agent of peptide-bond synthesis in the modern ribosome [164] and modified ribozymes are able to act as amino-acyl esterases [134] . Thus RNA seems able to serve synthetizing, transfer, messenger and ribosomal functions so that it can guide both its own replication and ordered polymerization of proteins.

3. Support for the RNA world pictures comes also from the fact that the ancient fossil nucleotide coenzymes including ATP , NAD, coenzyme A and vitamin B12 are all ribonucleotides. Eucariote organisms continue to posses massive RNA processing within the nucleus. Reverse transcriptase, whose function contradicts the Central Dogma, and encountered in retro-viruses (such as HIV), might have ancient origin. Reverse transcriptase is indeed crucial for the transition from RNA→RNA predecessor of genetic code to DNA→amino-acid genetic code in TGD framework.

10.2.6 How biochemical pathways and DNA-amino-acid code emerged?

The traditional viewpoint is that biochemical pathways have developed from some simple basic systems. This approach encounters difficulties when one tries to understand how integrated systems such as electron transport and metabolic machinery could have worked in primitive systems. TGD based solution to the problem is the universality of metabolism and other basic functions relying on super-conductivity and its breakdown by the leakage of various supra currents between space-time sheets.

Furthermore, one can also decompose the evolution to two parts corresponding to the development of genetically controlled structures and self-organizing structures not controlled genetically [41] . Chris King has formulated the same idea in a more concrete manner in his article [174] from the point of view of complex systems. According to King, the basic mechanisms developed without genetic control and were finally taken under control as the genetic takeover occurred. These kind of generic structures include proteins and nuclei acids, nucleotide coenzymes, bilayered membrane structures, ion transport and membrane excitability, membrane bound electron transport, glycolysis and the citric acide cycle. In TGD framework one can add to this list topologically quantized classical fields as universal structures.

A second open question is how DNA and amino-acids took the command. Here many-sheeted space-time provides a possible answer. DNA nucleotides are stable only inside regions containing ordered or liquid crystal water forming a macroscopic quantum phase. The transformation of DNA to RNA nucleotide requires water molecule which is not available in this kind of environment. The transition from RNA-RNA predecessor of genetic code to DNA-amino-acid genetic code is also a deep problem and here the trick might be very simple: reverse RNA transcriptase used by retro-viruses (also HIV) could have transformed RNA genes to DNA genes.

The model for the evolution of genetic code as a fusion of singlet and doublet codes in turn allows to understand the emergence of amino-acids as being due to a change in tRNA structure implying that amino-acids acting as catalyzers of the attachment of RNA to tRNA molecule began to stick to

tRNA, and were loosened only when tRNA was attached to RNA so that the used amino-acids began to form amino-acid sequences replacing RNA sequences as coded sequences.

10.2.7 Problems with the polymerization in primordial ocean

Polymerization occurs universally by dehydration in case of polynucleotides, polypeptides, polysaccharides and lipids serving as basic building blocks of living structures. The basic difficulty is that polymers are not stable in an aqueous environment. Several cures to this problem have been proposed.

1. Various mineral interfaces could serve as templates for the formation of polymers and the evaporation of water from these structures could give rise to polymers. For instance, mud flats might have made possible polymerization.

2. Fox has proposed that the heat flow from geoactive sites like hot springs, volcanic rims and submarine vents could have caused the dehydration [151] . Fox has indeed managed to show how to generate protenoids consisting of up to several hundred amino-acids possessing weak catalytic activities. The temperatures needed are typically above 100 C and somewhat too high. Archea as well as nanno-bacteria are indeed found in this kind of environments, and they utilize heat and sulphur compounds as a source of metabolic energy. The first objection is that the high temperature destroys the biological molecules in this kind of environment. Furthermore, the atmosphere around volcanoes contains CO_2 and water and only minor amounts of nitrogen, hydrogen sulfide and sulfur dioxide so that this kind of atmosphere does not give rise to the biomonomers in analogs of Urey-Miller experiments.

3. The un-stability of polymers against hydration is so serious a shortcoming for the primordial soup approach that it has inspired quite radical alternative proposals. For instance, Crick has concluded that pre-biotic life might have extraterrestrial origin. The panspermia hypothesis however only shifts the problem to the outer space. The evolution of life in intra-terrestrial environement is much less radical variant of this approach if one is ready to accept the notion of many-sheeted space-time.

4. Dr. Cairns-Smith has proposed that so called clay genes appeared as predecessors of genes [116] . For instance, Al atoms in the lattice containing Si and O can have three states at each site so that enormous information storage capacities become available. These structures would have acted as scaffolding for present day bio-molecules of RNA and DNA. This idea might create more problems than it solves. One could however turn the idea around and ask whether primitive life-forms such as nanno-bacteria could express their genetic code with the help of kaolinite clays.

To my personal opinion, an invention of a clever mechanism is probably not enough to solve the basic problem. Polymerization in modern cells is basically a process involving metabolic control, and it seems that the metabolic control must have been present from the beginning in some primitive form. TGD predicts that magnetosphere can perform quantum control in astrophysical length scales from the magnetic flux tubes of the Earth's magnetic field B_E or, rather, from the flux quanta of dark magnetic field accompanying it and having strength $B_E = 2B_E/5$. A further prediction is that metabolism is completely universal and existed in primitive form already during the primordial period. This in turn makes possible the option that the pre-biotic life need not have developed through stages differing dramatically from the recent life forms. One could even assume that a generalization of ontogeny recapitulates phylogeny principle holds true for the intracellular dynamics so that it would give precise information about pre-biotic evolution.

One must also clarify what one really means when one speaks of aqueous environment. Water allows an extremely rich variety of structures. Liquid crystal water/ordered water encountered inside cells might automatically stabilize polymers, and provide also a solution to how DNA and polymers were stabilized. Sol-gel transition giving rise to macroscopic quantum coherence would generate this liquid crystal phase.

10.2.8 The notion of protocell

The emergence of membrane bounded structures has certainly been decisive for the evolution of life. Cell membrane made possible differentiation forced by the competition for metabolic resources. Cell

membrane imports metabolics, exports waste products, and acts as a signalling system. In TGD universe the receptors at cell membrane also serve as cellular sensory receptors.

A variety of answers to the question about the predecessor of the cell has been proposed. The natural constraint is that the membrane in question results via self-organization. If one requires consistency with the generalization of ontogeny recapitulates phylogeny principle (ORP), the number of options is reduced dramatically.

1. Lipid bi-layers are certainly a natural guess since they formed spontaneously in solutions on biological conditions. There is thus a consistency with the generalized ontogeny recapitulates phylogeny principle requiring that all primordial structures appear also in modern cells.

2. An elegant an plausible candidate for protocell is the gel phase resulting in sol-gel transition inside cell [196, 174] . Gel phase has indeed many properties of cell membrane bound region and is routinely generated also inside modern cells. A compact ordered liquid crystal type phase is in question. Negatively charged proteins are generated inside the gel phase and gel phase rejects Na_+ ions and attracts K_+ ions just as cell interior. Also negatively charged proteins are stable inside gel phase. In TGD framework gel phase is a macroscopic quantum phase so that new physics is necessary involved. In particular, the evolution by quantum jumps is expected to lead to this kind of self-organized structures automatically. In TGD framework one expects that the liquid crystal/ordered water phase leads to the stabilization of RNA and that even DNA nucleotides become stable.

3. The proposal of Sidney Fox [151] is that protocells could correspond to the called micro-spheres formed from protenoids in geolocically active sites like hots springs and volcanic rims. He also demonstrated that this really occurs. Protedoids are amino-acid sequences differing from ordinary peptides in that peptide bonds are different: hence this option is not consistent with the generalization of ORP. When proteneids are washed into a warm water allowed to cool, micro-spheres are formed. Micro-spheres are bilayered structures able to divide. A concentration roughly 10 million times higher than believed to appear in primordial soup is required so that either the idea of protenoid or of primordial soup is wrong. Further objections are that micro-spheres do not perform any functions of cell, and that the structure is like an inpermeable cell wall or spore coat rather than a cell membrane [125, 172] .

The common problem of all these options is that the required concentrations of biomonomers are much higher than those expected in the primordial soup. This forces to question the notion of primordial soup and even the assumption about the occurrence of the pre-biotic evolution at the surface of Earth.

10.3 TGD based scenario about pre-biotic evolution

TGD framework leads to a radical view about life. Magnetosphere can be seen as a living system controlling the evolution of life and chicken-egg question can be seen in a totally new perspective. Super-conducting magnetosphere can be seen as a higher level life-form which controls and guides the biological evolution from the very beginning. Second key element is dark matter hierarchy.

10.3.1 Basic prerequisites

A short summary of basic requirements and problems is in order.

1. A stable star and planet providing appropriate conditions such as temperature for liquid water is needed.

2. Atoms like C, N, and O and smaller amounts of P and S giving rise to bio-monomers, and metals like Al, Fe, and Zn are the basic building blocks. The formation of various chemical bonds like hydrogen bonds, covalent bonds, and peptide bonds is necessary.

3. The formation of biological monomers (amino acids, nucleotides, fatty acids, sugars) is an essential element of life. Except for DNA nucleotides, basic monomers evolve in the circumstances simulating to what have been believed to be the primordial atmosphere. These bio-monomers are

found even in the interstellar space and in galactic clouds so that the question is not whether the pre-biotic life can develop but whether our recent day materialistic science allows to understand how it develops. The standard wisdom about primordial atmosphere as a reducing environment (containing no oxygen) indeed leads to grave difficulties. Also the concentrations in the primordial ocean seem to be quite too low for the bio-monomers to be synthesized [172] .

4. The formation of the biological polymers such as proteins, nucleic acids, lipids, and carbohydrates occurs universally by dehydration. The problem is that in water environment polymers are unstable against decay by hydration: it would seem that a metabolic energy feed is required already at this stage to guarantee non-equilibrium situation. The assembly of these macro-molecules into organized aggregates like chromosomes, micro-tubules and cell organelles suggests the emergence of symbolic representations and only a weak independence of hard facts of chemistry which makes the problem even more difficult from the point of view of standard physics.

5. The emergence of catalysts and metabolism, should be understood. Here one encounters an egg-hen problem. Standardized metabolic currency seems to be necessary for effective catalysis but metabolism according to the standard view involves extremely complex web of reaction pathways needing refined catalytic actions.

6. Membrane bound structures are essential for life and one should understand how they emerge and even predict correctly basic facts about them.

7. The emergence of the genetic code has remained a mystery in various scenarios of pre-biotic evolution.

8. How the incredible ability of the components of bio-systems to co-operate pops up from primordial soup is not always included to the list of mysteries since everything smelling "holism" is regarded as pseudo science in reductionistic circles.

10.3.2 TGD based vision about pre-biotic evolution

The prevailing mechanistic world view forces to conclude that life emerged accidentally in young Earth during a relatively short time period of about .3 billion years. On basis of extensive computer simulations, one can fairly say that a spontaneous generation of life in primordial ocean seems extremely implausible [125] .

TGD replaces materialistic view with a continual re-creation in which classical universe in 4-dimensional sense is replaced by a new one in each quantum jump. p-Adic length scale hypothesis allows to formulate the notion of evolution precisely as a generation of increasingly larger space-time sheets characterized by preferred p-adic primes meaning also a sequence of symmetry breakings. A second aspect is the emergence of new levels in dark matter hierarchy meaning great leaps in evolution. A crucially new element is the predicted fractal hierarchy of copies of electro-weak and color physics. Dark weak bosons and gluons thus become an essential part of the physics of living matter.

Macroscopic and even astrophysical quantum coherence becomes a key feature of living matter. Theory is partially non-deterministic also in classical sense but the variational principle for Kähler action implying that space-time surfaces are analogous to Bohr orbits and self-organization lead to Darwinian selection of selected patterns.

Is life really a result of accident?

Life is often regarded as an extremely improbable accident. The estimates for the probability of the formation of amino-acids, DNA, and of emergence of genetic code from random soup of molecules are indeed found to be extremely small. In TGD Universe the situation is different.

1. Intentional action is basic aspect of TGD Universe. Negentropy Maximization Principle [44] states that the dynamics of quantum jumps maximizes the information content of the conscious experience and implies evolution as a continual recreation of the Universe eventually leading unavoidably to the emergence of information rich systems and explaining also why the values of "fundamental constants" seem to be tailored for the emergence of life as we are used to identify it. p-Adic dynamics for cognitive space-time sheets implies local randomness but long range fractal correlations for the real dynamics.

2. The hierarchy of Planck constants implies macroscopic and macro-temporal quantum coherence in all length scales. Universe becomes single conscious organism in this framework. This has many implications. For instance, low frequency photon can have arbitrarily high energy. This makes it possible control of short length and time scales by the dynamics in long scales, say by EEG. The enormous values of gravitational Planck constant for dark matter and the assumption that visible matter condenses around dark matter imply that planetary orbits correspond to Bohr orbits [65, 51] . Only very few orbital radii are possible and for a star with mass around solar mass planets at distance of Earth are possible and probable irrespective of the mass of the planet. Hence solar systems are standardized to high degree. Also the quantization of masses of stars is highly suggestive and the number of stars with mass not far from solar mass is large. Obviously this raises the probability for having Earth like environments dramatically.

3. TGD based nuclear physics [1] , [1] explains cold fusion [6] , [14] as well as biological nuclear transmutations for which there is considerable empirical support [5] . The direct empirical evidence comes from the observation that the abundances of heavier elements in an astrophysical object at distance of order 10 billion light years are essentially the same as in solar system [7] . If elements are created only in the stellar interiors, the abundances should be much smaller. This suggests that the heavier elements result by cold fusion in the interstellar space. The implication is that environments allowing life have existed much earlier than believed hitherto.

4. The hierarchy of Planck constants and the notion of magnetic body allow a mechanism of topological quantum computation [26] based on the representation of braids represented as flux tubes of wormhole magnetic field whose presence might provide a definition for what it is to be living. The first implication is an explanation for the miraculous ability of biomolecules to find each other in terms of the reduction of Planck constant inducing a shortening of the flux tubes connecting reactants and catalysts. The structure of flux tube patterns connecting various molecules allows to program complex series of biochemical reactions to the structure of braids connecting the molecules since given spots of molecules can be forced to meet each other in reaction. Conserved braid color allowing to identify whether the braid strand comes from A,T,C or G implies even stronger selection rules. One can assign also to amino-acid a 3-braid corresponding to one of the DNA codons coding for it. These extremely selective interactions between living bio-molecules give good hopes of understanding why DNA and amino-acids were selected as molecules able to co-operate.

5. Many-sheeted space-time concept implies the existence of fundamental metabolic energy currencies [6] defined by the differences of zero point kinetic energies of particles for space-time sheets labeled by different value of p-adic prime p. The existence of standardized metabolic currencies simplifies the situation dramatically and living matter must face only the problem of storing metabolic energy. Plasmoid like life forms suggest themselves as predecessors of biological life. p-Adic length scale hypothesis $p \simeq 2^k$ is what implies standardization of zero point kinetic energies and follows from zero energy ontology which also assigns to a particle labeled by prime p a time scale $T_p = \sqrt{p}L_p/c = L_p(2)/c$ characterizing the temporal size of the space-time sheet having particle and its negative energy counterpart at its time-like boundaries. The fact that the fundamental 10 Hz biorhythm corresponds to the time scale assignable to electron suggests that fundamental biological time scales are hidden in the space-time structure of fundamental particles.

The notions of magnetic body and plasmoid

The model of high T_c super-conductivity and the general vision about dark matter hierarchy have led to a rather precise model for magnetic body as an intentional agent utilizing biological body or its part as motor instrument and sensory receptor [23] . Dark matter plasmoids and plasma oscillation patterns as representations of control commands are one important aspect of the model. The prediction is that plasmoids should have been predecessors of ordinary life forms. There is laboratory evidence that plasmoids behave like life forms [183] . Very high temperatures catastrophic for ordinary life forms could prevail at magnetic flux quanta associated with plasmoids. This forces a radical reconsideration of the question how pre-biotic life have evolved and forces to ask whether even the hot interior of Earth could have served or still serve as a seat of life.

Does the Earth's magnetic field have a dark counterpart?

The notion of dark matter as a hierarchy of phases characterized by arbitrarily large values of Planck constant has established itself as a part of TGD [27, 23] . This raises several questions. For instance: does the magnetic body of Earth have a dark counterpart and its the dark magnetic body relevant for functioning of living matter?

A partial answer to this question came from a frustrating realization that I had for years erratically believed that the magnitude of the magnetic field assignable to the biological body is $B_E = .5$ Gauss, the nominal value of the Earth's magnetic field. Probably I had made the calculational error at very early stage when taking Ca^{++} cyclotron frequency as a standard. I am grateful for Bulgarian physicist Rossen Kolarov for pointing to me that the precise magnitude of the magnetic field implying the observed 15 Hz cyclotron frequency for Ca^{++} is .2 Gauss and thus slightly smaller than the minimum value .3 Gauss of B_E. This value must be assigned to the magnetic body carrying dark matter rather than to the flux quanta of the Earth's magnetic field. This field value corresponds roughly to the magnitude of B_E at distance 1.4R, R the radius of Earth.

Dark matter hierarchy leads to a detailed quantitative view about quantum biology with several testable predictions [23] . In principle all integer and even rational values of Planck constant are allowed. Number theoretical arguments suggest a general formula for the favored values of $r \equiv \hbar/\hbar_0$ [27] as $r = n_1^{\pm 1} n_2^{\pm 1}$, where n_i characterizes the quantum phase $q = exp(i\pi/n_i)$ characterizing Jones inclusion [83] . The values of n_i for which quantum phase is expressible in terms of squared roots are number theoretically preferred and correspond to integers n expressible as $n_i = 2^k \prod_n F_{s_n}$, where $F_s = 2^{2^s} + 1$ is Fermat prime and each of them can appear only once The lowest Fermat primes are $F_0 = 3, F_1 = 5, F_2 = 17$. The prediction is that also r-multiples of p-adic length scales are possible as preferred length scales.

TGD inspired quantum biology and number theoretical considerations suggest preferred values for $r = \hbar/\hbar_0$. For the most general option the values of $\hbar$ are products and ratios of two integers n_a and n_b. Ruler and compass integers defined by the products of distinct Fermat primes and power of two are number theoretically favored values for these integers because the phases $exp(i2\pi/n_i)$, $i \in \{a, b\}$, in this case are number theoretically very simple and should have emerged first in the number theoretical evolution via algebraic extensions of p-adics and of rationals. p-Adic length scale hypothesis favors powers of two as values of r.

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1+i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that all the four p-adic length scales sith $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm) define scaled up copies of electro-weak and QCD type physics with ordinary value of $\hbar$ and that these physics are induced by dark variants of corresponding lower level physics leads to a prediction for the preferred values of $r = 2^{k_d}$, $k_d = k_i - k_j$, and the resulting picture finds support from the ensuing models for biological evolution and for EEG [23] . This hypothesis - to be referred to as Mersenne hypothesis - replaces the earlier rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant.

In the case of magnetic flux simplest quantization suggests the scaling $B \to B/r$ for the magnetic fields. This is assumed to hold true also in more general case when the quantization condition reads as $\oint (p - ZeA)dl = n\hbar$ and involves currents flowing at the boundaries of flux quanta so that magnetic flux need not be anymore quantized to a multiple of Planck constant. For axonal membranes the flux quantition with $n = 0$ is natural since the size of flux quantum does not depend on the value of Planck constant. Assuming flux quantization and standard value of Planck constant $B_{end} = .2$ Gauss would give flux tube radius $L = \sqrt{5/2} \times L(169) \simeq 1.58 L(169)$, which does not correspond to any p-adic length scale as such.

Concerning the interpretation of B_{end} there are two options. It could correspond to a personal magnetic body or to a dark variant of the Earth's magnetic field. At this moment it is impossible to say which if any hypothesis is right. However the fact that the ELF fields have no direct effect on conscious experience mildly supports the identification as the dark variant of B_E.

Emergence of symbols at molecular level and new view about hydrogen bond, water, and bio-catalysts

The hierarchy of dark matter leads to novel ideas about what distinguishes living matter from ordinary matter. The emergence of symbols and symbolic dynamics and what might be called "molecular sex" could be a fundamental step in the process and I have considered two visions for how this would take place.

1. First vision

First vision is relies on the model of DNA as tqc based on braids and has quite close contact with empirical reality [6, 26] . In this case DNA nucleotides are analogous to colors of braid strands and base pairing corresponds to molecular sex for DNA molecules. The color of braid strand implies long ranged highly selective interactions between DNA and distant molecules, such as lipids of the lipid layer of cell membrane or amino-acids. Free amino-acids inherit the colors of the first two nucleotides in the codon XYZ whereas the color of the third nucleotide corresponds to a quantum superposition of colors for codons coding for the amino-acidthis defines the quantum counterpart of wobble base pairing. Amino-acids can be divided into amino-acids and their conjugates analogous to opposite sexes and generalized base pairing determines the interactions of the amino-acids to a high degree. Hydrogen bond can be identified as a special case of flux tube. There are also flux tubes connecting acceptors of hydrogen bonds acting as plugs in the connection lines formed by the magnetic flux tubes and Y corresponds to this kind of plug at the level of amino-acids.

2. Second vision

The mathematical realization for the hierarchy of Planck constants leads to a generalization of the notion of imbedding space and this leads to four kinds of phases resulting as combinations of phases with increased or reduced unit of spin and quantum numbers associated with CP_2 degrees of freedom. Each phase corresponds to its own Planck constant and is characterized by a discrete symmetry group.

Especially interesting are phases with large value of Planck constant involving charge fractionization and increase of spin unit. The electrons of free electron pairs of aromatic cycle are reasonable candidates for dark electrons of this kind. One can consider variants of hydrogen atom containing $n \leq N$ fractionally charged electrons with with lepton number and electronic charge equal to n/N. The values n/N and $(N-n)/N$ for the fractional charge would correspond "name" and "conjugate name" since their combination would give a maximal charge and a state analogous to a full electron shell. Thermal stability poses strong constraints since atomic and molecular energy scales are reduced as Planck constant increases.

The notion of fractional electron inspires the notion of "half" hydrogen bond for which electron has a fractionized fermion number. The full hydrogen bond would be formed in the fusion of half hydrogen bonds and give rise to a structure analogous to a full electron shell expected to be especially stable. Catalyst sites might correspond to half hydrogen bonds and the basic recognition mechanism could be the fusion of half bond and its conjugate to form a full hydrogen bond. One could speak about "molecular sex". The sequences of half bonds would represent words so that molecules would have names. Also interpretation as quantum computer codes might make sense. The problem of this vision is the lack of direct contact with experimental facts and for this reason it will not be discussed in the sequel.

Universal metabolic currencies

In TGD framework a primitive many-sheeted metabolism is present from the beginning and becomes only refined during evolution. Most importantly, metabolic currencies identified as zero point kinetic energies liberated as particles drop to larger space-time sheets are constants of nature by the p-adic length scale hypothesis.

Phosphate-sugar polymers form the backbone of nucleic acids and metabolism is based on ADP and ATP formed from adenine and phosphate ions. It has been already earlier found that the generation of ATP and its metabolic utilization involve the flow of protons between the atomic space-time sheets and some larger space-time sheets, say magnetic flux tube of Earth [37]). It will be found that this mechanism is involved also with the dehydration leading to polymerization and phosphorylation. The reversal of this process also implies the in-stability of DNA in an ordinary aqueous environment.

The interpretation of the role of phosphate ions as metabolic energy batteries seems to be wrong in TGD framework: the main function of negatively charge phosphates would be to make bio-polymers critical against local modifications making them thus ideal for catalytic manipulations. Even deeper function would be the role as standard plugs to which magnetic flux tube can attach and which second flux tube can begin. $ATP \rightarrow$ADP would in this framework mean reconnection process for a magnetic flux tubes modifying the hardware of tqc.

Time mirror mechanism, intentional action, memory, and remote metabolism

Time mirror mechanism having negative energy MEs as space-time correlate has phase conjugate laser waves as standard physics counterparts. Essentially negative energy signals propagating to the geometric past and reflecting back is in question. Intentional action realized in terms of negative energy signals to the geometric past and appearing already at the level of molecular magnetic bodies, is expected to become an increasingly important when the complexity of the structures increases. The charge entanglement by negative energy W MEs is especially interesting control mechanism and makes also possible sharing of mental images. Time mirror mechanism allows also remote metabolism by inducing the dropping of population inverted system to the ground state liberating in this manner positive energy photons received by the sender of negative energy signal. What makes this mechanism so elegant is its enormous flexibility (credit card is the counterpart in economy). Time mirror mechanism provides also a mechanism of memory as communications with the geometric past.

Emergence of membrane bounded structures

Self-organization in many-sheeted space-time is expected to automatically lead to the generation of the ordered water phases which would have evolved to the gel phase defining in turn a natural predecessor of the membrane bounded structures. Self-organization would have also led to the emergence of membrane structures containing liquid crystal water stabilizing also DNA nucleotides.

In fact, the TGD inspired model for high T_c super-conductivity as quantum critical super-conductivity involving simultaneously two kinds of super-conductivities in a narrow range of temperatures around critical temperature (presumably $T \simeq 37$ °C) predicts correctly the double-layered structure of cell membrane and the length scales involved [12, 13] . A fractal hierarchy of super-conductivities and cell membrane like structures is predicted corresponding to the dark matter hierarchy and p-adic length scale hierarchy [23] . Josephson junctions and corresponding Josephson currents are in a crucial role in the model for the hierarchy of generalized EEGs responsible for the communication to and control by magnetic body.

According to unexpected findings about behavior of the cell membrane [196] discussed from TGD viewpoint in [57] , the usual picture based on pumps and channels for ions is not correct. Rather, cell interior is in gel phase in which water is in structured phase around charged bio-polymers intermediate between ice and water. One implication of this is stabilization of RNA and DNA polymers since hydrolysis is impossible due to the lack of free water molecules. Cell membrane would have guaranteed the long term stability of gel phase.

Second function of the membrane like structure consisting of lipids or perhaps even DNA or RNA molecules could relate to the topological quantum computation and memory in the manner discussed in [26] . The phase transitions changing the length of the wormhole magnetic flux tubes defining the braid strands and making possible tqc would also make possible biocatalysis via reconnection of flux tubes and via $\hbar$ changing phase transitions changing the length of flux tube.

In this framework water and lipids molecules playing the role of lipids could have been present in very early stage since they emerge as a result of self-organization process and are not genetically determined.

Did life evolve in Mother Gaia's womb?

The proposed framework poses strong conditions on pre-biotic environment and one ends up to to interpretations for the notion of Mother Gaia's womb, which are by no means mutually exclusive.

1. Mother Gaia's womb as underground seas?

Braiding in the proposed sense requires the presence negatively charged polymers and membranes consisting of lipids or their analogs. Water seems to be necessary but also gel phase is needed since

free water induces depolymerization. The coherent structure of gel would be due to the braiding of distant molecules. The phase transitions of gel phase are good candidates for a basic mechanism of bio-control and would stabilize these polymers via the formation of structured water around them preventing hydrolysis. The developing life forms should be shielded from UV radiation and meteor bombardment.

The combination of these constraints leads to the idea that life as we define it could have evolved in the womb of Mother Gaia in underground seas with the Earth's crust shielding from UV and meteors. The necessary ingredients of biomolecules, in particular phosphates making possible phosphorylation making DNA and RNA charged and appearing also in hydrophilic ends of phospholipids, would have dissolved to the water from the ground. Cambrian revolution would have meant the burst of these highly developed life-forms to the Earth surface and resulting as a phase transition increasing the value of Planck constant for Earth's space-time sheet by a factor of two would have occurred. This would also provide a justification of Expanding Earth theory explaining the strange finding that the continents fits nicely together to form a single super continent covering entire Earth's surface if the radius of Earth is one half of its recent value and actually the same as the recent radius of Mars, which is now known to contain reservoirs of underground water.

2. Mother Gaia's womb as mantle-core boundary?

What about the period before the life in underground seas?

1. The plasma like aspects of cytoplasm suggests that some kind of plasma phase must have been present. Also the postulated Bose-Einstein condensates of bosonic ions at dark magnetic flux quanta represent kind of quantum plasma.

2. Plasmoids involving magnetic flux tubes and charged particles could have been predecessors of more complex molecular life forms and could have developed in the interstellar space. Their metabolism could have been based on universal metabolic energy quanta. Simple metabolic cycles and short term chemical storage of energy based on fusion and decay of simple molecules induced by say UV radiation from the nearby stars might have developed during this era. Quite high temperatures can be considered so that after the interstellar period this kind of life forms could have survived and developed in the hot interior of planets receiving their metabolic energy from radiation by high temperature plasma. A possible candidate for the womb of Mother Gaia is the mantle-core boundary, where intensive self-organization processes are expected to take place.

3. Ultimately the charged molecules must have come in contact with ordinary water in underground seas. One can imagine that the polymerization of the charged molecules and the formation of structured water around them stabilizing them and giving rise to a gel phase took place simultaneously in presence of metabolic energy feed.

The primordial womb containing plasmoid like life forms could have been located somewhere below the boundary at which $k = 137$ atomic space-time sheets transform to very hot $k = 131$ space-time sheets: this should occur when the thermal de Broglie wave length becomes equal to the p-adic length scale $L(131)$. The transition occurs above the crust-mantle boundary (1300 K). Mantle-core boundary (4000 K) is a good candidate for a seat of high-T life forms.

The dropping of O, C, N ions from the hot $k = 131$ space-time sheets to larger space-time sheets generates light at visible frequencies replacing solar light so that even intra-terrestrial counterpart of photosynthesis could develop. The dropping of oxygen atoms could make also possible development of oxygen based metabolism.

Magnetic flux quantum structure of the magnetosphere acting as a nervous system and a metabolic circuitry of the magnetic Mother Gaia could make possible controlled metabolism already during the pre-biotic period and allow to circumvent these difficulties.

Model for the genetic code

The emergence of genetic code is one of the basic mysteries of models for pre-biotic life. The exact A-G symmetry and slightly broken T-C symmetry of the genetic code strongly suggest that the evolution of the triplet code occurred as a fusion of singlet and doublet codes. One ends up with a detailed

model for how this happened by studying the structure of tRNA molecule carrying in its fossilized parts detailed information about the evolution of the code.

Nanno-bacteria [153, 131] might correspond to some predecessor of the recent genetic code. Nanno-bacteria accompany mineral structures and actively manipulate them: this conforms with the view that mineral interfaces have been indeed important for the evolution of polymers.

Introns are the basic mystery of DNA. TGD predicts that language is a universal phenomenon appearing at level of eukaryotes. Memes represented as sequences of 21 DNA triplets and expressing themselves as field patterns associated with MEs would realized this universal language.

What makes possible the coherence of bio-chemical activities?

In TGD Universe the control of genome by magnetic body relies on magnetic flux sheets traversing through DNA strands [41, 23] . The model implies a generalization of the notion of gene. Super-genes correspond to sequences of genes inside single organism belonging to single magnetic flux sheet and organize like text lines at a page of a book. The expression of super-genes as an intentional action of magnetic body occurs therefore coherently at the level of entire organs. This explains to the miraculous coherence of bio-chemical activities at the level of single organism. Also hyper-genes involving genomes of several organisms, not necessary belonging to even same species, become possible. Collective gene expression at this level makes possible the development of co-operation and social structures and are predicted to be present already at the bacterial level.

Braiding defined by magnetic flux tubes of their wormhole counterparts carrying dark variants of charged particles seem to represent especially important part of the magnetic body and this leads to models of topological quantum computation and bio-catalysis.

10.3.3 Pre-biotic chemistry and new physics

The emergence of symbolic representations at dark matter level is certainly the most fascinating possibility suggested by dark matter hierarchy.

Overall view

The most important implications can be deduced readily.

1. The dropping of ions and atoms between space-time sheets involves a liberation of zero point kinetic energy. By p-adic length scale hypothesis these energies define a fractal hierarchy of universal metabolic currencies which have not changed at all during evolution and are the same in the entire universe. The presence of the metabolic machinery from the beginning helps enormously in the attempts to understand how life has evolved.

2. Chiral selection resulting in bio-polymers having a definite handedness is a deep mystery in standard physics framework. TGD predicts entire hierarchy of standard model physics meaning scaled up variants of electro-weak and color physics and dark variants of these. The hierarchy of dark weak gauge bosons predicted by TGD imply strong parity breaking effects in arbitrarily long length scales above atomic length scales, and the presence of the chiral selection supports the view that also dark weak bosons play key role in bio-control. Indeed, charge entanglement generated by W MEs would be in central position in TGD based model for how magnetic bodies control biological bodies.

3. The emergence of life means emergence of symbolic representations (including names), and also what might be called "molecular sex". Formation of wormhole magnetic flux tubes between biomolecules having quark pair and its conjugate is an attractive candidate for this process and means coding of DNA nucleotides to quarks and antiquarks appearing as dark matter at the flux tubes. This leads to a new view about bio-catalysis based on the temporary dropping of the liberated proton to a larger space-time sheets and ensuing liberation of metabolic energy quantum kicking the complex formed by reactants over the potential wall separating it from the final state. A new view about water and its role in bio-catalysis emerges. Stability considerations allow a general model for how first bio-polymers able to replicate emerged.

Dark matter and the emergence of symbolic representations at molecular level

The most important new physics element of pre-biotic chemistry has been already discussed and corresponds to the presence of dark matter hierarchy suggesting new views about hydrogen bond, water, and catalytic action. A highly attractive hypothesis is that symbolic representations at molecular level in the sense that quarks and antiquarks code for DNA nucleotides [26] and also for amino-acids [3] .

Evolution of pre-biotic chemistry as a sequence of bifurcations

In his article "Biocosmology" [174] Chris King discusses biochemistry from the point of view of mathematician using the notions of symmetry breaking and bifurcation. This discussion allows for a physicists to get a wider perspective to the complexities of biochemistry. In the following I modify the arguments of King to TGD framework. The first basic new element is that generation of new space-time sheets corresponds to a sequence of symmetry breakings.

Besides hydrogen C, N, and O atoms with charges 6, 7, and 8 are the most important elements appearing in basic bio-monomers. The bonds with hydrogen are formed between 1s and $2p^3$ orbitals. The covalent bonds between C, N, and O atoms are the bonds appearing in various bio-monomers like ribose. Also peptide bonds between C and N in amino-acid sequence are covalent bonds. In standard chemistry one can characterize the atom in given molecule by its electronegativity telling how effectively it attracts electrons.

Electronegativity increases in the sequence C, N, O so that the bonds are more and more polar. Also Si, P, and S in the next row of the periodic table form covalent bonds but the bond energy tends to be lower which reflects itself as lower boiling points. For instance, the boiling point of H_2S is below the freezing point of water). Consider now the bifurcations.

1. Polar-non-polar bifurcation is fundamental in biology. Non-polar molecules are hydrophobic and are not water-soluble whereas polar molecules are hydrophilic and water-soluble. For instance, the formation of biological membranes is based on hydrophobic character of the second ends of lipids. A rough characterization of amino-acids is by polar-non-polar dichotomy. Also DNA base stacking is based on polarity.

2. Second bifurcation corresponds to acid-base dichotomy. Acids are able to act as donors of positive and bases donors of negative charge. For instance, this allows to classify polar amino-acids to acidic and basic ones. A working hypothesis worth of studying is that many-sheeted physics is involved in the sense that the protons in acid and electrons in base have dropped to some larger space-time sheet from the atomic space-time sheet.

3. The third bifurcation corresponds to that between second and third row of the periodic table that is Na^+-K^+ and Mg^{++}-Ca^{++} bifurcations. The covalent bonds involving K and Ca are in general weaker. Na^+ concentration is higher outside cell whereas K^+ concentration is higher inside cell. Same applies to gel phase, a possible predecessor of cell membrane bound regions. Mg^{++} acts as stabilizer of polymers and Ca^{++} ions are key players in cellular and intracellular control. In particular, Ca^{++} waves appear in extremely wide range of frequencies and conduction velocities.

4. The fourth bifurcation corresponds to the d-orbital elements forming a catalytic group. Almost all transition elements Mn, Fe, Co, Cu, Zn are essential biological trace elements, promote pre-biotic synthesis and are optimal in their catalytic ligand-forming capacity and valency transitions. For instance, Zn^{2^+} catalyzes RNA polymerization in pre-biotic synthesis and occurs in both polymerases and DNA binding proteins.

5. The fifth bifurcation corresponds to chiral symmetry breaking not easy to understand in standard model predicting extremely small parity breaking. There is empirical evidence such as circular polarization of light from the region of star formation in the constellation of Orion suggests that parity breaking occurs also in interstellar space. Also the amino-acids in Murchison meteorite were found to be dominantly left handed.

In TGD Universe the interpretation of bifurcations is not quite the same as in the world obeying standard chemistry.

1. The polar-non-polar bifurcation corresponds to hydrophilic-hydrophobic dichotomy. The model for protein folding and bio-catalysis relies on the hypothesis that wormhole flux tubes connect conjugate amino-acids. This process is analogous to base pairing. Stating it roughly, amino-acid and its conjugate correspond hydrophilic and hydrophobic amino-acid. This bifurcation is thus important from the point of view of molecular symbolism and bio-catalysis if is based on the coding of DNA are nucleotides and amino-acids by quarks and antiquarks at the ends of wormhole magnetic flux tubes connecting them to other molecules. The emergence of wormhole magnetic flux tubes could be seen almost as a definition of emergence of life. This might have happened already during prebiotic molecular evolution if water molecules have been present from the beginning.

2. Acid-non-acid bifurcation brings in protons and there is obviously a connection with the role of protons in the basic mechanisms of metabolism and catalysis. What is also essential is the role of negative charge of bio-polymers making bio-polymers critical against local deformations so that a wide repertoire of catalytic actions using $\hbar$ changing phase transitions of wormhole magnetic flux tubes and their reconnections becomes possible. Phosphate ions would not serve as batteries of metabolic energy but make bio-polymers sensitive to catalytic actions.

3. Fifth bifurcation is difficult to understand in standard physics framework but is consistent with the presence long ranged weak fields predicted by TGD and possibly associated with dark matter. This bifurcation is not the last one in TGD Universe since already plasmoids identified as rotating magnetic systems break parity because the sign of the charge density generated by the induced radial ohmic current depends on the orientation of rotation and only the second orientation is favored energetically. W MEs induce charge entanglement giving rise to plasma oscillation patterns in turn inducing various physiological waves. This mechanism can be used as a control tool by magnetic bodies at various levels of hierarchy. Long range weak forces due to the exotic ionization of atomic nuclei could provide a tool for controlling conformations of nucleic acid polymers. Same applies to kaolinite clays consisting of Al, Si, O suggested to be of biological importance (Al can have three different states at a given lattice site): in this case the state of Al atoms in the lattice might be manipulated using weak forces.

4. The hierarchy of bifurcations defines also a hierarchy of decreasing cyclotron frequencies. The cyclotron frequencies would be associated with both with Bose-Einstein condensates of ordinary and exotic bosonic ions at magnetic flux sheets. For the bosonic ions cyclotron frequencies in the $B_{end} = 2B_E/5$ are in alpha band and in TGD Universe they play a fundamental role in communications to and control by magnetic body using hierarchy of generalized EEGs. Ca^{++} and other waves associated with bosonic ions are of special importance in the bio-control by magneticbody using plasmoids and plasma oscillation patterns.

What selected the bio-molecules?

The extremely low probabilities for the selection of bio-molecules from a super-astrophysical number of alternatives represents one of the bottleneck problems of biology relying on the prevailing view about biochemistry. The notion of braid could resolve this problem.

Suppose that the presence of braids distinguishes between living and dead matter, that the four nucleotides are mapped to colored braid strands (that is to 2 quarks + 2 anti-quarks), and that a given amino-acid is mapped in a non-deterministic manner to one of the 3-braids associated with the DNA triplets coding for it. Braids could be associated besides DNA, amino-acids, and lipids also to other bio-molecules and define more general analogs of genetic codes as correspondences between bio-molecules able to react.

The implication would be that the step of catalytic reactions bringing together the catalyst and reactants would occur by a temporary reduction of Planck constant only for subsets of bio-molecules connected by braid strands and the pattern of braid strands involved would define the geometro-dynamical pattern of the reaction. The outcome would be a selection of very restricted subsets of bio-molecules able to form reaction networks and of reaction pathways. This would imply Darwinian selection of subsets of bio-molecules able to co-exist and dramatically enhance the probability for the emergence of life as we know it.

One challenge is to predict what kind of braids can begin from a given bio-molecule, say nucleotide or amino-acid. The physicist's guess would be that the (electromagnetic only?) interaction energy between bio-molecule and given pattern of wormhole contacts having quark and anti-quark at its throats should select the preferred braids as minima of the interaction energy. How closely the presence of hydrogen bond relates to this is also an interesting question.

Polymerization, dehydration, phosphorylation, and new physics

The generation of phosphate polymers and polymers in general occurs by dehydration which quite generally seems to involve dropping of a proton to larger space-time sheet and liberation of metabolic energy quantum. It is interesting to find how one could understand these processes in TGD framework. Since the notion of wormhole magnetic flux tube playing a central role in the model of DNA as topological quantum computer and in the model of bio-catalysis, it is natural to look whether the basic steps of these processes could be understood in this conceptual framework.

1. $ATP \to ADP$ process

AMP, ADP , ATP are phosphorylated RNA nucleosides [5] and the hydrolysis of ATP to ADP [9] plays a key role in the metabolism. Obviously also the molecules XMP, X=U,C,G are important biologically. Each PO_3 in ATP corresponds to one unit of negative charge except for the last one which carries two units of negative charge. According to the standard chemistry $ATP \leftrightarrow ADP$ corresponds to the hydrolysis

$$ATP^{4-} + H_2O \leftrightarrow ADP^{2-} + P_i$$

where P_i denotes orthophosphate HPO_4^{-2}. In ADP the last phosphate group is $HO - PO_2^{-2}$ rather than $O = PO_2^{-2}$ as in the case of ATP .

The actual process is however much more complex than this.

1. The process involves several steps such that energy is liberated in two steps in which the change of Gibbs free energy is $\Delta G = .42$ eV and $\Delta G = .31$ eV making altogether .73 eV, which should closely relate to the liberated metabolic energy.

2. Three protons are accelerated in electric field during the generation of ATP . The interpretation would be in terms of driving of electrons from larger space-time sheet to $k = 137$ atomic space-time sheet. If the larger space-time sheet corresponds to $k = 139$, the increment of the zero point kinetic energy of proton is $(1 - 1/4) \times \times E_0(137) = .375$ eV for $E_0(137) = .5$ eV of metabolic energy quantum. Three protons would give net zero point kinetic energy increment of 1.125 eV which is higher than $\Delta G_{tot} = .73$ eV. The explanation of the discrepancy should relate to Coulombic binding energy of protons with ATP and F_1. This interpretation conforms with the observation that the liberated energy is higher for the third proton.

Consider now a more detailed model for the process. The binding of ATP to the catalytic site involves several steps.

Step 1: The binding $ATP + F_1 \to$ATP$\cdot F_1$ to the catalyst site is a complex process involving the break-up of the hydrogen bonds between cellular water and ATP molecule and cell water and catalyst site and generation of hydrogen bonds between catalyst site and ATP molecule. In TGD framework this means that protons can be kicked to and dropped back from atomic space-time sheets. Only the net number of protons dropped however matters.

This process involves liberation of Gibbs free energy about $\Delta G_{ATP} = .42$ eV. It was earlier believed that this energy is liberated instantaneously but the findings about the behavior of the F_1 motor coupled to dissipative load, lead Oster and Wang to suggest that the process is more complex and starts from a loose binding and ending up to a strong binding [190] .

Step 2 Hydrolysis: $F_1\cdot$ATP$\to$ $F_1\cdot$ADP$\cdot P_i$. The change of free energy is small during this step: $\Delta G \sim 0$.

Step 3: Ortophosphate is released from the catalyst site: $F_1\cdot$ADP$\cdot P_i \to F_1 \cdot ADP + P_i$. Free energy $\Delta G \sim .31$ eV is liberated at this step.

Step 4: ADP is released from the catalyst site: $F_1\cdot$ADP$+P_i \to F_1 + ADP + P_i$. $\Delta G \sim 0$ holds true also for this process.

This picture suggests that the notion of the high energy phosphate bond is not quite correct as suggested also by some empirical findings [22, 11] , [181] . The metabolic energy could be stored as the zero point kinetic energy of protons rather than in phosphate bonds. Perhaps one fundamental function of phosphates would be to make DNA and RNA polymers charged in turn making possible the formation of wormhole magnetic flux tubes and braiding making possible a wide repertoire of catalytic actions. Phosphorylation of say protein could mean a reconnection process for magnetic flux tubes with flux tubes attached to O= atom transferred from ATP to the target to which phosphate is attached.

2. Model of $ATP \rightarrow ADP$ based on wormhole magnetic flux tubes

Consider first the basic philosophy behind model.

1. In the model of DNA as topological quantum computer XMPs, $X = A, T, C, G$ can be connected to oxygen atoms by wormhole magnetic flux tubes having quark and antiquark at opposite throats of wormhole contact and charge conjugated quark-anti-quark pairs at the ends of the flux tubes. Dark u quark and its charge conjugate code for A, T and d quark and its conjugate for G, C so that the conjugation for nucleotides corresponds to charge conjugation for quarks and $A - G$ and $T - C$ symmetries of the third nucleotide of the codon to isospin symmetry.

2. Basic bio-catalytic processes are identified as a reconnection of the wormhole magnetic flux tubes and change of the length of the flux tube induced by the change of the value of Planck constant associated with it. It would not be too surprising if this kind of mechanism were involved also in $ATP \rightarrow$ADP+P_i. The reason for the special role of ATP among XTP might be that the positive charge $q(u) = 2/3$ of u-quark maximizes the attractive interaction between u quark and phosphate.

3. Flux tubes connect to oxygen atoms in the proposed model of bio-catalysis and protein folding [3] . The model is relies on ideas inspired by the model of DNA as topological quantum computer [26] . In this model hydrogen bonds are assumed to correspond or to be accompanied by (wormhole) magnetic flux tubes. Also flux tubes connecting acceptor atoms or molecules of hydrogen bonds are assumed to be connected long flux tubes and represent genuinely new physics. Examples of acceptors are $O =$ atoms in phosphates and amino-acids and aromatic rings in DNA and also in some amino-acids. The model for protein folding has tight connections with existing chemistry and leads to a very simple criterion for the formation of hydrogen bond between $N - H$ and $O =$ in the constant part of amino-acid and to a proposal for the folding code.

4. DNA as tqc model gives further constraints. The structure of the phospholipids suggest that in the case DNA nucleotides long flux tubes connect the aromatic ring of the nucleotide to the $O =$ atom at the hydrophilic end of the lipid acting as a standard plug which in turn can be connected to another acceptor and eventually terminates to a donor of hydrogen bond. The detailed charge structure of the aromatic ring(s) should determine the quark-nucleotide correspondence. The connection line to the lipid could involve several intermediate $O =$ plugs and the first plug in the series would be the $O =$ atom of the monophosphate of the nucleotide. Not surprisingly, phosphorylation would be absolutely essential for the operation of DNA as topological quantum computer. $O = -O =$ flux tubes could also act as switches inducing a shortcut of the flux tube connection by reconnecting with a hydrogen bond connecting two water molecules. This is an essential step in the model for how DNA acts as topological quantum computer.

A possible model (perhaps the simplest one found hitherto) for the reaction $ATP \rightarrow ADP + P_i$ is based on the assumption that it splits a flux tube connection defining strand of a braid defining topological quantum computation. A change of the hardware of topological quantum computer would be therefore in question.

1. Suppose that ATP defines a standard plug in flux tube connections. This would mean that aromatic ring and the oxygen atoms $O = 1$, $O =_2$, and $O =_3$ of the phosphates are connected by magnetic flux tubes to some molecules. These flux tubes represent genuinely new physics in accordance with the fact that "high energy phosphate bonds" are not really understood in the standard chemistry. Suppose that the flux tube assocaited with $O =_2$ connects it with $O =_3$ and defines the somewhat mysterious high energy phosphate bond. This bond would be formed

during cellular breathing and the metabolic energy would go the formation of the magnetic flux tube between $O =_2$ and $O =_3$. Suppose that $O =_1$- the innermost O has a fluix tube connecting it to catalyst in this case F_1.

2. At Step 1 F_1 and ATP molecule would find each other. This would be due to the shorterining of the magnetic flux tube connecting them and associated with the innermost phophate. This would liberate .42 eV of metabolic energy.

3. At Step 2 hydrolysis would induce $F_1 \cdot \mathrm{ADP} \cdot P_i \rightarrow F_1 \cdot ADP + P_i$. Since no energy is released at this step, there is temptation to concludde that a reconnection of $O_2 - O_2$ fluc tube and a flux tube associated with catalyst occurs. ADP and P_i fors now a high energy bond with catalyst. the reconnection of $(O =_2) - (O =_3)$ flux tube with the hydrogen bond connecting two water molecules leads to the disappaerence of this flux tubeso that the incoming and outgoing the flux tubes are shortcut by $(O =_2) - -H - (OH)$ *resp.* $(O =_3) - -H - (OH)$ hydrogen bonds (connection to ground is the analog in circuit theory). This would correspond in the usual terminology the liberation of the third phosphate: $ATP \rightarrow ADP + P_i$. P_i however remains at the end of flux tube to be attached later to another ADP . The resulting bonds to water molecules would have low energy and the liberated energy would be usable metabolic energy. In this case the function of the splitting would be purely energetic.

4. One can imagine also a function related to information processing. P_i could be also attached to some other molecule in phosphorylation process so that the outcome would be a reconnection in the web of magnetic flux tubes. Phosphorylation is ineed known to play a key role in activation and deactivation of proteins and in the formation of signal pathways. In the case of AMP associated with DNA there would be only single flux tube involved and it could connect DNA nucleotide to nuclear or cell membrane.

5. The process involves also hydration. $(OH)^-$ ion joins to the third P to give P_i^{-3} and H^+ to $O - P$ in second P to give $H^+ - O$ in ADP^{-1}. The exchange of electron would lead to the final state $ADP^{-2} + P_i^{-2}$.

A possible model for the dropping of protons would be following.

1. It is absolutely essential to realize that F_1 is an open system and that naive thermodynamic considerations can lead to misunderstandings. In particular, the notion of high energy phosphate bond does not make sense. The source of the metabolic energy is the chemical energy used to drive protons to the atomic space-time sheets of F_1. The function of the large negative charge of ATP is to increase the rate for the binding of ATP^{-4} to F_1. In the classical picture the binding to F_1 is followed by the dropping of two protons to larger space-time sheet. The value of the metabolic quantum could be reduced from .5 eV to about .21 eV by the Coulombic interaction energy of proton with PO^{4-}. The Coulombic binding energy of the remaining protons at F_1 with $ADP + P_i$ is smaller and the dropped proton liberates larger energy about .31 eV. In quantum picture the division of the process to this kind of sequence might not be a good approximation.

2. One function of the $ATP \rightarrow ADP$ would be to induce the dropping of the third proton from F_1 space-time sheet. Second function would relate to the topological quantum computation like process since the decay would correspond to a splitting of a braid strand coming to the aromatic ring of A and proceeding along string defined by the ring and three $O =$:s of phosphates and continuing further. This would make possible tqc as a braiding for both halves of the split flux tubes. After the reconnection the total braid structure would be different. Quite generally, reconnection process would make possible to modify the hardware of topological quantum computer.

3. The reason for why P_i leaves the catalyst site and proton is dropped (step 2) should be the in-stabilization of the bound state of positively charged proton with $ADP^{-2} + P_i^{-2}$ which does not have so strong Coulomb interaction energy with proton as ATP^{-4} As a consequence, proton can drop to the larger space-time sheet.

4. What remains open are the details of the transformation of the chemical energy to zero point kinetic energy of protons. Remote metabolism suggests that protons send negative energy phase

conjugate photons to the geometric past inducing a transition of an energy carrying molecule to a lower energy state (zero energy ontology gives justification for this picture). This would mean the failure of the standard description in terms of reaction kinetics. The catabolism of nutrients is the eventual provider of the metabolic energy and the coenzyme nicotinamid adenic dinucleotide NAD^+ [67] receives electron and the energy liberated in the catabolic reaction. In the proposed framework it is not an surprising that NAD^+ is analogous to RNA dinucleotide (perhaps as remnant from RNA era when dinucleotides defined the 2-codon code) and consists of two phosphates and adenine and nicotinamide nucleosides. The oxidation reaction $NADH \rightarrow NAD^+$ in turn liberates this energy. Protons could gain their energy by sending negative energy photons to $NADH$. Negative energy photons would propagate along "topological light rays" parallel to the flux tubes connecting the system in a precisely targeted manner to NADH aromatic rings. Alfwen waves propagating along magnetic field lines would be the standard electrodynamics counterpart for these topological light rays.

Many details of the process remain open but it would seem that the key ideas of TGD based quantum vision about living matter are fused together in rather detailed manner in this picture.

3. Polymerization of DNA and RNA

The polymerization of RNA and DNA by dehydration involves the fusion of $PO_4H_2^{2-}$ phosphate molecule with ribose. In this process the stub ...-O-H of the phosphate ion combines with H-O-C-... stub of ribose (here C is the carbon atom not belonging to the ribose cycle). This gives rise to ..-O-(H-O)$^-$-C-... plus proton dropping to a larger space-time sheet and liberating metabolic energy quantum. Too large negative charge of three units makes the complex unstable and (H-O)$^-$ ion splits out. Metabolic energy quantum might be also used in the process.

DNA as tqc model would suggest a possible interpretation. Perhaps the polymerization creates flux tube connections from nucleotides to to other molecules -say lipid molecules of the nuclear membrane or some catalyst molecule- via the attached O= attached to phosphate. Also the phosphorylation of proteins could involve this kind of reconnection process creating flux tube connection of protein with some other molecule.

Hydration destabilizes long polymers unless there is a continual feed of protons to the atomic space-time sheets. This could be achieved by irradiation with photons with energy equal to the metabolic energy currency. Situation changes also if water is ordered/structured water, in liquid crystal form, or as ice, and therefore unable to provide the water molecules needed for the hydration. Stabilization of RNA and DNA polymers could be achieved in this manner in gel phase.

Clay structures are known to act as catalyzers of RNA polymerization. The general model of catalysis based on the recombination and $\hbar$ changing transition for magnetic flux tubes should explain also this.

Why DNA is stable inside cell nucleus?

Inside membrane bound surface both DNA and RNA nucleotides and polymers are stable. The un-stability of the DNA nucleotides and polymers outside membrane bound surfaces could involve many-sheeted physics.

1. What one expects that DNA transforms to RNA unless it is inside a membrane bound region. A possible reason is that water molecule is needed to transform DNA to RNA but not available inside membrane bound structure where water is structure water in gel phase.

2. In the case of A, G, and C nucleotides DNA$\rightarrow$ RNA transformation means simply an addition of one oxygen atom to the de-oxyribose ring, that is replacement of one C-H with C-O-H. If ordinary water is present this could be achieved by the dissociation of the water molecule to OH^-+H^+ followed by the replacement of C-H in the de-oxyribose cycle with C-OH^- so that a negative1ly charged ribose results. The outcome is free hydrogen atom. If H^+ drops to a larger space-time sheet, the liberated zero point kinetic energy is of order .5 eV. This process is basically the same which should occur when single ATP molecule is utilized in metabolism.

3. In the case of T nucleotide also CH_3 group differentiating T from U must be de-attached. This is achieved if the hydrogen atom from the water molecule is taken by the de-attached CH_3 group

to give CH_4 molecule. As a result a negatively charged U results. Inside cell nucleus or in gel phase this process is not favored because the water is in liquid crystal form and it costs energy to take the needed H_2O molecule from it.

10.3.4 Could high energy phosphate bond be negentropic bond with negative binding energy?

Most people assign the word "love" to the word "life" as their first association. There is a notable exception to this: scientists including biologists. Un-educated layman might however wonder whether one can understand life without identifying any physical counterpart for this notion (, which could be replaced with that of compassion, sex, or ability to act synergetically or just X if some of these notions sounds less un-scientific). Certainly the word "love" stimulates a deep feeling of disgust in a reductionistically conditioned scientist. But isn't the duty of scientist to win this kind of feelings and try to see whether this identification might be possible after all? The prize could be high: the understanding of what distinguishes between living and dead matter could change the entire culture. Who knows, maybe it could be possible to identify some poorly understood fundamental biological process allowing a quantitative model using a guess for what this physical correlate could be. The basic step of metabolism is at the core of life and indeed poorly understood, and I shall argue that the identification of the negentropic entanglement as the counterpart for the notion of love could allow to model quantititatively what happens in this process.

Basic ideas

Before continuing general motivating comments about implications of negentropic entanglement are in order.

1. Ordinary bound states are stable because they have positive binding energy. One can visualize this kind of binding as a jail: the second particle resides near the bottom of a potential well. Organized marriage is a social analogy for this situation. Negentropic entanglement makes possible bound states for which binding energy can have and perhaps even has always a wrong sign. The state is not prevented from decaying to free particles in state function reduction by energy conservation: Negentropy Maximization Principle (NMP) [44] takes care that they remain correlated. The social analogy would be a voluntary marriage based on love. Partners are competely free to leave but want to stay together. One implication could be explanation for the stability of highly charged basic molecules of life such as DNA and ATP.

2. The presence of the negentropic entanglement implies the directedness of the biological processes since the outcome of the state function reduction would be far from random since the behavior of negentropic bonds could be almost deterministic. In the case of time-like entanglement this would select only particular initial final state pairs so that determinism would emerge also in this sense and could lead to almost deterministic irreversible cellular automaton behavior characteristic for the living matter very different from the reversible determinism of classical physics and very difficult to understand in quantum context.

3. The determinism would of course be only partial and would allow volition not spoiled by randomness of quantum jump. This would provide a general explanation for the ability of the living matter to overcome the second law basically implied by quantum randomness predicted by the standard quantum theory. This would happen in time scales shorter than the time scale of the appropriate causal diamond (CD) only but one would have hierarchy of CD meaning that in arbitrary long time scales there are levels of hierarchy at which second law is broken. The hierarchy of Planck constants would be also crucial since it would allow zooming up to arbitrarily long time scale. Non-equilibrium thermodynamics and cellular automaton models could be seen as phenomenological descriptions for the actual breaking of second law in the intersection of real and p-adic worlds.

4. High energy negentropic bonds need not be present only in phosphates. O=s are are present in all important biomolecules. Phospates are present in DNA. Each peptide bond in aminoacid polymer contains O=. Also sugars contain it. Maybe O= indeed acts as a universal plug

defining then ends of negentropic flux tube bonds between biomolecules. For instance, protein folding for which a possible model is discussed in [3] from different view point could be more or less deterministic cellular automaton like process if the bonds are negentropic. Negentropic entanglement would also guarantee the stability of the folding pattern. Certainly the assumption that the process is random -as standard quantum theory would suggest- leads to Levinthal paradox stating that the rate of the process is quite too slow. The simplest possibility is that the flux tube bonds are between O=s of subsequent aminoacids before folding and the folding process involves formation of reconnections possibly drawing by a reduction of Planck constant certain aminoacids near to each other. O=s could also act as plugs connecting protein to other biomolecules. One must however notice that many neurotransmitters, hallucinogens, and alcohol having strong effects on consciousness have O-H groups instead of O=s. This inspires the question what happens to the flux tube in O=$\leftrightarrow$ O-H process.

General formulation of the model

Consider now the model. High energy phosphate bond [42] assigned with the two outer-most phosphates of ATP [5] is fundamental for the basic processes in living matter. The $ATP \to ADP + P_i$ liberates metabolic energy loaded to ATP in the cellular respiration process [16] or its equivalent and occurs again and again and defines a kind of Karma's cycle in living matter. The phosphate bond is assumed to have a high energy content liberated as ATP is hydrated to ADP [4] and phosphate ion $P_i = PO_4^{3-}$ [75] . The notion of high energy phosphate bond has been however challenged as being meaningless [22, 11] , [181] .

1. One can of course consider a high energy bond for which the interaction potential looks like a well at the top of mountain and spin glass degeneracy of quantum TGD would certainly allow to consider this kind of notion. I do not know whether models realizing this idea concretely have been really constructed.

2. My earlier proposal for $ATP \to ADP + P_i$ process is inspired by the notion of many-sheeted space-time and p-adic length scale hypothesis making sense in the intersection of real and p-adic worlds and involves the dropping of protons (or electrons) to larger space-time sheets and driven back in oxidative metabolism. The energy liberated in this process corresponds to the zero point kinetic energy of protons (or electrons), which is smaller at the larger space-time sheet. The maximum value of zero point kinetic energy is predicted to be $E_0 \simeq .5$ eV for $k = 137$ in the case of proton and for $k = 148$ in the case of electron (for electron the energy would be by a factor $2^{-11}m_p/m_e \simeq .94$ smaller).

3. With an inspiration coming from DNA as topological quantum computer model [26] I have also proposed that the magnetic flux tubes connecting bio-molecules to each other define a kind of Indra's net plays a key role in the biological information processing. For instance, topological quantum computations could be realized in terms of braids formed by flux tubes [26, 3] . O=:s associated with phosphates wold serve as universal plugs to which flux tubes could be connected connecting intronic nucleotides and lipid layers of nuclear or cell membrane. In particular, the innermost O= of ATP could be connected by a flux tube to any biomolecule needing metabolic energy- say some catalyst or the F_1 machine central for energy metabolism. The reduction of Planck constant would bring ATP and biomolecule near each other and lead to a formation of a weakly bound state making catalytic processes possible. The outer O=:s of the ATP molecule could be connected by a flux tube to each other, which could be rather long loop. This flux tube could provide the new physics realization of the high energy phosphate bond.

4. ATP (P_i) has 4 (3) units of negative charge and at least ordinary layman might wonder why this does not induce instability. Similar problem is encountered in the case of DNA, which contains two units of negative charge per nucleotide. This particular problem is regarded as completely real. The idea about life as something in the intersection of real and p-adic worlds [62] raises the question whether these high energy states could be made possible by the presence of negentropic bonds- most naturally associated with the flux tubes with large $\hbar$. This love marriage would stabilize ATP, ADP, and DNA and other charged biomolecules. The presence of phosphates would be a clear-cut signature of this stabilization mechanism. Also proteins involve phosphates

playing a key role in the bio-control: typically phosphorylation activates or de-actives the protein and is also involved with the generation of signal patways. Why this happens would be easy to understand in Indra's net model.

5. In $ATP \to ADP + P_i$ transformation the energy carried by the negentropic bonds would be liberated but leave the flux tube bonds negentropic. Cell respiration would take care of the loading of the batteries with negentropic metabolic energy. This would involve also the kicking of protons back to the smaller space-time sheets. Also the molecular lovers ADP and P_i would find each other again as the Planck constant for the flux tube connecting them would be reduced during the cellular respiration transform ADP and P_i back to ATP.

Quantitative estimates

Consider now a more detailed model for $ATP \to ADP + P_i$. The binding of ATP to the catalytic site involves several steps. I have described them in the previous section and in the following add to this template the interpretation suggested by the proposed picture.

1. **Step 1**: The binding $ATP + F_1 \to ATP \cdot F_1$ to the catalyst site is a complex process involving the break-up of the hydrogen bonds between cellular water and ATP molecule and cell water and catalyst site and generation of hydrogen bonds between catalyst site and ATP molecule. In TGD framework this means that protons can be kicked to and dropped back from atomic space-time sheets. Only the net number of protons dropped however matters.

   This process involves a liberation of Gibbs free energy per single attachment, which is about $\Delta g_{ATP} = .42$ eV. It was earlier believed that this energy is liberated instantaneously but the findings about the behavior of the F_1 motor coupled to dissipative load, lead Oster and Wang to suggest that the process is more complex and starts from a loose binding and ending up to a strong binding [190] .

   Comment: One can question the assumption that strong binding is generated. Instead of binding proton or electron would be dropped to a larger space-time sheet and liberate tzero point kinetic energy.

   (a) The simplest interpretation in the proposed picture is that the negentropic flux tube connecting ATP and F_1 molecule and behaving as high energy phosphate bond associated with the innermost O= is contracted via the reduction of Planck constant. Then proton is dropped from $k = 137$ space-time sheet to a much larger space-time sheet and liberates metabolic energy quantum $E(137) \simeq .5$ eV. Another possibility is that electron at $k = 148$ space-time sheet is dropped. This process would replace the instantaneous generation of binding energy and in zero energy ontology the time scale for this process would correspond to the time scale of appropriate causal diamond (CD).

   (b) Instead of single particle energy macroscopic Gibbs energy $G = E + PV - TS$ is the useful notion now since macroscopic quantities of matter are studied and pressures and temperature are typically constant in the situations considered ($dG = -SdT + VdP$). G is minimized for constant T and P prevailing in the situation considered.

   (c) In the attachment of ATP to catatyst S is reduced and a good guess is that volume is not affected so that PV term does not change. From this one can deduce that the liberated energy per catalyst particle -call it $\Delta e = e_i - e_f = \Delta g - T\Delta s$ (i and f refer to initial and final states) satisfies $\Delta e > \Delta g = .42$ eV.

   (d) One must estimate the value of Δe. The attachment reduces the kinetic energy of relative motion of catalyst and ATP to zero. If it makes sense to speak about thermal equilibrium for ATP an catalyst in translational degrees of freedom the reduction of kinetic energy is $\Delta e_K = 3T/2$, which is of order .045 eV at room temperature. Whether this energy remains in the catalyst-ATP system or is it liberated in the process is not clear. The energy liberated in the dropping of the proton or electron gives a contribution $\Delta e = E_0 = .5$ eV. This gives the condition

$$\Delta g_1 = E_0 + 3T/2 - T\Delta s = .42 \ \ eV \ \ . \tag{10.3.1}$$

If the liberated kinetic energy remains in the syste, the first guess is $\Delta e = E_0 = .5$ eV, where E_0 is the nominal value of zero point kinetic energy. This would give for $T\Delta s$ the estimate $T\Delta s = .08$ eV about 3 times thermal energy corresponding to three translational degrees of freedom. This looks rather reasonable order of magnitude estimate.

(e) NMP suggests-maybe even requires- that the bond remains negentropic. The binding energy associated with ATP- catalyst binding could be small- of the order of thermal energy about .045 eV.

2. **Step 2** Hydrolysis: $F_1 \cdot ATP \to F_1 \cdot ADP \cdot P_i$. The change of free energy is small during this step: $\Delta G \sim 0$.

   Comment: The simplest option explaining the fact that the change of energy is small is that hydrolysis leaves the flux tube between outer O=:s of ATP intract and removes only the P-O-P bond. This flux loop could have rather large $\hbar$.

3. **Step 3**: Ortophosphate is released from the catalyst site: $F_1 \cdot ADP \cdot P_i \to F_1 \cdot ADP + P_i$. Free energy $\Delta G \sim .31$ eV is liberated at this step.

   Comment: The simplest option is that the negentropic flux tube liberates its energy but remains negentropic. The increase of Planck constant might be involved.

   (a) The value of Δe is now smaller than ΔG, which suggests that the metabolic energy quantum in the case of proton corresponds to $\Delta e = E(139) \simeq .25$ eV. The average change of kinetic energy can be assumed to be equal to thermal energy in final state and is same as above. This gives the condition

   $$\Delta g_2 = E_0/2 - 3T/2 + T\Delta s = .32 \ \ eV \ \ .$$

   (b) By adding this equation with the similar equation for Step 1 (see Eq. 10.3.1) one obtains the condition

   $$\Delta g_1 + \Delta g_2 = 3E_0/2 = .74 \ \ eV \ \ .$$

   This gives $E_0 = .49$ eV so that the model seems to be internally consistent.

4. **Step 4**: ADP is released from the catalyst site: $F_1 \cdot ADP + P_i \to F_1 + ADP + P_i$. $\Delta G \sim 0$ holds true also for this process.

   Comment: $\hbar$ increases back to the original value for the innermost flux tube which could it still have small positive energy and be negentropic.

The model would predict that ADP and P_i and remain highly correlated (connected by flux tubes) as do also AXP and F_1. These predictions should be testable by marking ADP and P_i of ATP with the same "color" (say radioactively) and finding whether the colors of ADP and P_i remain the same during the subsequent cycles or whether they mix immediately. These love affairs at molecular level could be modified only by reconnections of flux tubes as also in human relationships. For instance, two ADPs could exchange their P_is or F_1s. Negentropic entanglement could gurantee the highly organized and directed nature of basic bio-catalytic processes.

10.3.5 DNA as a topological quantum computer

For years ago I developed a model of topological quantum computation combining TGD based view about space-time with basic ideas about topological quantum computation and ended up with the proposal that DNA might act as a topological quantum computer. One can imagine several manners in which DNA or RNA could act as a topological quantum computer and it good to try to state clearly what one wants.

1. Natural requirements are that the topological quantum computer programs can be naturally combined to larger programs and evolution means this kind of process; that the programs have a natural modular structure inherited from the previous stages of evolution; and that the computation is not restricted inside single nucleus.

2. DNA and/or RNA defines the hardware of topological computation and at least for more advanced topological quantum computers this hardware should be static so that only programs would be dynamical. This leaves only DNA in consideration and the entangled initial and quantum states at the ends of braids quantum states would be assignable to static DNA structures.

3. The program would be determined by different braidings connecting the states of DNA in time direction or in spatial direction. Since the genomes are identical in different nuclei, the strands could connect different nuclei or conjugate strands of double DNA strand. Reconnection process would allow to modify the hardware for tqc.

The recent progress in quantum TGD and TGD inspired quantum biology

After the advent of the first model for topological quantum computation in TGD Universe [81] , the mathematical and physical understanding of TGD has developed dramatically and the earlier quite speculative picture can be replaced with a framework which leads to a rather unique view about topological quantum computations by DNA.

1. Universe as a topological quantum computer

One can say that the recent formulation of quantum TGD states that the entire Universe behaves like a topological quantum computer. This notion of topological quantum computer differs however from the standard one in many respects.

1. The emergence of hierarchy of Planck constants realized as a generalization of the notion of imbedding space is now a basic piece of TGD allowing an elegant formulation of quantum TGD [83, 27] . The phases of matter with large Planck constant are interpreted as dark matter. Large values of Planck constant make possible topological quantum computations in arbitrary long time scales so that the most fundamental objection against quantum computation can be circumvented.

2. Zero energy ontology forces to unify S-matrix and density matrix to M-matrix - the product of the square root of density matrix and S-matrix- defined as time-like (or rather light-like) entanglement coefficients between positive and negative energy parts of zero energy state [17, 16] . Connes tensor product emerging naturally from the notion of finite measurement resolution described in terms of inclusions of hyperfinite factors of type II_1 defines highly uniquely the M-matrix. M-matrix would be natural candidate for defining topological quantum computation in light-like direction. Connes tensor product makes sense also in space-like direction and would define quantum storage of functions represented as entanglement coefficients.

3. The notion of number theoretic braid [14, 17] is now well-understood and has become a basic element of the formulation of quantum TGD based on the requirement of number theoretical universality. As a matter fact, the notion of braid is generalized in the sense that braid strands can fuse and decay. The physical interpretation is as motion of minima of the generalization eigenvalue of the modified Dirac operator which is function of transversal coordinates of light-like partonic 3-surface and has interpretation as vacuum expectation of Higgs field. Fusion of braid strands corresponds to fusion of minima.

   For generalized Feynman diagrams partonic light-like 3-surfaces meet at 2-dimensional vertices defined by partonic 2-surfaces [16] . This implies that braids replicate at vertices: the interpretation is as a copying of classical information. Quantum information is not copied faithfully. The exchange of partonic 2-surfaces in turn corresponds to quantum communications. Hence quantum communication and quantum copying emerge naturally as additional elements. Space-like Connes tensor product in turn defines quantum memory storage.

4. Computation time is a fundamental restriction in both ordinary and quantum computation. Zero energy ontology makes possible communications in both directions of geometric time, which suggests the possibility of geometric time loops in topological quantum computations. Could this mean that computation time ceases to be a restriction and ordinary computations lasting for infinite amount of geometric time could be performed in a finite time interval of observer's time? This is perhaps too much to hope. The subjective time taken by the computation would

be infinite if each step in the iteration corresponds to single quantum jump. If this is the case and if each quantum jump of observer corresponds to a finite increment of geometric time perceived by the observer, time loops would not allow miracles.

2. The notion of magnetic body and the generalization of the notion of genome

The evolution of ideas related to quantum biology provides also new valuable insights. In particular, the notion of magnetic body leads to a model of living system in which dark matter at magnetic flux quanta of the field body of biological system uses biological body as a motor instrument and sensory receptor [23] . Quantum control would be naturally via the genome and sensory input would be from cell membrane containing all kinds of receptors. This would suggest that magnetic flux sheets traverse through DNA strands and cell membranes.

The quantization of magnetic flux with unit defined by Planck constant having arbitrarily large values leads naturally to the notions of super-genome and hyper-genome [41] . Super-genome would consists of DNA strands of separate nuclei belonging to single magnetic flux sheet and these sequences of genomes would be like lines of text at the page of book. Super-genomes in turn can combine to form text lines at the pages of a bigger book, I have used the term hyper-genome. This hierarchy of genomes would give rise to a collective gene expression at the level of organs, individuals of a species, and at the collective level consisting of populations containing several species. Even biosphere could express itself coherently via all the genomes of the bio-sphere. The model of topological quantum computation performed by DNA should be consistent with this general picture.

Model for DNA based topological quantum computation

The most promising model of DNA as topological quantum computer relies on the hierarchy of genomes. The flux sheets or collections of parallel flux tubes assignable to a magnetic body would traverse the DNA strands of several nuclei so that strands would be analogous to lines of text on the page of a book.

DNA strands would define the intersections of magnetic or number theoretic braids with plane and braiding would be associated with with the magnetic field lines or flux tubes transversal to DNA. The M-matrix defining topological quantum computation would act on quantum states assignable to nucleotides.

1. The interpretation of nucleotides

The interpretation of the A,T,C,G degree of freedom is not obvious and one can consider several options.

1. The quantum numbers entangled by braids having nothing to do with (A,T,C,G) assignable to nucleotides and the braiding does not affect nucleotides.

2. The nucleotides (A,T,C,G) correspond to four different colors (a,t,c,g) for braid strands with conjugate nucleotides defining conjugate colors. The subgroup of allowed braidings would preserve the color patterns. The minimal assumption consistent with the mapping of nucleotides to quarks and antiquarks [26] is that braid strands connect only nucleotides and conjugate nucleotides.

3. The model requires that the genomes in different nuclei are identical: otherwise it is not possible to realize braidings as symmetry transformations mapping portions of DNA to their conjugates (as noticed, this map would not occur at the chemical level). An interesting question is whether also the permutations of nucleotides of different codons are allowed or whether only codons are permuted so that they would define fundamental sub-programs.

4. One can understand why the minimum number of nucleotides in a codon is three. The point is that braid group is non-commutative only when the number of strands is larger than 2. The braidings acting as symmetries would correspond to a subgroup of ordinary braidings leaving the color pattern of braid invariant. Obviously the group is generated by some minimal number of combinations of ordinary braid generators. For instance, for two braid strands with different colors the generator is e_1^2 rather than e_1 (two exchange operations/full 2π twist). For codons one would have four different subgroups of full braid group corresponding to codons of type XXX,

XYY, XXY, and XYZ. Each gene would be characterized by its own subgroup of braid group and thus by an M-matrix defining topological quantum computation.

5. It might be possible to understand the "junk DNA" character of introns. Introns are the most natural candidates for the portions of genome participating topological quantum computations. The transcription process would disturb topological quantum computation so that introns should be chemically passive. Since the portion of "junk DNA" increases with the evolutionary level of the species evolution would indeed correspond to an increase the amount of topological quantum computations performed.

2. Two realizations of topological quantum computation and their combination

One can imagine two basic realizations of topological quantum computation like processes- or to be more precise - entanglement by braiding. In TGD framework this entanglement could be interpreted in terms of Connes tensor product.

2.1 Space-like entanglement

The first realization would rely space-like braids. Braid strands would connect identical lines of text at the page of book defined by sequences of genomes of different nuclei. Inside nucleus the strands would connect DNA and its conjugate. The braiding operation would take place between lines.

In this case it would be perhaps more appropriate to speak about quantum memory storage of a function realized as entanglement. These functions could represent various rules about the behavior of and survival in the physical world. For this option A,T,C,G cannot correspond to entangled quantum numbers and the interpretation as braid colors is natural. Braiding cannot correspond to a physical braiding of nucleotides so that (A,T,C,G) could correspond to braid color (strands would connect only identical nucleotides).

Strands would not connect strand and its conjugate like hydrogen bonds do but would be like long flux lines of dipole field starting from nucleotide and ending to its conjugate so that braiding would emerge naturally. Color magnetic flux tube structures of almost atom size appear in the TGD based model of nucleus and have light quarks and anti-quarks at their ends [1] , [1] . This could be the case also now since quarks and anti-quarks appear also in the model of high T_c superconductivity which should be present also in living matter [23] .

2.2. Light-like entanglement

Second realization would rely on light-like braids at the boundaries of light-like 3-surfaces connecting 2-surfaces assignable to single genome at different moments of time. Braiding would be dynamical and dance metaphor would apply. The light-like surface could intersect genomes only at initial and final moments and strands would connect only identical nucleotides. Light-likeness in the induced metric of course allows the partonic 3-surface to look static at the level of imbedding space. The fundamental number theoretic braids defined by the minima of the Higgs like field associated with the modified Dirac operator would be very natural in this case.

Genes would define only the hardware unless they code for the magnetic body of DNA too, which looks implausible. The presence of quantum memory and quantum programs would mean a breakdown of genetic determinism since the braidings representing memories and programs would develop quantum jump by quantum jump and distinguish between individuals with the same genome. Also the personal development of individual would take place at this level. It would be these programs (that is magnetic bodies) which would differentiate between us and our cousins with almost identical genome.

2.3 Combination of the two realizations

These two variants of tqc accompany each other automatically if DNA nucleotides are connected to the lipids by magnetic flux tubes [26] . In this case the 2-D flow of lipids induced by the self organization pattern of the metabolically induced flow of cellular water would induce the tqc as dance and this in turn would would generate braiding of flux tubes connecting lipids to the nucleotides. Presumably a gel-sol transition of cytoplasm accompanies tqc in this kind of situation.

Biological evolution as an evolution of topological quantum computation

This framework allows to understand biological evolution as an evolution of topological quantum computation like processes in which already existing programs become building blocks of more complex programs.

1. The transition from RNA era to DNA era involving also the emergence of cell membrane bounded structures would mean the emergence of the topological quantum computation using a static hardware.

2. For mono-cellulars double DNA strands define space-like topological quantum computations involving only single step if the braids connect the nucleotides of the two DNA strands: obviously a reason why for double DNA strands.

3. For multicellular organisms more complex space-like topological quantum computations would emerge and could code rules about environment and multicellular survival in it. At this step also introns specialized to topological quantum computation would emerge.

4. A further evolution as a generation of super-genomes in turn forming hyper-genomes and even higher structures would have a concrete counterpart as the organization of braids of lower level to form braids at higher level so that topological quantum computations would become increasingly complex and program module structure would emerge very naturally.

subsectionWater memory and braids

There are several grand visions about TGD Universe. One of them is as a topological quantum computer in a very general sense. This kind of visions are always oversimplifications but the extreme generality of the braiding mechanism suggest that also simpler systems than DNA might be applying tqc.

Water memory: general considerations

With few exceptions so called "serious" scientists remain silent about the experiments of Benveniste and others relating to water memory [102, 186, 135, 136] in order to avoid association with the very ugly word "homeopathy".

The Benveniste's discovery of water memory initiated quite dramatic sequence of events. The original experiment involved the homeopathic treatment of water by human antigene. This meant dilution of the water solution of antigene so that the concentration of antigene became extremely low. In accordance with homeopathic teachings human basophils reacted on this solution.

The discovery was published in Nature and due to the strong polemic raised by the publication of the article, it was decided to test the experimental arrangement. The experimental results were reproduced under the original conditions. Then it was discovered that experimenters knew which bottles contained the treated water. The modified experiment in which experimenters did not possess this information failed to reproduce the results and the conclusion was regarded as obvious and Benveniste lost his laboratory among other things. Obviously any model of the effect taking it as a real effect rather than an astonishingly simplistic attempt of top scientists to cheat should explain also this finding.

The model based on the notion of field body and general mechanism of long term memory allows to explain both the memory of water and why it failed under the conditions described.

1. Also molecules have magnetic field bodies acting as intentional agents controlling the molecules. Nano-motors do not only look co-operating living creatures but are such. The field body of molecule contains besides the static magnetic and electric parts also dynamical parts characterized by frequencies and temporal patterns of fields. To be precise, one must speak both field and relative field bodies characterizing interactions of molecules. Right brain sings-left brain talks metaphor might generalize to all scales meaning that representations based on both frequencies and temporal pulse with single frequency could be utilized.

   The effects of complex bio-molecule to other bio-molecules (say antigene on basofil) in water could be characterized to some degree by the temporal patterns associated with the dynamical part of its field body and bio-molecules could recognize each other via these patterns. This

would mean that symbolic level in interactions would be present already in the interactions of bio-molecules.

If water is to mimic the field bodies of molecules using water molecule clusters, at least vibrational and rotational spectra, then water can produce fake copies of say antigenes recognized by basofils and reacting accordingly.

Also the magnetic body of the molecule could mimic the vibrational and rotational spectra using harmonics of cyclotron frequencies. Cyclotron transitions could produce dark photons, whose ordinary counterparts resulting in de-coherence would have large energies due to the large value of $\hbar$ and could thus induce vibrational and rotational transitions. This would provide a mechanism by which molecular magnetic body could control the molecule. Note that also the antigenes possibly dropped to the larger space-time sheets could produce the effect on basofils.

2. There is a considerable experimental support for the Benveniste's discovery that bio-molecules in water environment are represented by frequency patterns, and several laboratories are replicating the experiments of Benveniste as I learned from the lecture of Yolene Thomas in the 7:th European SSE Meeting held in Röros [23] . The scale of the frequencies involved is around 10 kHz and as such does not correspond to any natural molecular frequencies. Cyclotron frequencies associated with electrons or dark ions accompanying these macromolecules would be a natural identification if one accepts the notion of molecular magnetic body. For ions the magnetic fields involved would have a magnitude of order .03 Tesla if 10 kHz corresponds to scaled up alpha band. Also Josephson frequencies would be involved if one believes that EEG has fractally scaled up variants in molecular length scales.

3. Suppose that the representations of bio-molecules in water memory rely on pulse patterns representing bit sequences. The simplest realization of bit would be as a laser like system with bit 1 represented by population inverted state and bit 0 by the ground state. Bits could be arranged in sequences spatially or by variation of zero point energy defining the frequency: for instance increase of frequency with time would define temporal bit sequence. Many-sheeted lasers are the natural candidates for laser like systems are in question since they rely on universal metabolic energy quanta. Memory recall would involve sending of negative energy phase conjugate photons inducing a partial transition to the ground state. The presence of metabolic energy feed would be necessary in order to preserve the memory representations.

Water memory in terms of molecular braidings

It is interesting to look water memory from the point of view of tqc. Suppose that the molecules and water particles (space-time sheet of size of say cell length scale) are indeed connected by color flux tubes defining the braid strands and that splitting of the braid strands can take place so that water flow can gives rise to a braiding pattern and tqc like process.

The shaking of the bottle containing the diluted homeopathic remedy is an essential element in the buildup of water memories also in the experiments of Benveniste [135] . Just like the vigorous flow of sol near the inner monolayer, this process would create a water flow and this flow creates a braiding pattern which could provide a representation for the presence of the molecules in question. Note that the hardware of braiding could carry information about molecules (cyclotron frequencies for ions for instance.

The model for the formation of scaled down variants of memories in hippocampus discussed above suggests that each half period of theta rhythm corresponds to tqc followed by a non-computational period during which the outcome of tqc is expressed as 4-D nerve pulse patterns involving cyclotron frequencies and Josephson frequency. Josephson currents at the second half period would generate dark Josephson radiation communicating the outcome of the calculation to the magnetic body. Entire hierarchy of EEGs with varying frequency scale would be present corresponding to the onion like structure of magnetic body. This pattern would provide an electromagnetic representation for the presence of the antigene and could be mimicked artificially [136] , [23] .

This picture might apply be the case also in the case of water memory.

1. The shaking might drop some fraction of antigene molecules to dark space-time sheets where they generate a dark color magnetic field. Because of the large value of Planck constant super-

conductivity along color flux tubes running from molecular space-time sheets could still be present.

2. TGD based model of super conductivity involves double layered structures with same p-adic length scale scale as cell membrane [12] . The universality of p-adic length scale hierarchy this kind of structures but with a much lower voltage over the bilayer could be present also in water. Interestingly, Josephson frequency $ZeV/\hbar$ would be much lower than for cell membrane so that the time scale of memory could be much longer than for cell membrane for given value of $\hbar$ meaning longer time scale of memory recall.

3. Also in the case of homeopathic remedy the communication of the result of tqc to the magnetic body would take place via Josephson radiation. From the point of view of magnetic body Josephson radiation resulting in shaking induced tqc induced would replace the homeopathic remedy with a field pattern. The magnetic bodies of basophils could be cheated to produce allergic reaction by mimicking the signal representing the outcome of this tqc. This kind of cheating was indeed done in the later experiments of Benveniste involving very low frequency electromagnetic fields in kHz region allowing no identification in terms of molecular transitions (magnetic body and cyclotron frequencies) [136] .

Why experimenter had to know which bottle contained the treated water?

Why experimenter had to know which bottle contained the treated water? The role of experimenter eliminates the possibility that the (magnetic bodies of) clusters of water molecules able to mimic the (magnetic bodies of) antigene molecules electromagnetically are present in the solution at geometric now and produce the effect. The earlier explanation for experimenter's role was based on the idea that memory storage requires metabolic energy and that experimenter provides it. Tqc picture suggests a variant of this model in which experimenter makes possible the recall of memories of water represented as braiding patterns and realized via tqc.

1. Does experimenter provide the metabolic energy needed to store the memories of water?

What could be then the explanation for the failure of the modified experiment? Each memory recall reduces the occupation of the states representing bit 1 and a continual metabolic energy feed is needed to preserve the bit sequence representations of antibodies using laser light systems as bit. This metabolic energy feed must come from some source.

By the universality of metabolic energy currencies population inverted many-sheeted lasers in living organisms define the most natural source of the metabolic energy. Living matter is however fighting for metabolic energy so that there must be some system willing to provide it. The biological bodies of experimenters are the best candidates in this respect. In this case experimenters had even excellent motivations to provide the metabolic energy. If this interpretation is correct then Benveniste's experiment would demonstrate besides water memory also psychokinesis and direct action of desires of experimenters on physics at microscopic level. Furthermore, the mere fact that we know something about some object or direct attention to it would mean a concrete interaction of our magnetic with the object.

2. Does experimenter make possible long term memory recall?

The alternative explanation is that experimenter makes possible long term memory recall which also requires metabolic energy.

1. If braiding pattern represents, the water memory the situation changes since the robustness of the braiding pattern suggests that this representation is still in the geometric past (which is replaced with a new one many times). If the dark variants of molecules created in the process are still in the water, the braid representation of water memories could be available even in the geometric now but it is better to not make this assumption. The challenge is to understand how this information can be made conscious.

2. What is certainly needed is that the system makes the tqc again. This would mean a fractal quantum jump involving unitary U process and state function reduction leading to the generation of generalized EEG pattern. Only the sums and differences of cyclotron frequency and Josephson

frequency would matter so that the details of the flow inducing braiding do not matter. The shaking process might be continuing all the subjective time in the geometric past so that the problem is how to receive information about its occurrence. Experimenter might actually help in this respect since the mechanism of intentional action initiates the action in the geometric past by a negative energy signal.

3. If the magnetic body of the water in the geometric now can entangle with the geometric past, tqc would regenerate the experience about the presence of antigene by sharing and fusion of mental images. One can however argue that water cannot have memory recall in this time scale since water is quite simple creature and levels with large enough $\hbar$ might not be present. It would seem that here the experimenter must come in rescue.

4. The function of experimenter's knowledge about which bottle contains the homeopathic solution could be simply to generate time-like entanglement in the required long time scale by serving as a relay station. The entanglement sequence would be *water now - experimenter now - water in the past* with "now" and "past" understood in the geometric sense. The crucial entanglement bridge between the magnetic body of water and experimenter would be created in the manufacturing of the homeopathic remedy.

   Note that this explanation does not exclude the first one. It is quite possible that experimenter provides also the metabolic energy to the bit representation of water memories possibly induced by the long term memory recall.

This picture is of course just one possible model and cannot be taken literally. The model however suggest that magnetic bodies of molecules indeed define the braiding; that the generalized EEG provides a very general representation for the outcome of tqc; that liquid flow provides the manner to build tqc programs - and also that shaking and sudden pulses is the concrete manner to induce visible-dark phase transitions. All this might be very valuable information if one some day in the distant future tries to build topological quantum computers in laboratory.

10.4 Model for the hierarchy of Josephson junctions

As far as hierarchy of EEGs and its generalizations is considered the hierarchy of Josephson junctions assignable to cell membrane itself is relevant. Dark matter hierarchy and p-adic fractality allow to imagine a fractal hierarchy of structures analogous to cell membrane with arbitrarily large thickness. One can even imagine scaled up variants of cell membrane with different p-adic length scale and value of Planck constant but possessing same membrane potential as ordinary cell membrane. The generalization of the imbedding space helps to understand what is involved and is discussed in Appendix.

10.4.1 The most recent model for the generation of nerve pulse

For some time ago I learned [7, 9, 27, 28, 26] (thanks to Ulla Mattfolk) that nerve pulse propagation seems to be an adiabatic process and thus does not dissipate: the authors propose that 2-D acoustic soliton is in question. Adiabaticity is what one expects if the ionic currents are dark currents (large $\hbar$ and low dissipation) or even supra currents. Furthermore, Josephson currents are oscillatory so that no pumping is needed. Combining this input with the model of DNA as topological quantum computer (tqc) [26] leads to a rather precise model for the generation of nerve pulse.

1. The system would consist of two superconductors- microtubule space-time sheet and the space-time sheet in cell exterior- connected by Josephson junctions represented by magnetic flux tubes defining also braiding in the model of tqc. The phase difference between two super-conductors would obey Sine-Gordon equation allowing both standing and propagating solitonic solutions. A sequence of rotating gravitational penduli coupled to each other would be the mechanical analog for the system. Soliton sequences having as a mechanical analog penduli rotating with constant velocity but with a constant phase difference between them would generate moving kHz synchronous oscillation. Periodic boundary conditions at the ends of the axon rather than chemistry determine the propagation velocities of kHz waves and kHz synchrony is an automatic

consequence since the times taken by the pulses to travel along the axon are multiples of same time unit. Also moving oscillations in EEG range can be considered and would require larger value of Planck constant in accordance with vision about evolution as gradual increase of Planck constant.

2. During nerve pulse one pendulum would be kicked so that it would start to oscillate instead of rotating and this oscillation pattern would move with the velocity of kHz soliton sequence. The velocity of kHz wave and nerve pulse is fixed by periodic boundary conditions at the ends of the axon implying that the time spent by the nerve pulse in traveling along axon is always a multiple of the same unit: this implies kHz synchrony. The model predicts the value of Planck constant for the magnetic flux tubes associated with Josephson junctions and the predicted force caused by the ionic Josephson currents is of correct order of magnitude for reasonable values of the densities of ions. The model predicts kHz em radiation as Josephson radiation generated by moving soliton sequences. EEG would also correspond to Josephson radiation: it could be generated either by moving or standing soliton sequences (latter are naturally assignable to neuronal cell bodies for which $\hbar$ should be correspondingly larger): synchrony is predicted also now.

3. The previous view about microtubules in nerve pulse conduction can be sharpened. Microtubular electric field (always in the same direction) could explain why kHz and EEG waves and nerve pulse propagate always in same direction and might also feed energy to system so that solitonic velocity could be interpreted as drift velocity. This also inspires a generalization of the model of DNA as tqc sine also microtubule-cell membrane systems are good candidates for performers of tqc. Cell replication during which DNA is out of game seems to require this and microtubule-cell membrane tqc would represent higher level tqc distinguishing between multi-cellulars and mono-cellulars.

4. New physics would enter in several manners. Ions should form Bose-Einstein cyclotron condensates. The new nuclear physics predicted by TGD [1] , [1] predicts that ordinary fermionic ions (such as K^+, Na^+, Cl^-) have bosonic chemical equivalents with slightly differing mass number obtained by replacing one or more neutral color flux tubes connecting nucleons of neutral atom with a charged one. Anomalies of nuclear physics and cold fusion provide experimental support for the predicted new nuclear physics. Electronic supra current pulse from microtubules could induce the kick of pendulum inducing nerve pulse and induce a small heating and expansion of the axon. The return flux of ionic Josephson currents would induce convective cooling of the axonal membrane. A small transfer of small positive charge into the inner lipid layer could induce electronic supra current by attractive Coulomb interaction. The exchange of exotic W bosons which are scaled up variants of ordinary $W^{\pm}$ bosons is a natural manner to achieve this if new nuclear physics is indeed present.

10.4.2 Quantum model for sensory receptor

This original model of nerve pulse and EEG was still based on the implicit assumption that the space-time sheet carrying the Josephson currents is far from vacuum. The model for sensory receptor and sensory qualia however led to a the proposal that the space-time sheet in question is near vacuum extremal [31, 56] . Near vacuum extremal property does not affect the general structure of the model in an essential manner.

1. The only change [56, 57] is the replacement of charges ± 1 of ions with effective charges given as

$$Q_{eff} = -\frac{Z-N}{2p} + 2Z + q_{em} \quad . \tag{10.4.1}$$

Z and N denote nuclear charge and neutron number. $p = sin^(\theta_W)$ corresponds to Weinberg angle. For K^+, Cl^-, Na^+, Ca^{++} one has $Z = (19, 17, 11, 20)$, $Z - N = (-1, -1, -1, 0)$, and $q_{em} = (1, -1, 1, 2)$. Table 1 below gives the values of Josephson energies for some values of resting potential for $p = sin^(\theta_W) = .0295$ reproducing the frequencies of peak sensitivity for photoreceptors. Rather remarkably, they are in IR or visible range.

2. The energies are in UV and visible range. Hence one can consider also Josephson junctions with considerably lower membrane potentials of order mV are possibly without losing the thermal stability. For instance, one could consider $k = 151, 157, 163, 167$ Josephson junctions with a membrane potential scaling as $1/L(k)$. For $k = 167$ the energies would be scaled down by a factor $2^{-(167-151)/2} = 2^{-8}$ giving for $V_{eff} = .09$ V a photon energy somewhat below the thermal energy at room temperature. On the other hand, the fact that Josephson junctions with a vanishing Z^0 field are at the verge of thermal instability suggests that also they might be present in living matter.

3. From Table 1 one can evaluate the value of Planck constant for a given Josephson frequency for various ions. For $f_J = 5$ Hz giving a first estimate for neuronal Josephson frequency and V=-55 mV corresponding to the critical voltage for the generation of action potential one obtains the values $r = \hbar/\hbar_0 = (1.51, 1.89, 2.11, 1.59) \times 2^{46}$ for $(Na^+, Cl^-, K^+, Ca^{++})$. For V=-70 mV corresponding to the resting potential of neuron and same Josephson frequency one obtains $r = (0.961.201.341.01) \times 2^{47}$. For Ca^{++} ion r is very near to a power of 2. A good mnemonic is that the Josephson energies of biologically inportant ions vary in an interval, which is in a reasonable approximation half octave $(E_J(K^+)/E_J(Na^+) = 1.3958 \simeq \sqrt{2} \simeq 1.4142)$.

Ion	Na^+	Cl^-	K^+	Ca^{++}
$E_J(40\ mV, p = .0295)/eV$	1.60	2.00	2.23	1.68
$E_J(50\ mV, p = .0295)/eV$	2.00	2.49	2.79	2.10
$E_J(55\ mV, p = .0295)/eV$	2.20	2.74	3.07	2.31
$E_J(65\ mV, p = .0295)/eV$	2.60	3.25	3.64	2.73
$E_J(70\ mV, p = .0295)/eV$	2.80	3.50	3.92	2.94
$E_J(75\ mV, p = .0295)/eV$	3.00	3.75	4.20	3.15
$E_J(80\ mV, p = .0295)/eV$	3.20	4.00	4.48	3.36
$E_J(90\ mV, p = .0295)/eV$	3.60	4.50	5.04	3.78
$E_J(95\ mV, p = .0295)/eV$	3.80	4.75	5.32	3.99
Color	R	G	B	W
E_{max}	2.19	2.32	3.06	2.49
energy-interval/eV	1.77-2.48	1.97-2.76	2.48-3.10	

Table 1. The table gives the prediction of the model of photoreceptor for the Josephson energies for typical values of the membrane potential. For comparison purposes the energies E_{max} corresponding to peak sensitivities of rods and cones, and absorption ranges for rods are also given. R,G,B,W refers to red, green, blue, white. The values of Weinberg angle parameter $p = sin^2(\theta_W)$ are assumed to be .23 and .0295. The latter value is forced by the fit of Josephson energies to the known peak energies.

It interesting to try to interpret the resting potentials of various cells in this framework in terms of the Josephson frequencies of various ions. Table 1 gives the values of Josephson frequencies of basic biological ions for typical values of the membrane potential.

1. The maximum value of the action potential during nerve pulse is +40 mV so that Josephson frequencies are same as for the resting state of photoreceptor. Note that the time scale for nerve pulse is so slow as compared to the frequency of visible photons that one can consider that the neuronal membrane is in a state analogous to that of a photoreceptor.

2. For neurons the value of the resting potential is -70 mV. Na^+ and Ca^{++} Josephson energies 2.80 eV and 2.94 eV are in the visible range in this case and correspond to blue light. This does not mean that Ca^{++} Josephson currents are present and generate sensation of blue at neuronal level: the quale possibly generated should depend on sensory pathway. During the hyperpolarization period with -75 mV the situation is not considerably different.

3. The value of the resting potential is -95 mV for skeletal muscle cells. In this case Ca^{++} Josephson frequency corresponds to 4 eV metabolic energy quantum.

4. For smooth muscle cells the value of resting potential is -50 mV. In this case Na^+ Josephson frequency corresponds to 2 eV metabolic energy quantum.

5. For astroglia the value of the resting potential is -80/-90 mV for astroglia. For -80 mV the resting potential for Cl^- corresponds to 4 eV metabolic energy quantum. This suggests that glial cells could also provide metabolic energy as Josephson radiation to neurons.

6. For all other neurons except photo-receptors and red blood cells Josephson photons are in visible and UV range and the natural interpretation would be as biophotons. The biophotons detected outside body could represent sensory leakage. An interesting question is whether the IR Josephson frequencies could make possible some kind of IR vision.

10.4.3 The role of Josephson currents

The general vision is that Josephson currents of various ions generate Josephson photons having dual interpretations as bio-photons and EEG photons. Josephson photons can in principle regenerate the quale in the neurons of the sensory pathway. In the case of motor pathways the function would be different and the transfer of metabolic energy by quantum credit card mechanism using phase conjugate photons is suggested by the observation that basic metabolic quanta 2 eV *resp.* 4 eV are associated with smooth muscle cells *resp.* skeletal muscle cells.

As already found in the previous section, the energies of Josephson photons associated with the biologically important ions are in general in visible or UV range except when resting potential has the value of -40 mV which it has for photoreceptors. In this case also IR photons are present. Also the turning point value of membrane potential is +40 mV so that one expects the emission of IR photons.

Josephson photons could be used to communicate the qualia to the magnetic body.

1. If Josephson currents are present during the entire action potential, the entire range of Josephson photons down to frequencies of order 2 kHz range is emitted for the standard value of $\hbar$. The reason is that lower frequencies corresponds to cycles longer than the duration of the action potential. The continuum of Josephson frequencies during nerve pulse makes it possible to induce cyclotron transitions at the magnetic body of neuron or large structure. This would make possible to communicate information about spatial and temporal behavior of the nerve pulse pattern to the magnetic body and build by quantum entanglement a sensory map.

2. The frequencies below 2 kHz could be communicated as nerve pulse patterns. When the pulse rate is above $f = 28.57$ Hz the sequence of pulses is experienced as a continuous sound with pitch f. f defines the minimum frequency for which nerve pulses could represent the pitch and there remains a 9 Hz long range to be covered by some other communication method.

3. The cyclotron frequencies of quarks and possibly also of electron would make possible a selective reception of the frequencies emitted during nerve pulse. Same applies also to the Josephson frequencies of hair cell (, which does not fire). If the value of Planck constant is large this makes possible to communicate the entire range of audible frquencies to the magnetic body. Frequency would be coded by the magnetic field strength of the flux tube. Two options are available corresponding to the standard ground state for which Z^0 field is very weak and to almost vacuum extremals. For the first option one as ordinary cyclotron frequencies. The cyclotron frequency scales for them differ by a factor

$$r(q) = \frac{Q_{eff}(q)}{Q_{em}(q)} = \frac{\epsilon(q)}{2pQ_{em}(q)} + 1 \quad , \quad \epsilon(u) = -1 \quad , \epsilon(d) = 1 \tag{10.4.2}$$

from the standard one. For $p = .0295$ one obtains $(r(u), r(d), r(e) = (24.42, 49.85, 15.95)$. The cyclotron frequencies for quarks and electron with masses m(u)=2 MeV, m(d)=5 MeV, and m(e)=.5 MeV are given the table below for the two options. If one assumes that B_{end} defines the upper bound for field strength then he standard option would require both d quark and electron. Gor $d$quark with kHz CD the upper bound for cyclotron frequencies would be 20 kHz which corresponds to the upper limit of audible frequencies.

fermion	$f_c(e)/MHz$	$f_c(u)/MHz$	$f_c(d)/MHz$
standard	.564	.094	.019
nearly vacuum extremal	8.996	2.275	.947

Table 2. Cyclotron frequencies of quarks and electron in magnetic field $B_{end} = .2$ Gauss for standard vacuum with very small Z^0 field and nearly vacuum extremal.

4. Besides cyclotron frequencies also the harmonics of the fundamental frequencies assignable to quark and electron CDs could be used and in case of musical sounds this looks a highly attractive option. In this case it is now however possible to select single harmonics as in the case of cyclotron transitions so that only the rate of nerve pulses can communicate single frequency. Lorentz transform sub-CD scales up the frequency scale from the secondary p-adic time scale coming as octave of 10 Hz frequency. Also the scaling of $\hbar$ scales this frequency scale.

10.4.4 What is the role of the magnetic body?

The basic vision is that magnetic body receives sensory data from the biological body- basically from cell membranes and possibly via genome - and controls biological body via genome. This leaves a huge amount of details open and the almost impossible challenge of theoretician is to guess the correct realization practically without any experimental input. The following considerations try to clarify what is involved.

Is magnetic body really needed?

Libet's findings and the model of memory based on time mirror hypothesis suggests that magnetic body is indeed needed. What is the real function of magnetic body? Is it just a sensory canvas? The previous considerations suggest that it is also the seat of geometric qualia, in particular the pitch of sound should be coded by it. It would be relatively easy to understand magnetic body as a relatively passive sensory perceiver defining sensory map. If one assumes that motor action is like time reversed sensory perception then sensory and motor pathways would be just sensory pathways proceeding in opposite time directions from receptors to the various layers of the magnetic body. Brain would perform the information processing.

Certainly there must exist a region in which the motor and sensory parts of the magnetic body interact. What comes in mind is that these space-time sheets (or actually pairs of space-time sheets) are parallel and generate wormhole contacts between them. This interaction would be assignable to the region of the magnetic body could receive positive energy signals from associative sensory areas and send negative energy signals to motor motor neurons at the ends of motor pathways wherefrom they would progate to premotor cortex, supplementary motor cortex and to frontal lobes where the abstract plans about motor actions are generated.

Is motor action time reversal of sensory perception in zero energy ontology?

One could argue that the free will aspect of motor actions does not conform with the interpretation as sensory perception in reversed direction of time. On the other hand, also percepts are selected -say in binocular rivalry [24] . Only single alternative percept need to be realized in a given branch of the multiverse. This makes possible metabolic economy: for instance, the synchronous firing at kHz frequency serving as a correlate for the conscious percept requires a lot of energy since dark photons at kHz frequency have energies above thermal threshold. Similar selection of percepts could occur also at the level of sensory receptors but quantum statistical determinism would guarantee reliable perception. The passivity of sensory perception and activity of motor activity would reflect the breaking of the arrow of time if this interpretation is correct.

What magnetic body looks like?

What magnetic body looks like has been a question that I have intentionally avoided as a question making sense only when more general questions have been answered. This question iseems how unavoidable now. Some of the related questions are following. The magnetic flux lines along various parts of magnetic body must close: how does this happen? Magnetic body must have parts of size

at least that defined by EEG wavelengths: how do these parts form closed structures? How the magnetic bodies assignable to biomolecules relate to the Earth sized parts of the magnetic body? How the personal magnetic body relates to the magnetic body of Earth?

1. The vision about genome as the brain of cell would suggest that active and passive DNA strands are analogous to motor and sensor areas of brain. This would suggests that sensory data should be communicated from the cell membrane along the passive DNA strand. The simplest hypotesis is that there is a pair of flux sheet going through the DNA strands. The flux sheet through the passive strand would be specialized to communicate sensory information to the magnetic body and the flux sheet through the active strand would generate motor action as DNA expression with transcription of RNA defining only one particular aspect of gene expression. Topological quantum computation assignable to introns and also electromagnetic gene expression would be possible.

2. The model for sensory receptor in terms of Josephson radiation suggests however that flux tubes assignable to axonal membranes carry Josephson radiation. Maybe the flux tube structures assigned to DNA define the magnetic analog of motor areas and flux tubes assigned with the axons that of sensory areas.

3. A complex structure of flux tubes and sheets is suggestive at the cellular level. The flux tubes assignable to the axons would be parallel to the sensory and motor pathways. Also microtubules would be accompanied by magnetic flux tubes. DNA as topological quantum computer model assumes and the proposed model of sensory perception and cell membrane level suggests transversal flux tubes between lipids and nucleotides. The general vision about DNA as brain of cell suggest flux sheets through DNA strands.

   During sensory perception of cell and nerve pulse the wormhole flux tube connecting the passive DNA strand of the first cell to the inner lipid layer would recombine with the flux tube connecting outer lipid layer to some other cell to form single flux tube connecting two cells. In the case of sensory organs these other cells would be naturally other sensory receptors. This would give rise to a dynamical network of flux tubes and sheets and axonal sequences of genomes would be like lines of text at the page of book. This structure could have a fractal generalization and would give rise to an integration of genome to super-genome at the level of organelles, organs and organism and even hypergenome at the level of population. This would make possible a coherent gene expression.

4. This vision gives some idea about magnetic body in the scale of cell but does not say much about it in longer scales. The CDs of electrons and quarks could provide insights about the size scale for the most relevant parts of the magnetic body. Certainly the flux tubes should close even when they have the length scale defined by the size of Earth.

Additional ideas about the structure follow follow if one assumes that magnetic body acts a sensory canvas and that motor action can be regarded as time reversed sensory perception.

1. If the external world is represented at part of the magnetic body which is stationary, the rotation of head or body would not affect the sensory representation. This part of the magnetic body would be obviously analogous to the outer magnetosphere, which does not rotate with Earth.

2. The part of the magnetic body at which the sensory data about body (posture, head orientations and position, positions of body parts) is represented, should be fixed to body and change its orientation with it so that bodily motions would be represented as motions of the magnetic , which would be therefore analogous to the inner magnetosphere of rotating Earth.

3. The outer part of the personal magnetic body is fixed to the inner magnetosphere, which defines the reference frame. The outer part might be even identifiable as the inner magnetosphere receiving sensory input from the biosphere. This magnetic super-organism would have various life forms as its sensory receptors and muscle neurons. This would give quantitative ideas about cyclotron frequencies involved. The wavelengths assignable to the frequencies above 10 Hz would correspond to the size scale of the inner magnetosphere and those below to the outer magnetosphere. During sleep only the EEG communications with outer magnetic body would remain intact.

4. Flux quantization for large value of $\hbar$ poses an additional constraint on the model.

   (a) If Josephson photons are transformed to a bunch of ordinary small $\hbar$ photons magnetic flux tubes can correspond to the ordinary value of Planck constant. If one assumes the quantization of the magnetic flux in the form

   $$\int BdA = n\hbar$$

   used in super-conductivity, the radius of the flux tube must increase as $\sqrt{\hbar}$ and if the Josephson frequency is reduced to the sound frequency, the value of $\hbar$ codes for the sound frequency. This leads to problems since the transversal thickness of flux tubes becomes too large. This does not however mean that the condition might not make sense: for instance, in the case of flux sheets going through DNA strands the condition might apply.

   (b) The quantization of magnetic flux could be replaced by a more general condition

   $$\oint (p - ZeA)dl = n\hbar \ , \tag{10.4.3}$$

   where p represents momentum of particle of super-conducting phase at the boundary of flux tube. In this case also $n = 0$ is possible and poses no conditions on the thickness of the flux tube as a function of $\hbar$. This option looks reasonable since the charged particles at the boundary of flux tube would act as sources of the magnetic field.

   (c) Together with the Maxwell's equation giving $B = ZeNv$ in the case that there is only one kind of charge carrier this gives the expression

   $$N = \frac{2m}{RZ^2e^2} \tag{10.4.4}$$

   for the surface density N of charge carrier with charge Z. R denotes the radius of the flux tube. If several charge carriers are present one has $B = \sum_k N_k Z_k e v_k$, and the condition generalizes to

   $$N_i = \frac{2m_i v_i}{RZ_i \sum_k Z_k v_k e^2} \ . \tag{10.4.5}$$

   It seems that this condition is the most realistic one for the large $\hbar$ flux sheets at which Josephson radiation induces cyclotron transitions.

What are the roles of Josephson and cyclotron photons?

The dual interpretation of Josephson radiation in terms of bio-photons and EEG photons seems to be very natural and also the role of Josephson radiation seems now relatively clear. The role of cyclotron radiation and its interaction with Josephson radiation are not so well understood.

1. At least cell membrane defines a Josephson junction (actually a collection of them idealizable as single junctions). DNA double strand could define a series of Josephson junctions possibly assignable with hydrogen bonds. This however requires that the strands carry some non-standard charge densities and currents- I do not know whether this possibility is excluded experimentally. Quarks and antiquarks assignable to the nucleotide and its conjugate have opposite charges at the two sheets of the wormhole flux tube connective nucleotide to a lipid. Hence one could consider the possibiliy that a connection generated between them by reconnection mechanism could create Josephson junction.

2. The model for the photoreceptors leads to the identification of biophotons as Josephson radiation and suggests that Josephson radiation propagates along flux tubes assgnable to the cell membranes along sensory pathways up to sensory cortex and from there to motor cortex and back to the muscles and regenerates induced neuronal sensory experiences.

3. Josephson radiation could be used quite generally to communicate sensory data to/along the magnetic body: this would occur in the case of cell membrane magnetic body at least. The different resting voltages for various kinds of cells would select specific Josephson frequencies as communication channels.

4. If motor action indeed involves negative energy signals backwards in geometric time as Libet's findings suggest, then motor action would be very much like sensory perception in time reversed direction. The membrane resting potentials are different for various types of neurons and cells so that one could speak about pathways characterized by Josephson frequencies determined by the membrane potential. Each ion would have its own Josephson frequency characteristizing the sensory or motor pathway.

The basic questions concern the function of cyclotron radiation and whether Josephson radiation induces resonantly cyclotron radiation or vice versa.

1. Cyclotron radiation would be naturally associated with the flux sheets and flux tubes. The simplest hypothesis is that at least the magnetic field $B_{end} = .2$ Gauss can be assigned with the some magnetic flux quanta at least. The model for hearing suggests that B_{end} is in this case quantized so that cyclotron frequencies provide a magnetic representation for audible frequencies. Flux quantization does not pose any conditions on the magnetic field strength if the above discussed general flux quantization condition involving charged currents at the boundary of the flux quantum are assumed. If these currents are not present, $1/\hbar$ scaling of B_{end} for flux tubes follows.

2. The assumption that cyclotron radiation is associated with the motor control via genome is not consistent with the vision that motor action is time reversed sensory perception. It would also create the unpleasant question about information processing of the magnetic body performed between the receival of sensory data and motor action.

3. The notion of magnetic sensory canvas suggests a different picture. Josephson radiation induces resonant cyclotron transitions at the magnetic body and induces entanglement of the mental images in brain with the points of the magnetic body and in this manner creates sensory maps giving a third person perspective about the biological body. There would be two kind of sensory maps. Those assignable to the external world and those assignable to the body itself. The Josephson radiation would propagate along the flux tubes to the magnetic body.

4. There could be also flux tube connections to the outer magnetosphere of Earth. It wuold seem that thee reconnections could be flux tubes traversing through inner magnetosphere to poles and from there to the outer magnetosphere. These could correspond to rather low cyclotron frequencies. Especially interesting structure in this respect is the magnetic flux sheet at the Equator.

10.4.5 Dark matter hierarchies of Josephson junctions

The hierarchy of Josephson junctions assignable to cell membrane and characterized by values of Planck constant provides a rather nice model for cell membrane but one can consider also more general dark hierarchies of Josephson junctions. This model conforms with the general vision that living matter processes information by locating it to various pages of the "Big Book".

Maximization of Planck constant in quantum control and communication in living matter

The sectors of the imbedding space for which CD and CP_2 are replaced with their n_a- *resp.* n_b-fold coverings define the most promising candidates concerning the understanding of living matter, at least the quantum control of living matter. The reason is that the value of the Planck constant is maximized and given by $r = \hbar/\hbar_0 = n_a n_b$. Also the number of pages with same Planck constant would be finite unlike for the more general option allowing rational values of Planck constant. In particular, infinite number of pages with the standard value of Planck constant would be possible and this might lead to mathematical difficulties.

Experimental constraints allow to consider also the possibility that only covering spaces are possible. One must be however very cautious in making hasty conclusions. If also factor spaces are allowed one can have G_a or G_b as discrete and exact symmetry groups at the level of dark matter and these symmetries would be manifested as approximate symmetries of the visible matter topologically condensed around the dark matter.

1. In M^4 degrees of freedom since the restriction to the orbifold $\hat{M}^4/G_a$ is equivalent to the exact G_a-invariance of dark matter quantum states. Molecular rotational symmetries correspond typically to small groups G_a and might relate to this symmetry. Small values of n_a would not affect dramatically the value of Planck constant if n_b is large.

2. $G_a = Z_n$, $n = 5, 6$ are favored for molecules containing aromatic cycles. Also genuinely 3-dimensional tedrahedral, octahedral, and icosahedral symmetries appear in living matter.

In the sequel only integer values of Planck constant will be considered. An especially interesting hierarchy corresponds to ruler and compass integers expressible as a product of power of two and distinct Fermat primes (see Appendix). The reason is that these integers correspond to number theoretically very simple quantum phases. This hierarchy includes as a special case powers of two and one can imagined a resonant interaction between p-adic length scale hierarchy and hierarchy of Planck constants.

Dark hierarchy of Josephson junctions with a constant thickness

The model for EEG relies on fractal hierarchy of cell membrane like structures with a fixed thickness and membrane potential. Therefore cell membrane thickness is not scaled by $\hbar$ as one might naively expect. Same applies to magnetic flux tubes: this is possible since the condition for the quantization of magnetic flux can be replaced with a more general one if one allows charged currents at the boundaries of flux quanta [56] . In this model the value of $\hbar$ becomes a measure for the evolutionary level of cell and neurons in hippocampus, associative regions of cortex and their motor counterparts, and frontal lobes are expected to correspond to the largest values of $\hbar$ measuring also the time scale of long term memory and planned action. Note that cell membrane corresponds to twin primes $k = 149$ and $k = 151$ with $k = 151$ defining a Gaussian Mersenne so that it is indeed very special.

Page of a book is rather precise metaphor for the magnetic flux sheet going through a linear array of strings of nuclei and also for a collection flux tubes parallel to axons. This raises several questions. Do the lines of the text of this book correspond to axons in neural circuits? Do the pages correspond to larger structures formed by the axons?

The quantum model for qualia [56] implies that Josephson radiation travels through flux tubes parallel to sensory pathways and there could be also a horizontal organization of the neurons- at least at the level of sensory receptors in the sense that magnetic flux tubes connecting DNA nucleotides to lipids of cell membrane fuse to form longer flux tubes between DNA nucleodites of different cells when sensory receptor is active. Axons could thus be seen as the analogs of text lines which however can interact with each other. Similar organization would appear at the level of flux sheets traversing through DNA strands.

Books are made for reading and one can thus ask whether the book metaphor extends. Could the observed moving brain waves scanning cortex relate to the "reading" of the information associated with these sheets of book by the magnetic body and does our internal speech correspond to this "reading"? One is also forced to ask whether these brain waves are induced by waves propagating along magnetic flux quanta of the magnetic body of Earth or personal magnetic body in the case that it has components other than magnetic flux sheets serving as Josephson junctions.

An objection against a fractal hierarchy of Josephson junctions with thickness scaling as $\hbar$

One can consider also a hierarchy of Josephson junctions with a scaled up thickness proportional to $\hbar$ instead of constant thickness. If these junctions have same voltage at all levels of the hierarchy a resonant interaction between various levels of the hierarchy would become possible.

One can represent common sense objections against this idea. The electric field involved with the higher levels of Josephson junction hierarchy is very weak: something like 10^{-7} V/m for litoionospheric Josephson junctions (of thickness about 176 km from the scaling of the cell membrane

thickness by $\lambda^4 = 2^{44}$) which might be responsible for EEG. The electric field of the Earth at space-time sheets corresponding to ordinary matter is much stronger: about $10^2 - 10^4$ V/m at the surface of Earth but decreasing rapidly as ionosphere is approached being about .3 V/m at 30 km height. The estimate for the voltage between ionosphere and Earth surface is about 200 kV [40] .

The many-sheeted variant of Faraday law implies that on order to have a voltage of order .08 V over lito-ionospheric Josephson junction at dark matter space-time sheet, the voltage over ionospheric cavity must be almost completely compensated by an opposite voltage over litosphere so that lito-ionospheric double layer could be seen as a pair of capacitor plates in a radial electric field of order 10^{-7} V/m generated by the charge density in sub-litospheric part of Earth. This condition requires fine-tuning and therefore looks unrealistic.

A natural distance scale in which the electric field is reduced would correspond to 10-20 km thick layer in which whether phenomena are present. The mirror image of this layer would be Earth's crust. The cell membrane counterpart would be a dipole layer like charge density between the lipid layers of the cell membrane. Note that the electric field at dark matter space-time can be constant. However, as far as Josephson junction is considered, it is only the net voltage what matters.

10.4.6 p-Adic fractal hierarchy of Josephson junctions

p-Adic length scale hypothesis allows to imagine a hierarchy of Josephson junctions at least in length scales regarded usually as biologically relevant. The voltage through the junction need not however be same as for the ordinary cell membrane anymore. Twin primes are especially interesting since they would naturally correspond to pairs of structures analogous to a pair of lipid layers defining cell membrane.

In particular, twin primes abundant in the p-adic length scale range assignable to living matter could define double layered structures acting as Josephson junctions.

$(k, k+2)$	$(137, 139)$	$(149, 151)$	$(167, 169 = 13^2)$	$(179, 181)$
$L(k)$	.78 A	5 nm	$2.5\mu m$	.32 mm
$(k, k+2)$	$(191, 193)$,	$(197, 199)$		
$L(k)$	1 cm	8 cm		

Table 3. Twin primes define especially interesting candidates for double membrane like structures defining Josephson junctions. Also included the pair $(137, 13^2 = 169)$ although $k = 169$ is not prime. The two largest scales could relate to structures appearing in brain.

Also Gaussian Mersennes define highly interesting p-adic length scales and the length scale range between cell membrane thickness and the size of cell contains as many as four Gaussian Mersennes corresponding to $k = 151, 157, 163, 167$. Only the smallest one is associated with a twin prime but p-adic length scale hypothesis allows also non-prime values of k.

The possibility of a p-adic hierarchy of membrane like structures accompanied by Josephson junctions

One can imagine the existence of fractally scaled up variants of cell membrane defining hierarchy of Josephson junctions possibly realized as magnetic flux tubes. The possible existence of this hierarchy is however not relevant for the model of EEG in its recent form.

The first hierarchy correspond to the p-adic length scales varying in the range of biologically relevant p-adic length scales $L(k)$ involving membrane like structures. Twin primes $(k, k+2)$ are good candidates here (Table 3). Second hierarchy corresponds to dark matter hierarchy for which length scales come as $\sqrt{r}L(k)$), $r = \hbar/\hbar_0$. Later the question which values of r are favored will be discussed.

The size of cell nucleus varies in the range $(L(169) = 5\ \mu m, 2L(169) = 10\ \mu m)$. This is consistent with the assumption that cell nucleus provides the fundamental representation for this block. This would mean that at least the multiply coiled magnetic flux quantum structures associated with DNA appear as fractally scaled up copies.

Each dark matter level corresponds to a block of p-adic length scales $L(k)$, $k = 151, ..., 169$. Also new length scales emerge at given level and correspond to $L(k)$, $k > 169$. The dark copies of all these length scales are also present. Hence something genuinely new would emerge at each level.

Fractal hierarchy of magnetic bodies assignable to cell

Second hierarchy corresponds to a dark matter hierarchy involving values of Planck constant. The original hypothesis was that the values of Planck constant comes as $r \equiv \hbar/\hbar_0 = 2^{11k}$ of given p-adic length scale assignable to biological membrane like structure. A possible justification for the hypothesis is that the ratio of electron and proton masses is rather near to 2^{11} and that this number appears in quantum TGD in the role of fundamental constant. This hypothesis is however un-necessarily restrictive and it is better to consider at least the values of r given as products of two ruler and compass integers n_F expressible as a product of distinct Fermat primes and some power of two. The justification comes from the number theoretic vision about evolution and number theoretical simplicity of the phases $q = exp(i2\pi/n_F)$ (Appendix).

The emergence of a genuinely new structure or function in evolution would correspond to the emergence of new level in this fractal hierarchy. Quantum criticality would be essential: phases corresponding different values of Planck constant would compete at quantum criticality.

The flux sheet or tubes through cell membranes should integrate to larger structures at the higher levels of dark matter hierarchy implying the integration of sensory inputs from a large number of cells to single coherent input at higher levels of dark matter hierarchy. One can think two options: the sensory inputs from cell membranes are communicated directly to the magnetic body or via the DNA. The second option would require that the flux sheets or tubes starting from cell membrane traverse also the DNA.

10.5 Physical model for genetic code and its evolution

The original number theoretic models for genetic realied on the idea that genetic code has deeper number theoretical significance. The neglect of some obvious physical inputs however generated some pseudo problems. These models however led to what I believe is the correct track concerning the understanding of the prebiotic evolution. The original model for the evolution of genetic code as a fusion of singlet and doublet codes to triplet code has been discussed in [1] . The model to be discussed here is obtained from this model by some dramatic simplifications.

The basic questions are following.

1. What were the physical counterparts of the pre-amino-acids and pre-tRNAs for singlet and doublet codes?

2. How the triplet code emerged from the singlet and doublet codes? How the tRNA molecules evolved and how the amino-acids replaced pre-amino-acids?

3. Can one identify singlet and doublet life-forms or at least some predecessors of triplet life forms as existing life-forms?

In an attempt to answer these questions p-adic length scale hypothesis and the vision about the molecular evolution as a sequence of spontaneous symmetry breakings induced by the generation of new space-time sheets serve as valuable guide lines. The following biological input is needed.

1. RNA world [158] as a model for pre-biotic evolution allows to identify pre-amino-acids as RNA sequences (RNA_1 for short) differing somehow from the ordinary RNA sequences (RNA_2 for short). 1-code was associated with the transformation of $RNA_2 \rightarrow RNA_1$ and 2-code in the simplest case with the transcription of RNA_2 to its conjugate.

2. The cross like structure of tRNA molecule identifiable as a composite of its singlet and doublet predecessors allows to read directly the main steps in the evolution of the triplet code as a fusion of singlet and doublet codes and also gives detailed and highly non-trivial information about RNA_1.

3. The reverse transcriptase, appearing in retro-viruses like HIV and acting also as a transcriptase [12] , provides the mechanism transforming RNA sequences to DNA sequences inside pre-nucleus so that DNA→RNA code emerged and also evolved rapidly since reverse transcriptase makes a lot of errors.

4. The basic idea is that the fusion of $tRNA_1$ and $tRNA_2$ to to $tRNA_3$, the recent tRNA, made $RNA_2 \to RNA_1$ and $RNA_2 \to RNA_2$ transformations impossible and the amino-acids originally catalyzing the attachment of RNA_2 doublet in RNA_2 transcription began to be attached to a growing amino-acid sequence and mRNA$\to$ amino-acid part of genetic machinery was established. The emergence of reverse transcriptase brought in DNA. DNA as topological quantum computer idea generalized to RNA context provides tight additional conditions on the course of events: in particular, membrane like structures, most naturally consisting of RNA_1 should have been present already at RNA era.

5. Nanno-bacteria claimed to be even the dark bio-matter are excellent candidates for singlet and doublet life-forms or at least, predecessors of the recent life-forms. There are reasons to believe that RNA era is still continuing inside cell nucleus.

Second group of questions relates to the quantum control of the translation process. There are many questions also now.

1. What makes a codon stopping codon?

2. What is behind the symmetries of the code with respect to the third codon.

3. What is the origin of breaking of the canonical A-T, C-G rules for mRNA-tRNA association?

The model for the transition from RNA era to RNA-amino-acid era allows to answer these questions and te DNA as tqc picture leads to a physical interpretation of these symmetries and their breaking.

10.5.1 RNA world

The hypothesis that pre-biotic life before the emergence of the cell membrane structures was RNA dominated (the notion of RNA world) is based on a strong empirical evidence summarized in detail in [174] . For instance, only RNA can be generated spontaneously in the absence of cell membrane bounded structures. There is also a lot of support for the ability of RNA to take care of functions like replication, translation, and transfer (see the [174] and references therein). Ribozymes could even replace enzymes as RNA based catalyzing agents so that even amino-acids might be un-necessary in RNA world and the system could consist of RNA only. This of course does not mean that this system could yet realize genetic code and evolve.

An important implication is that pre-amino-acids might be identifiable as $2', 5'$ RNA, which was produced in the classical experiments of Leslie Orgel at 1980s mimicking primordial ocean. There are however also other candidates and the structure of tRNA more or less fixes identification to a high degree.

Ontogeny recapitulates phylogeny principle suggests that if RNA coded RNA during primordial period, the remnants of these RNAs could still exist and be coded by specific genes. This is indeed the case [205] (for an article about RNA genes and RNA world see [126]). RNA genes were discovered already 1990 in the genome of Caenorhabditis elegans, the small nematode worm but it took years to realize that they do not code proteins but small RNA molecules that somehow turn off other genes that play a role in worm development. Later these small RNA coding genes were found in flies, mollusks, fish, and even humans. As many as 200 microRNA genes in C. elegans were known at time of the writing of the article, which would represent about 1 percent of the genes of its genes. There is also evidence that centrosomes possess their own genome based on RNA rather than DNA [18] .

10.5.2 Programming of bio-molecular self assembly pathways from TGD point of view

The beautiful results (for a popular summary see [107]) about programming of bio-molecular self assembly - described above - when combined with the earlier model for the pre-biotic evolution - inspire interesting insights about the role of braiding in translation. The basic observation is that the structure of tRNA- although more complex than that of hairpin- has much common with that of hairpins. Therefore it is interesting to look this structure from the point of view of TGD. For instance, one can find whether the notions of braiding, anomalous em charge and quark color could provide additional insights about the structure and function of tRNA.

The brief summary of the resulting picture is as follows. According to the TGD based model of prebiotic evolution, 3-code should have resulted as a fusion of 1- and 2- codes to 3-codes involving fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3 \equiv tRNA$. Second hypothesis is that during RNA era the function of $tRNA_2$ was to generate RNA_2 double helix from single RNA strand and that amino-acids catalyzed this process. The considerations that follow strongly suggest that $tRNA_1$ was involved with a non-deterministic generation of new RNA sequences essential for the evolution. After the establishment of 3-code these two process fused to a deterministic process generating amino-acid sequences. RNA era could still continue inside cell and play an important role in evolution.

There is an interesting work about programming bio-molecular self assembly pathways [85] . The catalytic self assembly of complexes of nuclei acids is carried out automatically by a program represented implicitly as a mixture of linear DNA strand acting as catalyst and so called hairpin DNA:s containing three nucleation sites a_t, b_t, c_t - so called toeholds.

Key ideas

The basic idea is that a set of bio-molecular reactions can be programmed to occur in a desired order by using a generalization of lock and key mechanism. The simplest self assembly pathway can be specified by a collection of keys and locks. In the beginning there is only one key and the this key fits to only one door, which leads into a room with several doors. The lock eats the key but gives one or more keys. If the room contains several doors to which the keys fits, the reaction corresponds to addition of several branches to the already existing reaction product. By continuing in this manner one eventually ends up to the last room and at the last step the lock gives back the original key so that it can act as a catalyst.

The translation of this idea to a program defining self assembly pathway is following.

1. DNA hairpin define key structural element of the self-assembly program. Hairpin is a single-stranded DNA strand in meta-stable configuration having form A+B+C [201] such that B forms a loop and C is a palindrome [73] . The formal expression for palindromy is $C = A_t^*$: this means that C read backwards (C_t) is conjugate A^* of A implying that A and C running in opposite direction can form a double helix (duplex) by hydrogen bonding. As catalytic a^* acting as key forms a double helix with a, the hairpin molecule opens to a linear DNA molecule and energy is liberated. In this process original key is lost but the two other toe-holds b_t and c_t contained by the hairpin become available as keys. Each hairpin in the mixture of catalyst and hairpin molecules has its own lock and two keys.

2. The process of opening new doors continues until all hairpin molecules are used. The key given by the last lock must be catalyst strand a^*. The outcome is a molecule consisting of pieces of DNA strands and can possess a very complex topology. For instance, the formation trees and star like structures can be easily programmed.

3. To run this program one needs only an optimal mixture of catalyst molecule and hairpin DNA molecules. In the applications discussed in [85] hairpins have length of order 10 nm which corresponds to p-adic length scale $L(151)$ defining also cell membrane thickness. That $L(151)$ corresponds also to the length of 30-nucleotide sequence defining the codon of the code associated with Mersenne prime $M_{61} = 2^{61} - 1$ might not be an accident. The simplest applications are autocatalytic formation of DNA dublex molecules and of branched junctions, nucleated dendritic growth, and autonomous locomotion of a bipedal walker.

The basic idea in the realization of the autonomous motion of bipedal walker is to cheat the walker to follow a track marked by food. The walker literally eats the food and receives in this manner the metabolic energy needed to make the step to the next piece of food. The menu contains two kinds of hairpins as foods: hairpins A attached regularly along the desired path of the walker (second DNA strand) and hairpins B but not attached to the strand. The front leg l of the walker attaches to A and this catalyzes the formation of the duplex $A \cdot B$ as a waste and the liberated metabolic energy allows to make a step in which hind leg becomes the front leg.

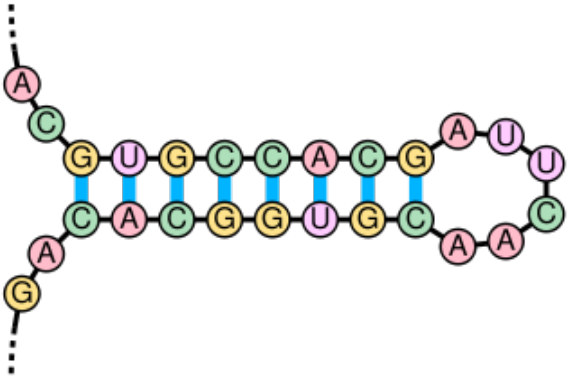

Figure 10.1: The structure of DNA hairpin (stem loop)

TGD view about the situation

The possibility to program the self-assembly relies on the almost deterministic realization of the lock and key mechanism. The presence of braid strands could make this possible.

1. Consider first the hypothesis about the cancelation of anomalous DNA charge. The palindromic character of A means that the neck of the hairpin has vanishing anomalous em charge and also vanishing color charge is possible. Hence palindromes are favored in TGD Universe. The circular piece B is not in general color singlet. It could have braid strands connecting it to it to some other DNA or nuclear membrane but this is not necessary. Same applies to the toehold a_t at the end of the other strand of neck.

2. The attachment of the lock to key could be seen as a process in which a braid consisting of magnetic flux tubes connecting lock and key strands (DNA and its conjugate) is formed spontaneously and followed by a phase transition reducing $\hbar$ contracting the flux tubes and in this manner guiding the key to the lock.

If one assumes that only paired nucleotides of single DNA strand possess braid strands, one must assume the same for mRNA. As a consequence one would loose the nice interpretation for the formation of AAA... tail of mRNA as a manner to guarantee integer valuedness and small value (or even vanishing) of the anomalous em charge. If there is braid strands associated with entire mRNA, it could end at the nuclear membrane. In this case the transfer of tRNA to mRNA during translation by a phase transition reducing $\hbar$ of braid strands could be initiated by the fusion of the braid strand ends coming from mRNA codon and from its conjugate codon at tRNA at nuclear membrane.

10.5.3 The archeology of tRNA molecules as a guideline

The study of the structure of the ordinary tRNA molecule is of considerable help in the attempts to guess what might have been its predecessor.

The structure of the tRNA molecule

The shape of the tRNA molecule [99] in 2-D representation is that of cruciform.

1. tRNA molecule has a cross like appearance, and decomposes into a body coded by tRNA gene and an acceptor stem which is same for all amino-acids and added separately and can be replaced during the lifetime of the tRNA molecule. Acceptor stem, to which the amino-acid is attached with the mediation of amino-acyl-tRNA synthase, can be said to be a passive component and is same for all tRNAs so that its structure does not determine which amino-acid is attached to it. The stem is not coded by genes and contains 4 nucleotides.

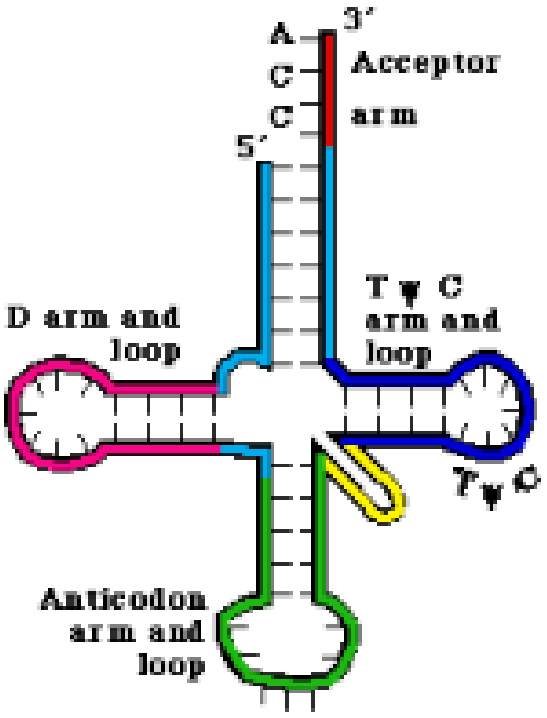

Figure 10.2: The structure of tRNA

2. tRNA molecule can be seen as single RNA strand just as hairpin. The five stems are double helices analogous to the necks of the hairpin. Strand begins at $5'$ end of the acceptor stem directed upwards. The second strand of acceptor stem continues as a toehold ending to $3'$ end of tRNA. The toehold has at its end ACC to which the amino-acid (rather than conjugate DNA) attaches.

3. tRNA molecule contains three arms with hairpin structure. A arm containing the anticodon is directed downwards. D and T arms are horizontal and directed to left and right. Between T arm and A arm there is additional variable hairpin like structure but with highly degenerate loop is degenerate. It has emerged during evolution.

4. The structure of tRNA minus anticodon depends on anti-codon which conforms with the fact T and D arms are related to the binding of amino-acid so that their nucleotide composition correlates with that of anticodon.

5. Anticodon arm contains the anticodon of mRNA codon and thus corresponds to RNA. For doublet part of the mRNA codon the correspondence is 1-1 but for the third nucleotide the correspondence is more complex due to wobble base pairing to be discussed below. Wobble base pairing indeed leads to the recent simplified model for the evolution of the triplet code as a fusion of 1-code and 2-code.

Wobble base pairing

The phenomenon of wobble base pairing [103] is very important. There are only about 40 tRNA molecules instead of 61 which means that one-to-one map between mRNA nucleotides and tRNA conjugate nucleotides is not possible. Crick suggests that so called wobble base pairing resolves the problem. What happens that the first nucleotide of anticodon is either A, G, U, or I(nosine) [46] . The base-pairings for third nucleotide are $\{A-U, G-C, U-\{A,G\}, I-\{U,A,C\}\}$. The explanation

for the non unique base pairing in the case of U is that its geometric configuration is quite not the same as in ordinary RNA strand. I is known to have 3-fold base pairing.

Minimization of the number of tRNAs requiring that only three mRNA codons act as stopping signs predicts that the number of tRNAs is 40.

1. It is convenient to classify the 4-columns of code table according to whether all four codons code for the same amino-acid ($(T,C,A,G) \to X$, whether 4-column decomposes into two doublets: $[(T,C),(A,G)] \to [X,Y]$, or whether it decomposes to triplet and singlet ($[(T,C,A),G] \to [ile, met]$). There are also the 4-columns containing stop codon: $[(U,C),(A,G)] \to [(tyr,tyr),(stop,stop)]$ and $[(U,C),A,G] \to [(cys,sys),stop,trp]$. Mitochondrial code has full A-G and T-C symmetries whereas for vertebrate nuclear code 3 4-columns break this symmetry.

2. Consider first 4-columns for which the doublet symmetry is broken. $[tyr,tyr,top,stop]$ column must correspond to first tRNA nucleotide which is A or G (tyr). The absence of anti-codons containing U implies stop codon property. For $[cys,sys,stop,trp]$ one must have A,G and C but U is not allowed. ile-met column can correspond to tRNAs with I and C as the first nucleotide.

3. For 4-columns coding for two doublet amino-acids the minimal set of first tRNA codons is $\{A,G,U\}$. For completely symmetric 4-columns the minimal set of tRNA codons is $\{I,U\}$. Thus $\{A,G,U,I\}$ would replace $\{A,G,U,C\}$.

4. There are 9 completely symmetric 4-columns making 18 tRNAs, 5 doublet pairs making 15 tRNAs, ile-met giving 2 tRNAs, and the columns containing stopping codons giving 5 tRNAs. Altogether this gives 18+15+2+5= 40. Also the deviations from the standard code can be understood in terms of the properties of tRNA.

Consider the interpretation of wobble base pairing in TGD framework assuming the braiding picture and the mapping of nucleotides to quarks. The completely symmetric 4-columns correspond to unbroken isospin and matter-antimatter asymmetries. 4-columns decomposing into doublets result from the breaking of matter-antimatter asymmetry at quark level. ile-met column corresponds to the breaking of both symmetries. The base pairings of I obviously break both symmetries.

The non-unique based pairing of U and I means that they cannot correspond to a unique quark or anti-quark in braiding U pairs with both A and G so that the braid strands starting from these RNA nucleotides must both be able to end to tRNA U. Hence tRNA U is not sensitive to the isospin of the quark. This non-uniqueness could relate to the assumed anomalous geometric character of the binding of U codon to tRNA sequence. The braid strands beginning from U, A, and C must be able to end up to I so that I can discriminate only between $\{U,C,A\}$ and G.

Anomalous em charge and color singletness hypothesis for tRNA

One can test also whether the vanishing of anomalous em charge of tRNA leads to testable predictions. One can also try understand translation process in terms of the braiding dynamics. One must distinguish between the states of tRNA alone and tRNA + amino-acid for which braidings are expected to be different.

Before continuing it must be made clear that braiding hypothesis is far from being precisely formulated. One question is whether the presence of the braiding could distinguish between matter in vivo and vitro. For instance, the condition that anomalous em charge is integer valued or vanishing for DNA hairpins in vivo gives strong condition on the loop of the hairpin but or hairpins in vitro there would be no such conditions. Second point is that amino-acids and I and U in tRNA_1 could carry variable anomalous em charge allowing rather general compensation mechanism.

1. tRNA without amino-acid

1. The minimal assumption is that braiding hypothesis applies only to the stem regions of tRNA in this case. In this case the strands can indeed begin from strand and end up to conjugate strand. The possibility of color singletness and vanishing of total anomalous em charge are automatically satisfied for the stem regions as a whole in absence of non-standard base pairings. In general the acceptor stem contains however $G*U$ base pair which is matter-antimatter asymmetric but breaks isospin symmetry and gives unit anomalous charge for the acceptor stem. Also other

stems can contain $G*U$, $U*G$ pairings as also $P*G$ and $L*U$ pairings (P and L denote amimno-acids Pro and Leu). The study of concrete examples [89] shows that single G*U bond is possible so that anomalous em charge can be non-vanishing but integer valued for double strand part of tRNA. Suppose that a given amino-acid can have anomalous of any codon coding for it. If P in $G*P$ pair has the anomalous em charge of the codon CCG, $G*P$ pair has vanishing anomalous em charge. If L corresponds to CUA the value of anomalous em charge is integer.

2. The anomalous em charge in general fails to vanish for the loops of hairpins. For the braids possibly associated with the loops of tRNA the strands can only end up to tRNA itself or nuclear membrane. If there are no braid strands associated with these regions, there is no color or anomalous em charge to be canceled so that the situation trivializes. On the other hand, in the case of tRNA I and U associated with the first nucleotide of the anticodon of tRNA can have a varying value of anomalous em charge. Therefore integer valued em charge and color singletness become possible for tRNA. tRNA can also contain amino-acids. If the amino-acids can carry a varying anomalous em charge with a spectrum corresponding to its values for DNA codons coding it, also they could help to stabilize tRNA by canceling the anomalous em charge.

2. tRNA plus amino-acid

1. Amino-acyl tRNA synthetase, which is the catalyst inducing the fusion of amino-acid with ACC stem [100], could have braid strands to both amino-acid and tRNA and have regions with opposite anomalous em charges compensating separately that of amino-acid and of the active part of tRNA. The required correlation of amino-acid with anticodon would suggest that both D and T loops and A-loop are included. The simplest option is however that the anticodon is connected by braid to amino-acid so that braiding would define the genetic code at the fundamental level and the many-to-one character of genetic code would reflect the 1-to-many character of amino-acid-quark triplet correspondence. This hypothesis is easy to kill: for the portion of catalyst attaching to a given portion of DNA strand amino-acids and codons should have opposite anomalous em charges: $Q_a(amino) = -Q_a(codon)$.

2. After the catalysis involving reduction of $\hbar$ amino-acid and tRNA would form a system with a vanishing net anomalous em charge but with a braiding structure more complex than that before the fusion.

3. In the translation process the braiding structure of tRNA- amino-acid system should re-organize: the braid strands connecting anticodon with amino-acid are transformed to braid strands connecting it to mRNA codon with a subsequent reduction of $\hbar$ of braid strands bringing tRNA into the vicinity of mRNA. In the transcription the anticodon-codon braiding would be replaced with amino-acid-mRNA braiding forcing formation of the amino-acid sequence. It will be later found that the simpler option without this step corresponds to the earlier hypothesis according to which amino-acids acted originally as catalysts for the formation of RNA double helix.

4. tRNA is basically coded by genes which suggests that the general symmetries of the genetic code apply to to the variants of tRNA associated with same anticodon. Hence the variants should result from each other by isospin splits and modifications such as permutations of subsequent nucleotides and addition of AT and CG pairs not changing overall color and isospin properties. Also anomalous base pairs $X*Y$ can be added provide their net anomalous em charge vanishes.

5. tRNA has a complex tertiary (3-D) structure [97] involving base pairing of distant nucleotides associated with the roots of the stem regions where tRNA twists sharply. This pairing could involve formation of braid strands connecting the nucleotides involved. The reduction of Planck constant for these strands could be an essential element of the formation of the tertiary structure.

The fossilized components of tRNA as record about the evolution of the recent form of the genetic code

The ordinary tRNA indeed seems to contain in its structure fossilized components providing a record about how the molecular evolution proceeded. tRNA_1 and tRNA_2 correspond naturally to the horizontal and vertical segment in the recent tRNA formed as a fusion of tRNA_1 and tRNA_2 to form a

cross like structure (see figure above). Hence tRNA_1 and trNA_2 should represent in their structures the respective genetic codes.

1. tRNA_2 should contain both the conjugate of the coding RNA nucleotide attaching to RNA_2 plus the conjugate of the coded nucleotide to which RNA nucleotide was attached and then transferred to RNA_2 and added to the growing RNA sequence. This means that the structure of tRNA should help to deduce the doublet code experimentally. The pairs formed by the RNA triplet XYZ at the end of the anticodon arm of the ordinary tRNA and the pair formed by the triplet $X'Y'Z'$ and its conjugate on right and left sides of XYZ should provide detailed information about the doublet code. The pairs $XY - X'Y'$ should represent the doublet code apart from possible symmetry breaking effects. These effects might be induced at the level of $X'Y'Z'$-amino-acid correspondence level and thus not visible in the structure of tRNA.

2. The transition to the triplet code added one RNA nucleotide to both the exotic doublet $(XY)_2$ and the doublet $X'Y'$ and its conjugate coded by it. The exotic $2',5'$ doublet plus the added singlet transformed to ordinary triplet. The simplest assumption is that these RNAs came from D arm and TψC arm. This is possible since all loops are physically near to each other. The structure of D and Tψ loops conforms with the assumption that the predecessor of the first *resp.* second loop has lost the coding *resp.* coded RNA. The structure of these loops forces also to conclude that all tRNA loops have been stem like structures before their de-activation just as the acceptor stem is. Deactivation of RNA_1 translation process must have meant the completion of these stems to loops by addition of a conjugate of the conjugate of the coded RNA.

The components of tRNA as ribozymes which have acted originally as RNA polymerases

The mechanism of ribozyme catalyzed polymerization for both the exotic RNA with mono- *resp.* disphosphate backbones, and their their double strand can be guessed from the fact that the process can be seen as an unfaithful replication. Hence the tRNAs involved would play a role analogous to DNA polymeraze in the polymerization of DNA. The only difference is that, instead of the conjugate of the template strand, a copy of strand is reproduced and the copy can be un-faithful.

DNA replication utilizes the conjugate strand as a template and occurs with the mediation of DNA polymerase enzyme, which brings dXTP, $X = A, T, C, G$ rather than dXMP, to the vicinity of the DNA conjugate strand [180] . The di-phosphate is cleaved out from dXTP and the liberated energy makes it possible to add the resulting dXMP to the growing DNA strand.

The prediction is that tRNA_1 and tRNA_2 have originally been ribozymes acting as exotic RNA polymerases. In the case of DNA strand dXMP pairs with its conjugate in the template strand by hydrogen bonds and $3',5'$ bond is formed between monophosphate deoxiribose of previous nucleoside. In the case of exotic RNA strand the XMP associated with the tRNA pairs with its conjugate in the template RNA strand, $2',5'$ bond with the ribose of the previous RNA unit is formed. tRNA is not so selective as a polymerase as DNA polymerase and this ultimately gives rise to the many-to-one correspondence crucial for the non-triviality of the genetic code.

1. RNA_2 consists of exotic RNA doublets with nucleotides connected by $2',5'$ monophosphate bonds. tRNA_2 brings $2',5'$ doublet $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ to the growing strand and glues it to the $5'$ position of the ribose in the already existing polymer. The YTP suffers the cleavage $\mathrm{YTP}_2 \to \mathrm{YMP}_2$ as in the case of DNA polymerization and the amount of metabolic energy provided by the cleavage is the same. The formation of $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ proceeds by gluing of XTP_2 to YTP_2 by a similar process so that the net metabolic energy used per nucleotide is essentially the same as in the ordinary DNA polymerization.

2. RNA_1 consists of exotic RNA singlets connected by $2',5'$ diphosphate bonds. tRNA_1 brings XTP_2 near the growing strand, the cleavage $\mathrm{XTP}_2 \to \mathrm{XDP}_2$ occurs, and XDP_2 is glued to the $5'$ position of the ribose of the previous RNA nucleotide. The amount of metabolic energy provided by the cleavage is roughly one half of that in the case of RNA_2 polymerization, and this might partially explain why diphosphate exotic RNA strands are rare whereas monophosphate exotic DNA strands can be found inside cells. On the other hand, it is $ATP \to ADP$ cleavage, which usually occurs in the ordinary metabolism instead of $ATP \to$ AMP cleavage: only during a very intense metabolism $ATP \to$ AMP cleavage occurs. Since ATP metabolism is a functional

fossil from a very early period of evolution, one might expect that $ATP \to$ ADP cleavage has in fact occurred naturally, if not even more naturally, also in the polymerization of $2', 5'$ RNA during (exotic) RNA era.

3. In the case of double exotic RNA strand of ordinary and exotic RNA the predecessor of the recent tRNA formed by tRNA_1+tRNA_2 would be a ribozyme bringing energized singlet and doublet RNAs to the double strand acting as a template with tRNA_1 component catalyzing the cleavage of the monophosphate and tRNA_2 component catalyzing the cleavage of the diphosphate.

The crucial and testable prediction is that the ribozymes responsible for the exotic mono- and diphosphate $2', 5'$ RNA polymerization should have a strong resemblance with the two structural components of the recent tRNA. Furthermore, the replication catalyzed by these ribozymes should be unfaithful, perhaps in a manner consistent with the genetic code before the breaking of its symmetries. Ribozymes responsible for the ordinary RNA polymerization are known but I am not aware about how much is known about the corresponding ribozymes in the case of $2', 5'$ RNA. The building blocks of recent tRNA would however provide a good starting point for innovative RNA engineers. In any case, the very fact that this form of RNA does not even allow DNA, makes it a more natural candidate for the basic building block of RNA life than $3', 5'$ RNA.

10.5.4 Recent genetic code as a fusion of singlet and doublet codes?

There are several guidelines helping to answer the question how DNA-amino-acid translation might have emerged from singlet and doublet codes producing only RNA from RNA.

The following vision about evolution leading from RNA era to the recent DNA-RNA-amino-acid era inspired by a combination of RNA world vision [158] with the detailed study of the structure of tRNA suggesting the presence of 1- and 2-codes during RNA era with the DNA as tqc vision suggesting the presence of cell membrane like structures as a necessary ingredient making possible topological quantum computation like processes already during RNA era. The recent model is considerably simpler than the earlier models [1] .

RNA era and the transition to RNA-amino-acid era

1. Translation of mRNA to amino-acid sequences separates from the transcription of DNA to mRNA. One expects that during RNA two different kinds of RNAs, call them RNA_2 and RNA_1, analogous to mRNA and proteins existed. RNA_2 can be identified as the ordinary $3', 5'$ RNA acting in the role of mRNA. A natural candidate for RNA_1 playing the role of proteins is $2', 5'$ RNA since it is generated in the experiments of Orgel and appears also in genomes. Of course, also other candidates can be considered and the structure of tRNA gives valuable information about the character of this RNA. The copying of RNA_2 to its conjugate was the counterpart of RNA replication. The transcription of RNA_2 to RNA_1 was the counterpart of translation.

2. The structure of tRNA, call it tRNA_3, gives valuable information about the course of events leading to the translation of mRNA to amino-acids. The cross like structure of tRNA_3 and the decomposition of RNA triplet appearing in it to 2-codon and 1-codon suggests that it resulted as a fusion of two hairpin like molecules tRNA_1 and tRNA_2. tRNA_2 brought pairs of nucleotides forming the 2-codon part of RNA triplet to the growing RNA_2 sequence during replication and 2-code was simply RNA conjugation. tRNA_1 was involved with transcription of RNA_2 to RNA_1 bringing RNA_1 nucleotides one-by own to the growing sequence. In tRNA_3 the third nucleotide does not quite correspond to ordinary RNA but to to A, G, U or I(nositol) and is believed to differ geometrically from ordinary nucleotide, and one can assume that these nucleotides were the building blocks of RNA_1 possibly appearing in $2', 5'$ form. The phenomenon of the wobble pairing can be assumed to have been present already during RNA era so that correspondence 1-code was not not 1-to-1 nor deterministic but given by the correspondence $\{U \to A, C \to G, \{A, G\} \to U, \{U, A, C\} \to I\}$ deduced from the number 40 of tRNAs and assigning unique 1-codon to only G could be interpreted as a many-to-one and non-deterministic correspondence generating new RNA sequences from existing ones. If there was RNA_2 sequence coding for tRNA_1, this sequence appearing in hairpin structure could have coded the inverse of the translation. As a consequence, the occurrence of transcription and its reversal generated a rapid evolution by creating new kinds of RNA_2 sequences.

3. From the fact that amino-acids are attached to the ACC stem of $tRNA_2$, one can guess that the role of amino-acids during RNA era was to catalyze the replication. If single amino-acid would have catalyzed the attachment of given RNA doublet to the growing sequence, there would be at most 16 amino-acids and genetic coded would not depend at all on the third nucleotide. This is indeed the case for roughly half of the code table (both matter antimatter symmetry and isospin symmetry with respect to third codon). For those mRNA codons for which A,G and T,C correspond to different amino-acids (breaking of matter antimatter asymmetry but isospin symmetry) two amino-acids catalyzed the attachment. Same amino-acid could also catalyzed two different attachments (ser, arg, leu for standard genetic code).

4. The crucial step was the fusion of the 1-code and 2-code to 3-code took place via fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3$ along their ends containing RNA_1 nucleotide and RNA_2 doublet which thus combined to RNA triplet. Presumably $tRNA_3$ in its original form was translated from a linear mRNA molecule and transformed spontaneously to the cross like shape because of the presence of palindrome structures in both. The original functions of tRNAs were not possible anymore since the triplet was not at the end of the molecule. The catalyzing amino-acid however was at the ACC end of and the function of $tRNA_3$ became to assist the translation of mRNA to amino-acid sequence. For those 3-codons for which single amino-acid catalyzed the fusion of 2-codon, a full matter antimatter and isospin symmetry resulted. For those 3-codons for which two amino-acids catalyzed the fusion, a breaking of matter antimatter symmetry took place in the sense that for given mRNA codon only the $tRNA_3$ corresponding to single amino-acid was stable. Isospin symmetry was broken only weakly or not at all (human mitocondrial code). Thus codons with A,G as third nucleotide almost always coded the first amino-acid and those with T,C as the third nucleotide the second one. Stopping codons resulted when all $tRNA_3$ corresponding to mRNA triplet were unstable. That same RNA can code for both amino-acid and act as a stop codon in certain situations, can be understood if the stability of corresponding $tRNA_3$ depends on the chemical environment.

Symbiosis with membrane bounded structures

In DNA as tqc picture nuclear and cell membranes make possible topological quantum computation. The magnetic flux tubes connecting DNA nucleotides to lipids of the cell membrane could also explain why DNA is stabile inside cell. The emergence of cell membranes consisting of lipids and generated via self-organization rather being coded by genes would have stabilized DNA generated in this manner during DNA-RNA-amino-acid era. Membrane bounded structures emerged when the space-time sheets corresponding to the p-adic length scale $k = 151$ emerged in the condensate.

Topological quantum computation should have taken place already during RNA era. This suggest that the counterpart of the cell membrane was present already at that time. Quite recently it was reported [146] that DNA duplexes of length 6 to 20 base pairs can join to longer cylinders which in turn form liquid crystals and that the liquid crystal phase separates from the phase formed by single DNA strands. Long strands had been already earlier known to form liquid crystals. This encourages to think that also RNA duplexes are able to self-organize in this manner so that the analog of cell nucleus containing RNA double helices as genetic material could have existed already during RNA era.

The latter option would allow to distinguish between RNA_2 and RNA_1 used as building block of various structures. This suggests that RNA_1, which disappeared in the transition to RNA-amino-acid era, might have formed liquid membranes containing inside then RNA_2 such that RNA_2 nucleotides were connected by magnetic flux tubes to RNA_1 nucleotides. The minimal function of RNA_1 would have been to make possible the buildup of cell membrane. In this case the lengths of RNA_1 needed to be only of order $L(151) = 10$ nm. The sequences consisting of 30 RNA_1 base pairs would correspond roughly to the thickness of cell membrane and to the codon of M_{61} code. Lipid layer of thickness 5 nm would correspond to roughly 16 base pairs and to the codon assignable to M_{17}. If magnetic flux tubes indeed stabilize DNA, the presence of RNA_1 membrane might have been enough to stabilize also DNA so that RNA era could have been followed by DNA-RNA era and eventually by DNA-RNA-amino-acid era with RNA_1 membrane being replaced by double lipid layer membrane.

Reverse transcription of RNA to DNA

The basic problem was how to build DNA sequences which would later take the command. If one, in conflict with the Central Dogma, assumes the presence of the predecessor of the so called reverse RNA transcriptase [12] associated with retro-viruses (in particular HIV virus), one can understand how this step occurred. Reverse RNA transcriptase allowed to transform ordinary RNA sequences to DNA sequences inside newly emerged pre-nuclei. The reverse transcriptase catalyzes also the transcription of DNA back to RNA so that DNA began to produce new RNA.

Reverse transcriptase requires amino-acids sequences. Amino-acids appeared as catalysts in $tRNA_2$ already during RNA era but the spontaneous emergence of reverse transcriptase before RNA$\rightarrow$ amino-acids translation look improbable. After the fusion of $tRNA_1$ and $tRNA_2$ RNA_2 could replicate only if $tRNA_1$, $tRNA_2$ and $tRNA_3$ continued to live in symbiosis for some time. This could have led naturally to the generation of reverse transcriptase and DNA. After that DNA could have taken care of the production of RNA and $tRNA_1$ and $tRNA_2$ might have lost in the fight for molecular survival or at least their importance could have diminished. The emergence of DNA could have been associated with the replacement of RNA_1 membrane with ordinary cell membrane. For instance, it might be that DNA was able to form only magnetic flux tubes only with lipid bilayer membrane.

The reverse transcription is not reliable (one error per about 1000 nucleotides), and this led to a rapid evolution of DNA analogous to that of HIV virus. This meant an escape from the fixed point situation, and a genuine DNA $\rightarrow$ RNA predecessor of the genetic code emerged. Together with the emergence of membrane bounded structures this meant genuine evolution at DNA level. Reverse transcription is possible only for the ordinary RNA and explains why exotic doublet RNA has disappeared from cell.

What were the first self replicators?

The TGD inspired model of pre-biotic evolution suggests a reasonable guess for the first self-replicating molecular entities. Both $tRNA_1$ and $tRNA_2$ molecules must have resulted as more or less copies of corresponding RNA_2 sequences (amino-acid was added after transcription to $tRNA_2$) and the minimal self-reproducing system could have consisted of $tRNA_1$, $tRNA_2$ and corresponding RNA_2 molecules. Since $tRNA_1$ and $tRNA_2$ are hairpins in the usual configuration and the mechanism making possible biochemical reaction series suggests that these hairpin molecules catalyzed the opening of the corresponding RNA_2 pieces and their coding to $tRNA_1$ or $tRNA_2$.

Note that double strands in the sense they occur for DNA are not necessary since the double strand part of hairpin is analogous to DNA double strand and the opening of hairpin structure is analogous to the opening of DNA double strand during transcription and replication. The non-determinism of 1-code could have rapidly led to a genuine evolution and one can also imagine a spontaneous generation of RNA_2 sequences as oligonucleotides consisting of copies of pieces of RNA_2 coding for $tRNA_2$.

Also more general hairpin might be used to construct a self-catalyzing system. Since exotic and normal RNA do not differ too much, a reasonable amount of guess work might allow to identify $tRNA_1$ and $tRNA_2$, and perhaps even create simple pre-biotic life-forms in the laboratory.

10.5.5 Is RNA era continuing inside cell nuclei?

The last issue of [121] contains an article about the discovery that only roughly one half of DNA expresses itself as amino-acid sequences. A detailed summary of the results has been published in Nature [45] . The Encyclopedia of DNA Elements (ENCODE) project has quantified RNA transcription patterns and found that while the "standard" RNA copy of a gene gets translated into a protein as expected, for each copy of a gene cells also make RNA copies of many other sections of DNA. In particular, intron portions ("junk DNA", the portion of which increases as one climbs up in evolutionary hierarchy) are transcribed to RNA in large amounts. What is also interesting that the RNA fragments correspond to pieces from several genes which raises the question whether there is some fundamental unit smaller than gene.

None of the extra RNA fragments gets translated into proteins, so the race is on to discover just what their function is. TGD proposal is that the RNA gets braided and performs a lot of topological quantum computation [81] . Topologically quantum computing RNA fits nicely with replicating number theoretic braids associated with light-like orbits of partonic 2-surfaces and with their spatial "printed text" representations as linked and knotted partonic 2-surfaces giving braids. An interesting

question is how printing and reading could take place. Is it something comparable to what occurs when we read consciously? Is the biological portion of our conscious life identifiable with this reading process accompanied by copying by cell replication and as secondary printing using amino-acid sequences?

This picture conforms with TGD view about pre-biotic evolution. Plasmoids [183] , which are known to share many basic characteristics assigned with life, came first: high temperatures are not a problem in TGD Universe since given frequency corresponds to energy above thermal energy for large enough value of $\hbar$ [27] . Plasmoids were followed by RNA, and DNA and amino-acid sequences emerged only after the fusion of 1- and 2-letter codes fusing to the recent 3-letter code. The cross like structure of tRNA molecules carries clear signatures supporting this vision. RNA would be still responsible for roughly half of intracellular life and perhaps for the core of "intelligent life".

I have also proposed that this expression uses memetic code which would correspond to Mersenne $M_{127} = 2^{127} - 1$ with 2^{126} codons whereas ordinary genetic code would correspond to $M_7 = 2^7 - 1$ with 2^6 codons. Memetic codons in DNA representations would consist of sequences of 21 ordinary codons. Also representations in terms of field patterns with duration of .1 seconds (secondary p-adic time scale associated with M_{127} defining a fundamental bio-rhythm) can be considered.

A hypothesis worth of killing would be that the DNA coding for RNA has memetic codons scattered around genome as basic units. It is interesting to see whether the structure of DNA could give any hints that memetic codon appears as a basic unit.

1. In a "relaxed" double-helical segment of DNA, the two strands twist [93] around the helical axis once every 10.4 base pairs of sequence. 21 genetic codons correspond 63 base pairs whereas 6 full twists would correspond to 62.4 base pairs.

2. Nucleosomes [70] are fundamental repeating units in eukaryotic chromatin [21] possessing what is known as 10 nm beads-on-string structure. They repeat roughly every 200 base pairs: integer number of genetic codons would suggest 201 base pairs. 3 memetic codons makes 189 base pairs. Could this mean that only a fraction $p \sim 12/201$, which happens to be of the same order of magnitude as the portion of introns in human genome, consists of ordinary codons? Inside nucleosomes the distance between neighboring contacts between histone and DNA is about 10 nm, the p-adic length scale L(151) associated with the Gaussian Mersenne $(1 + i)^{151} - 1$ characterizing also cell membrane thickness and the size of nucleosomes. This length corresponds to 10 codons so that there would be two contacts per single memetic codon in a reasonable approximation. In the example of Wikipedia [70] nucleosome corresponds to about 146=126+20 base pairs: 147 base pairs would make 2 memetic codons and 7 genetic codons. The remaining 54 base pairs between histone units + 3 ordinary codons from histone unit would make single memetic codon. That only single memetic codon is between histone units and part of the memetic codon overlaps with histone containing unit conforms with the finding that chromatin accessibility and histone modification patterns are highly predictive of both the presence and activity of transcription start sites. This would leave 4 genetic codons and 201 base pairs could decompose as memetic codon+2 genetic codons+memetic codon+2 genetic codons. The simplest possibility is however that memetic codons are between histone units and histone units consist of genetic codons. Note that memetic codons could be transcribed without the straightening of histone unit occurring during the transcription leading to protein coding.

10.5.6 Could nanno-bacteria correspond to predecessors of the triplet life-forms?

The experiments of Leslie Orgel (at 1980) imitating the primordial ocean demonstrate the emergence of the exotic RNA for which doublet effectively replaces the triplet. The so called nanno-bacteria represent a mystery at the borderline between living and non-living matter. The web article of Robert L. Folk [153] , who is one of the pioneers in the field besides Y. Morita [187] and E. O. Kajander [131] , provides a brief summary about nanno-bacteria and contains also references. A priori one cannot exclude the possibility that nanno-bacteria might represent a predecessor of the triplet code, perhaps even singlet or doublet life-form or their symbiosis.

Basic facts about nanno-bacteria

Nanno-bacteria (often called also nanobacteria) are considerably smaller than ordinary bacteria. The sizes of the nanno-bacteria vary from about 20 nm to .2 micro-meters. Thus the smallest nanno-bacteria have size scale not much above $L(151)$ so that optical microscope does not allow to study them. Indeed, geologists discovered nanno-bacteria by using scanning electron microscope.

Nanno-bacteria can originate a precipitation in calcite and argonite crystals by providing the seed of the crystal. Nanno-bacteria act also as catalysts by attracting cations to their negatively charged cell walls. They appear as dense clumps in various minerals and rocks such as limestones, dolomites, native sulphur crystals, and metallic sulfide minerals [153] . Nanno-bacteria produce complex silicates such as clays, where their sizes can be as small as 30 nanometers. They are involved even with the construction of birds' eggs! Nanno-bacteria of size about .1 micro-meters were found in the Martian meteorite ALH84001 [5] , and there is evidence that carbonaceous chondrite meteorite Allende [153] contains them. According to Folk, the nanno-bacteria might the biological counterpart of the dark matter perhaps dominating over the ordinary bio-matter in the entire universe. An interesting question is how deep in the rock nanno-bacteria based life forms can survive. The hypothesis about intra-terrestrial life suggests that there is no limit here!

Although nanno-bacteria have been demonstrated to replicate [153] , the prevailing belief has been that nanno-bacteria cannot be real life forms since by their small size they cannot contain the usual genetic apparatus. A Finnish biologist Kajander and his collaborators have done a lot of self-funded pioneering work in the study of the nanno-bacteria [131] . It has not been demonstrated that nanno-bacteria possess DNA-mRNA-amino-acid translation machinery, the existence of which is often taken almost as a definition for what it is to be a living system (a size larger than .2 micro-meters has been the second prevailing definition of a living system!). This failure could be understood if nanno-bacteria contain only replicating DNA or if only the RNA-to-RNA translation machinery exists possibly accompanied by RNA-DNA transcriptase transforming the code to DNA-RNA code. Due to the hard cell wall of nanno-bacteria, the study of DNA/RNA is very difficult but according to the Kajander's private communication to Folk [153] , the nanno-bacterial DNA exists and consists of very short strands.

Nanno-bacteria as RNA life?

Nanno-bacteria could correspond to some predecessor of the recent genetic code. One can consider several options.

1. Nanno-bacteria represent an RNA life form involving two kinds of RNA sequences and closed inside RNA_1 membrane. This does not require DNA.

2. If the claim of Kajander about about nanno-bacterial DNA is correct, then two options remain.

   i) Nanno-bacteria are able to just replicate DNA and do not possess genetic code. Thus nanno-bacteria would be at a higher level than viruses.

   ii) RNA-DNA reverse transcription is utilized so that nanno-bacteria could realize DNA-RNA code and would probably be at a higher developmental level than RNA life-forms but had not yet realized DNA-amino-acid code. The objection against this is that the reverse transcriptase enzyme probably requires RNA-aminoacid translational machinery.

One can ask what what RNA life-forms (option 1) would look if they still exist.

1. Singlet RNA would express itself as RNA sequences containing only U (or C) and A (or G) nucleotides. The tRNAs used by these life-forms should appear as fossil remnants in the ordinary tRNA.

2. In the case of a singlet life-form the layer could correspond to the length scale $L(2,73)" = "L(146)$ and be formed by doublet atomic layer corresponding to the twin pair of p-adic length scales formed by $L(16,9)" = "L(144)$ and $L(2,73)" = "L(146)$.

3. In the case of doublet life-forms the length scale $L(2,29)" = "L(145)$ and the tertiary p-adic length scale $L(3,7^2)" = "L(147)$ form a twin pair and could define a double-layered structure. The reported hard cell wall could correspond to this double layered structure. A cell wall

consisting of minerals (also nanno-bacteria induce also the precipitation of mineral crystals) might however be most appropriate for life-forms living in the pores of rock, and possibly utilizing tectonic energy in some form to satisfy their metabolic needs.

The generation of the triplet code would have been accompanied by the generation of double lipid layers and possibly a transition to water environment. The most natural location for the primitive RNA-RNA translation machinery is at the inner surface of a lipid membrane if present inside nanno-bacteria.

The singlet or doublet RNA life-forms and their fusions could correspond to what I have christened plasmoids. Intelligent looking plasma balls occur repeatedly in UFO reports and they are also reported to occur around crop formations. There is even a report about a plasma ball in the act of constructing the crop formation. The plasmoid like life forms serving as couriers of ITs could be also seen as multicellulars consisting of nanno-bacterial cells or, more probably, of their predecessors. The immune response against nanno-bacteria and their predecessors generated during very early evolution would make possible encounters with crops and even humans (abduction experiences) without fatal consequences. The reported immune response against exotic doublet RNA suggests that plasmoids contain exotic doublet RNA. The visible light from plasmoids suggests that the metabolism indeed involves also the hot $k = 131$ space-time sheet so that ITs or IPs might be in question.

Was the encounter of nanno-bacteria and plasmoids the moment of Gaian fertilization?

Earth consists mostly of ancient meteorites known as chondrites. Carbonaceous chondrites are shown to contain not only basic bio-monomers but even nanno-bacteria. The meteoritic material can end up to the interior of Earth along magnetic flux tubes even today. Recall that this mechanism actually explains the magnetized iron from meteors found in crop circles [20]).

Thus IT life might have developed nanno-bacteria contained by meteorites in the womb of Mother Gaia. The bio-molecules/nanno-bacteria contained by the meteorites from outer space would thus take the role of the sperm as in panspermia theory.

There is a temptation to develop the fertilization metaphor to a more concrete level in order to understand what happened when the symbiosis of pre-nucleus containing DNA and and pre-cell containing RNA was established and led to the development of the genetic code and established a genuine evolution.

1. The simple nanno-bacteria in the meteorites having only replicating DNA or perhaps only the ability to produce DNA nucleotides would have been the sperm. Cell nucleus is much smaller than cell and might itself be regarded as having originated from ancient nanno-bacteria. The much more complex pre-cells containing RNA, amino-acids, and reverse transcriptase as well as the potentiality for the realization of the genetic code plus the needed metabolic machinery, were located in the interior of Earth and played the role of the egg. Since the hot $k = 131$ space-time sheets essential for the metabolic machinery were also involved, primitive plasmoid is an excellent candidate for the egg.

2. The encounter of nanno-bacteria and plasmoids led to the fertilization of Mother Gaia. What is fascinating that balls of light reported to appear near the crop circles and reported to even fabricate them migh be there in order to get fertilized by nanno-bacteria contained by meteors! Alternatively, the simultaneous appearance of pre-biotic egg and sperm might be interpreted as a symbolic hint about what happened in the key event of the pre-biotic evolution.

10.6 Did life evolve in the womb of Mother Gaia?

The idea that Earth interior, even the hot regions at the boundary of core and mantle, could serve as a seat for life, sounds totally outlandish in the standard physics framework. The many-sheeted space-time and hierarchy of Planck constants however allow to consider at least half seriously this idea although I hasten to admit that during these years I have very often had the feeling that this is one of those painfully stubborn fix idees that like to tease imaginative theoretician. This idea has variants characterized by a varying degree of craziness. It is a fact that rocks contain simple life forms down to surprising depths. A crazier idea is that underground lakes could have served as seats for evolving

life. The really crazy variant of the idea is that the boundary between mantle and Earth's core as a regions containing strong gradients has been a seat of self organization leading to the emergence of life in some form.

Recently however completely unexpected support for this idea came as I learned that the geological evolution of Earth involves an anomaly. The continents would fit nicely to form a single super continent (Wegener's theory does not predict complete fit) if the radius of Earth would have been at the time of Cambrian explosion by factor of 1/2 smaller than now. The fact that Cambrian explosion is one of the biggies mysteries of biology puts bells ringing. For long time ago this anomaly has inspired what have been called Expanding Earth Theory but the physical mechanism giving rise to expansion has been lacking.

Quantum TGD provides this mechanism. TGD predicts that cosmic expansion does not take place smoothly but via quantum jumps induces by the growth of the Planck constant by a factor of 2 for space-time sheet considered. This holds true also in planetary scales and TGD variant of Expanding Earth theory predicts relatively fast expansion of Earth's radius with a factor 2. The sudden appearance of completely new life forms in Cambrian explosion could be understood as a burst of various multicellular life forms which have developed in the womb of Mother Gaia sheltered from UV light and meteoric bombardment. What remains open is how deep in Earth's interior life is possible. This of course depends also on the definition of life: probably biological life would not be possible at core mantle boundary but one can consider much more general forms of molecular life.

In the following I will proceed in stepwise manner from not totally crazy (I hope so) to really crazy and discuss first the quantum version of Expanding Earth theory and its possible connection with Cambrian explosion and only after consider the really crazy possibilities.

10.6.1 Quantum version of Expanding Earth theory and Cambrian explosion

TGD predicts that cosmic expansion at the level of individual astrophysical systems does not take place continuously as in classical gravitation but through discrete quantum phase transitions increasing gravitational Planck constant and thus various quantum length and time scales. The reason would be that stationary quantum states for dark matter in astrophysical length scales cannot expand. One would have the analog of atomic physics in cosmic scales. Increases of $\hbar$ by a power of two are favored in these transitions but also other scalings are possible.

This has quite far reaching implications.

1. These periods have a highly unique description in terms of a critical cosmology for the expanding space-time sheet. The expansion is accelerating. The accelerating cosmic expansion can be assigned to this kind of phase transition in some length scale (TGD Universe is fractal). There is no need to introduce cosmological constant and dark energy would be actually dark matter.

2. The recently observed void which has same size of about 10^8 light years as large voids having galaxies near their boundaries but having an age which is much higher than that of the large voids, would represent one example of jerk-wise expansion.

3. This picture applies also to solar system and planets might be perhaps seen as having once been parts of a more or less connected system, the primordial Sun. The Bohr orbits for inner and outer planets correspond to gravitational Planck constant which is 5 times larger for outer planets. This suggests that the space-time sheet of outer planets has suffered a phase transition increasing the size scale by a factor of 5. Earth can be regarded either as n=1 orbit for Planck constant associated with outer planets or n= 5 orbit for inner planetary system. This might have something to do with the very special position of Earth in planetary system. One could even consider the possibility that both orbits are present as dark matter structures. The phase transition would also explain why n=1 and n=2 Bohr orbits are absent and one only n=3,4, and 5 are present.

4. Also planets should have experienced this kind of phase transitions increasing the radius: the increase by a factor two would be the simplest situation.

The obvious question - that I did not ask - is whether this kind of phase transition might have occurred for Earth and led from a completely granite covered Earth - Pangeia without seas - to the

recent Earth. Neither it did not occur to me to check whether there is any support for a rapid expansion of Earth during some period of its history.

Situation changed when my son visited me and told me about a Youtube video [36] by Neal Adams, an American comic book and commercial artist who has also produced animations for geologists. We looked the amazing video a couple of times and I looked it again yesterday. The video is very impressive artwork but in the lack of references skeptic probably cannot avoid the feeling that Neal Adams might use his highly developed animation skills to cheat you. I found also a polemic article [1] of Adams but again the references were lacking. Perhaps the reason of polemic tone was that the concrete animation models make the expanding Earth hypothesis very convincing but geologists refuse to consider seriously arguments by a layman without a formal academic background.

The claims of Adams

The basic claims of Adams were following.

1. The radius of Earth has increased during last 185 million years (dinosaurs [28] appeared for about 230 million years ago) by about factor 2. If this is assumed all continents have formed at that time a single super-continent, Pangeia, filling the entire Earth surface rather than only 1/4 of it since the total area would have grown by a factor of 4. The basic argument was that it is very difficult to imagine Earth with 1/4 of surface containing granite and 3/4 covered by basalt. If the initial situation was covering by mere granite -as would look natural- it is very difficult for a believer in thermodynamics to imagine how the granite would have gathered to a single connected continent.

2. Adams claims that Earth has grown by keeping its density constant, rather than expanded, so that the mass of Earth has grown linearly with radius. Gravitational acceleration would have thus doubled and could provide a partial explanation for the disappearance of dinosaurs: it is difficult to cope in evolving environment when you get slower all the time.

3. Most of the sea floor is very young and the areas covered by the youngest basalt are the largest ones. This Adams interprets this by saying that the expansion of Earth is accelerating. The alternative interpretation is that the flow rate of the magma slows down as it recedes from the ridge where it erupts. The upper bound of 185 million years for the age of sea floor requires that the expansion period - if it is already over - lasted about 185 million years after which the flow increasing the area of the sea floor transformed to a convective flow with subduction so that the area is not increasing anymore.

4. The fact that the continents fit together - not only at the Atlantic side - but also at the Pacific side gives strong support for the idea that the entire planet was once covered by the super-continent. After the emergence of subduction theory this evidence as been dismissed.

5. I am not sure whether Adams mentions the following objections [6] . Subduction only occurs on the other side of the subduction zone so that the other side should show evidence of being much older in the case that oceanic subduction zones are in question. This is definitely not the case. This is explained in plate tectonics as a change of the subduction direction. My explanation would be that by the symmetry of the situation both oceanic plates bend down so that this would represent new type of boundary not assumed in the tectonic plate theory.

6. As a master visualizer Adams notices that Africa and South-America do not actually fit together in absence of expansion unless one assumes that these continents have suffered a deformation. Continents are not easily deformable stuff. The assumption of expansion implies a perfect fit of *all* continents without deformation.

Knowing that the devil is in the details, I must admit that these arguments look rather convincing to me and what I learned from Wikipedia articles supports this picture.

The critic of Adams of the subduction mechanism

The prevailing tectonic plate theory [24] has been compared to the Copernican revolution in geology. The theory explains the young age of the seafloor in terms of the decomposition of the litosphere to

tectonic plates and the convective flow of magma to which oceanic tectonic plates participate. The magma emerges from the crests of the mid ocean ridges representing a boundary of two plates and leads to the expansion of sea floor. The variations of the polarity of Earth's magnetic field coded in sea floor provide a strong support for the hypothesis that magma emerges from the crests.

The flow back to would take place at so called oceanic trenches [17] near continents which represent the deepest parts of ocean. This process is known as subduction. In subduction oceanic tectonic plate bends and penetrates below the continental tectonic plate, the material in the oceanic plate gets denser and sinks into the magma. In this manner the oceanic tectonic plate suffers a metamorphosis returning back to the magma: everything which comes from Earth's interior returns back. Subduction mechanism explains elegantly formation of mountains [18] (orogeny), earth quake zones, and associated zones of volcanic activity [34] .

Adams is very polemic about the notion of subduction, in particular about the assumption that it generates steady convective cycle. The basic objections of Adams against subduction are following.

1. There are not enough subduction zones to allow a steady situation. According to Adams, the situation resembles that for a flow in a tube which becomes narrower. In a steady situation the flow should accelerate as it approaches subduction zones rather than slow down. Subduction zones should be surrounded by large areas of sea floor with constant age. Just the opposite is suggested by the fact that the youngest portion of sea-floor near the ridges is largest. The presence of zones at which both ocean plates bend down could improve the situation. Also jamming of the flow could occur so that the thickness of oceanic plate increases with the distance from the eruption ridge. Jamming could increase also the density of the oceanic plate and thus the effectiveness of subduction.

2. There is no clear evidence that subduction has occurred at other planets. The usual defense is that the presence of sea is essential for the subduction mechanism.

3. One can also wonder what is the mechanism that led to the formation of single super continent Pangeia covering 1/4 of Earth's surface. How probable the gathering of all separate continents to form single cluster is? The later events would suggest that just the opposite should have occurred from the beginning.

Expanding Earth theories are not new

After I had decided to check the claims of Adams, the first thing that I learned is that Expanding Earth theory [6] , whose existence Adams actually mentions, is by no means new. There are actually many of them.

The general reason why these theories were rejected by the main stream community was the absence of a convincing physical mechanism of expansion or of growth in which the density of Earth remains constant.

1. 1888 Yarkovski postulated some sort of aether absorbed by Earth and transforming to chemical elements (TGD version of aether could be dark matter). 1909 Mantovani postulated thermal expansion but no growth of the Earth's mass.

2. Paul Dirac's idea about changing Planck constant led Pascual Jordan in 1964 to a modification of general relativity predicting slow expansion of planets. The recent measurement of the gravitational constant imply that the upper bound for the relative change of gravitational constant is 10 time too small to produce large enough rate of expansion. Also many other theories have been proposed but they are in general conflict with modern physics.

3. The most modern version of Expanding Earth theory is by Australian geologist Samuel W. Carey. He calculated that in Cambrian period (about 500 million years ago) all continents were stuck together and covered the entire Earth. Deep seas began to evolve then.

Summary of TGD based theory of Expanding Earth

TGD based model differs from the tectonic plate model but allows subduction which cannot imply considerable back-flow of magma. Let us sum up the basic assumptions and implications.

1. The expansion is or was due to a quantum phase transition increasing the value of gravitational Planck constant and forced by the cosmic expansion in the average sense.

2. Tectonic plates do not participate to the expansion and therefore new plate must be formed and the flow of magma from the crests of mid ocean ridges is needed. The decomposition of a single plate covering the entire planet to plates to create the mid ocean ridges is necessary for the generation of new tectonic plate. The decomposition into tectonic plates is thus prediction rather than assumption.

3. The expansion forced the decomposition of Pangeia super-continent covering entire Earth for about 530 million years ago to split into tectonic plates which began to recede as new non-expanding tectonic plate was generated at the ridges creating expanding sea floor. The initiation of the phase transition generated formation of deep seas.

4. The eruption of plasma from the crests of ocean ridges generated oceanic tectonic plates which did not participate to the expansion by density reduction but by growing in size. This led to a reduction of density in the interior of the Earth roughly by a factor 1/8. From the upper bound for the age of the seafloor one can conclude that the period lasted for about 185 million years after which it transformed to convective flow in which the material returned back to the Earth interior. Subduction at continent-ocean floor boundaries and downwards double bending of tectonic plates at the boundaries between two ocean floors were the mechanisms. Thus tectonic plate theory would be more or less the correct description for the recent situation.

5. One can consider the possibility that the subducted tectonic plate does not transform to magma but is fused to the tectonic layer below continent so that it grows to an iceberg like structure. This need not lead to a loss of the successful predictions of plate tectonics explaining the generation of mountains, earthquake zones, zones of volcanic activity, etc...

6. From the video of Adams it becomes clear that the tectonic flow is East-West asymmetric in the sense that the western side is more irregular at large distances from the ocean ridge at the western side. If the magma rotates with slightly lower velocity than the surface of Earth (like liquid in a rotating vessel), the erupting magma would rotate slightly slower than the tectonic plate and asymmetry would be generated.

7. If the planet has not experienced a phase transition increasing the value of Planck constant, there is no need for the decomposition to tectonic plates and one can understand why there is no clear evidence for tectonic plates and subduction in other planets. The conductive flow of magma could occur below this plate and remain invisible.

The biological implications might provide a possibility to test the hypothesis.

1. Great steps of progress in biological evolution are associated with catastrophic geological events generating new evolutionary pressures forcing new solutions to cope in the new situation. Cambrian explosion indeed occurred about 530 years ago (the book "Wonderful Life" of Stephen Gould [161] explains this revolution in detail) and led to the emergence of multicellular creatures, and generated huge number of new life forms living in seas. Later most of them suffered extinction: large number of phylae and groups emerged which are not present nowadays.

   Thus Cambrian explosion is completely exceptional as compared to all other dramatic events in the evolution in the sense that it created something totally new rather than only making more complex something which already existed. Gould also emphasizes the failure to identify any great change in the environment as a fundamental puzzle of Cambrian explosion. Cambrian explosion is also regarded in many quantum theories of consciousness (including TGD) as a revolution in the evolution of consciousness: for instance, micro-tubuli emerged at this time. The periods of expansion might be necessary for the emergence of multicellular life forms on planets and the fact that they unavoidably occur sooner or later suggests that also life develops unavoidably.

2. TGD predicts a decrease of the surface gravity by a factor 1/4 during this period. The reduction of the surface gravity would have naturally led to the emergence of dinosaurs 230 million years

ago as a response coming 45 million years after the accelerated expansion ceased. Other reasons led then to the decline and eventual catastrophic disappearance of the dinosaurs. The reduction of gravity might have had some gradually increasing effects on the shape of organisms also at microscopic level and manifest itself in the evolution of genome during expansion period.

3. A possibly testable prediction following from angular momentum conservation ($\omega R^2 = constant$) is that the duration of day has increased gradually and was four times shorter during the Cambrian era. For instance, genetically coded bio-clocks of simple organisms during the expansion period could have followed the increase of the length of day with certain lag or failed to follow it completely. The simplest known circadian clock is that of the prokaryotic cyanobacteria. Recent research has demonstrated that the circadian clock of Synechococcus elongatus can be reconstituted in vitro with just the three proteins of their central oscillator. This clock has been shown to sustain a 22 hour rhythm over several days upon the addition of ATP : the rhythm is indeed faster than the circadian rhythm. For humans the average innate circadian rhythm is however 24 hours 11 minutes and thus conforms with the fact that human genome has evolved much later than the expansion ceased.

4. Scientists have found a fossil of a sea scorpion with size of 2.5 meters [200] , which has lived for about 10 million years for 400 million years ago in Germany. The gigantic size would conform nicely with the much smaller value of surface gravity at that time. The finding would conform nicely with the much smaller value of surface gravity at that time. Also the emergence of trees could be understood in terms of a gradual growth of the maximum plant size as the surface gravity was reduced. The fact that the oldest known tree fossil is 385 million years old [189] conforms with this picture.

Did intra-terrestrial life burst to the surface of Earth during Cambrian expansion?

Intra-terrestrial hypothesis is one of the craziest TGD inspired ideas about the evolution of life and it is quite possible that in its strongest form the hypothesis is unrealistic. One can however try to find what one obtains from the combination of the IT hypothesis with the idea of pre-Cambrian granite Earth. Could the harsh pre-Cambrian conditions have allowed only intra-terrestrial multicellular life? Could the Cambrian explosion correspond to the moment of birth for this life in the very concrete sense that the magma flow brought it into the day-light?

1. Gould emphasizes the mysterious fact that very many life forms of Cambrian explosion looked like final products of a long evolutionary process. Could the eruption of magma from the Earth interior have induced a burst of intra-terrestrial life forms to the Earth's surface? This might make sense: the life forms living at the bottom of sea do not need direct solar light so that they could have had intra-terrestrial origin. It is quite possible that Earth's mantle contained low temperature water pockets, where the complex life forms might have evolved in an environment shielded from meteoric bombardment and UV radiation.

2. Sea water is salty. It is often claimed that the average salt concentration inside cell is that of the primordial sea: I do not know whether this claim can be really justified. If the claim is true, the cellular salt concentration should reflect the salt concentration of the water inside the pockets. The water inside water pockets could have been salty due to the diffusion of the salt from ground but need not have been same as that for the ocean water (higher than for cell interior and for obvious reasons). Indeed, the water in the underground reservoirs in arid regions such as Sahara is salty, which is the reason for why agriculture is absent in these regions. Note also that the cells of marine invertebrates are osmoconformers able to cope with the changing salinity of the environment so that the Cambrian revolutionaries could have survived the change in the salt concentration of environment.

3. What applies to Earth should apply also to other similar planets and Mars [2] is very similar to Earth. The radius is .533 times that for Earth so that after quantum leap doubling the radius and thus Schumann frequency scale (7.8 Hz would be the lowest Schumann frequency) would be essentially same as for Earth now. Mass is .131 times that for Earth so that surface gravity would be .532 of that for Earth now and would be reduced to .131 meaning quite big dinosaurs! have learned that Mars probably contains large water reservoirs in it's interior and that there

is an un-identified source of methane gas usually assigned with the presence of life. Could it be that Mother Mars is pregnant and just waiting for the great quantum leap when it starts to expand and gives rise to a birth of multicellular life forms. Or expressing freely how Bible describes the moment of birth: in the beginning there was only darkness and water and then God saidLet the light come!

To sum up, TGD would provide only the long sought mechanism of expansion and a possible connection with the biological evolution. It would be indeed fascinating if Planck constant changing quantum phase transitions in planetary scale would have profoundly affected the biosphere.

10.6.2 Did pre-biotic life evolve in mantle-core boundary?

In the sequel this question is taken to mean simple prebiotic life forms preceding the life that possibly developed in underground seas near to the surface of Earth. One can imagine that pre-biotic life moved from high temperature environment in the Earth's interior to the underground seas and charged molecules polymerized in this process and generated gel like phase around them.

Some arguments supporting IT life

The following arguments favor IT hypothesis.

1. Life would have originated already in interstellar space via evolution of primitive metabolic cycles involving temporary chemical storage of metabolic energy. The decay of molecules would have been induced by incoming radiation in UV and visible range and fusion would have occurred spontaneously liberating energy quantum. As stars and planetary systems formed these primordial predecessors of life would have naturally ended into the planetary and even interiors and received their metabolic energy from the hot environment. The dropping of particles, in particular protons and electrons, to large space-time sheets would have provided fundamental metabolic energy quanta, and the anomalies lines in the IR, visible, and UV radiation from interstellar space indeed contains this kind of lines with energies which can be understood in terms of the spectrum of these quanta [6] .

2. Boundary layers are ideal places for self-organization since they contain gradients which give rise to energy currents feeding self-organization. Liquid state is certainly crucial for life since this makes it possible quantum control the atomic space-time sheets very effectively. Ordinary life relies actually on the liquid crystal property of water which suggests that the same is the case quite generally. Thus those parts of the planetary core which correspond to boundary regions between solid and liquid phases and thus analogous to ordered water, could be ideal places for IT life forms to flourish, and it is actually difficult to imagine any other state of matter making possible life able to control the surrounding world effectively.

3. This picture is consistent with and would realize concretely the general vision about magnetosphere as a living system. In Earth's interior the mantle-core and core-inner core boundaries are especially interesting in this respect since these boundaries represent solid liquid boundaries.

4. Mg, Fe, Al, Si, and O are the dominant elements in mantle. Also Ca is present. These are the basic minerals involved with life. Also the minerals believed to be important for the evolution of polymer structures (like kaolinites consisting of Al, Si, and O) could form both at the hot space-time sheets and atomic space-time sheets. Below mantle-core boundary Fe and S are the prevailing elements. Fe-S centers play a key role in high temperature and pressure models for photosynthesis pathways [174] . The establishment of the photosynthesis has been proposed to occur first in a sulphur containing environment with S replacing O. Inner core contains mainly Fe at hot space-time sheets.

5. A further possibly important aspect is the transparency of the liquid glass state at mantle-core boundary implying that visible light propagates over long distances without absorption. This might be absolutely essential for the possibility of visible photons to propagate through sufficiently long distances. For dark photons situation changes, and the transparency of liquid glass might be due the fact that some fraction of photons propagate as dark photons through it.

Hence quartz is transparent in liquid state, and thus an optimal candidate for a medium whose behavior is quantum controlled from larger space-time sheets.

6. Magnetic body means the presence of both magnetic nervous system and the analog of blood circulation which could bring in sufficient amounts of elements needed for the synthesis of bio-polymers. The low concentrations of the elements needed to build up bio-monomers need not be a problem anymore since magnetic Mother Gaia could control them.

Structure of the Earth's interior and IT life

Combining the above described general ideas with the knowledge about Earth interior, one ends up with a more detailed picture.

1. Earth's interior decomposes into a relatively thin crust of thickness 30-60 km; a plastic mantle consisting mainly of Si, O, Mg, Fe, and Al mostly in form of silicates FeO-SiO_2 and MgO-SiO_2; a liquid core containing mainly Fe and S; and the inner core consisting mainly of solid Fe. There are thus two solid-liquid boundary regions. The upper boundary region could contain at least glass in liquid crystal form and the lower boundary region Fe in liquid crystal form.

2. Theoretically, the thickness for the mantle-core layer is expected to be of order few meters. The reflection of tectonic waves from mantle-core boundary has given evidence for a rich structure at this boundary and suggests that this expectation is not quite correct [49] . Structures of thickness about 150 meters and with of several kilometers and between liquid and solid state have been identified at the top of the liquid core. One explanation is that lighter elements in the core-inner core boundary saturate and condense to solid form and being lighter than iron, raise up and form kind of puddles at the highest points of core.

   A more radical explanation is that these structures relate to a highly developed self-organization patterns which have given rise to some kind of life-forms. In the mantle-core layer the velocity of tectonic waves gets ultra-low. The velocity of sound in solid phase is quite generally higher than in liquid phase: this reflects directly the fact that the approximately harmonic forces between atoms are stronger. If liquid crystal phase is present the velocity in transversal liquid directions should be low. What is fascinating that sooner or later the analysis of reflected tectonic waves could give detailed information about mantle-core boundary.

3. Earth contains a previously unidentified core region with size of 300 km [35] . Assuming that the magnetic field behaves like a dipole field down to the distances of order 300 km, the electronic cyclotron frequency at this distance is 5 GHz which corresponds to the wave length of about 6 cm, the size scale of BOLs for the dark companion $B_{end} = 2B_E/5$ of B_E. If the magnetization density below this distance is constant (so that the core would be like ordinary magnet), the magnetic field would be constant below this length scale.

Also some other experimental findings support this picture. It has been found that the times for of the compressional waves to travel through Earth in magnetic north-south direction and equatorial direction differ by 2-3 seconds [45] . This suggests a gigantic crystal structure with symmetry axis parallel to magnetic field. If the join along boundaries condensate associated with atomic space-time sheets is hollow with a hole of radius 300 km, and if only $k = 151$ space-time sheet consisting of cold and magnetized iron is at this space-time sheet one can understand the crystal structure and how Earth's magnetic field results by magnetization. The estimated velocity of propagation for compressional waves in the crystal is about 3 km/s which is rather near to the 5 km/s for steel at room temperature. The appearance of a relatively small hole at the atomic space-time sheet is not so surprising since typically the field equations of TGD imply hole like singularities at given space-time sheet, and the hole could be analogous to black hole like singularity carrying inertial and gravitational masses at its boundary.

The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth. This would mean that some kind of plasmoid like life forms could reside also at the boundary layer associated with the new core. If the $k = 151$ space-time sheet is not ferromagnet above the radius $r = 300$ km, the boundary region could be in spin glass type magnetic phase and the bio-control from magnetic flux tubes would operate on the local direction of magnetization of the magnetized regions in the boundary region.

10.6.3 What conditions can one pose on life at mantle-core boundary?

In the following some conditions on life at high temperatures at pressures are discussed as a mere intellectual exercise certainly not to meant taken deadly seriously. The speculations rely on the ideas which should be already familiar such as presence of strong gradients driving self-organization as indeed found in mantle-core boundary, magnetic bodies as controllers of biological bodies, dark matter as phases with large value of Planck constant able to form macroscopic quantum phases even at high temperatures, and the notion of universal metabolic currencies. Gel-sol phase transitions are also key element in the model of life. The condition that topological quantum computation like information processing based on braids requires existence of some kind of polymers defining braids and consisting of some basic building blocks stable under the conditions in question. The presence of analogs of lipids and cell membranes might be argued to be also necessary.

Plasmoid life as minimum option

The least non-realistic assumption is that IT life corresponds to plasmoid like life forms having magnetic body containing dark matter with large Planck constant controlling visible matter at high temperatures and in plasma phase. Fractality suggests that the high frequency analog of EEG is present and allows magnetic body to use the visible body as a sensory receptor and motor instrument. Frequencies and the values of Planck constant should be such that the energies of dark photons are above thermal energy. General vision about evolution suggests that the values of Planck constant are not very high so that frequency scale should be rather high.

1. Only biologically important ions and relatively simple molecules are expected to be present. Primitive metabolic cycles based on the fusion and decay of molecules induced by the radiation coming from environment can be considered. Cyclotron Bose-Einstein condensates of ions at magnetic flux tubes correspond to energies above thermal threshold only if the magnetic field is strong enough.

2. At temperature of about 4000 K at mantle core interior hydrogen bonds are still stable and metabolic energy quantum of $E_0 = .5$ eV is near thermal energy. There exists of course other metabolic quanta comings as power of two multiples of this quantum. Hence one can assumes that the dropping of protons and possibly of electrons from larger space-time sheets is responsible for metabolic energy quanta also now. One might argue that the typical p-adic length scale associated with the space-time sheets corresponds to the de-Broglie wave length a $\lambda_{dB} = \sqrt{3}\hbar/\sqrt{2mT}$ associated with electron. For electron this wavelength is around 35 slightly below $L(149) = 50$ A defining the thickness of the lipid layer of ordinary cell membrane. This scale increases with increasing $\hbar$.

3. Dark micro-waves amplified by quartz crystals might be crucial for the metabolism of plasmoid life-forms and replace visible light serving as the "food" of the terrestrial life forms. Tectonic activity might be as important for these life-forms as solar radiation is for us. The crust and mantle could serve as amplifiers of em waves is a wide wave length range and make possible communications between IT and us.

Could topological quantum computation like activities be considered?

Could even more advanced life forms have evolved in the environment provided by mantle-core boundary? The presence of magnetic body makes possible braidings and simple versions for the mechanisms of memory, of topological quantum computation like information processing, and of catalysis. The presence of braids could be taken almost as a basic prerequisite of life. The presence of polymers of some basic molecules seems necessary if one wants something resembling DNA as tqc.

1. The presence of polymers consisting of some thermally stable basic units is the basic requirement. Hydrocarbons, lipids, aminoacids, and nucleotide polymers are not chemically stable at temperatures considered and mantle contains carbon only in trace amounts. The dominating elements in mantle are O, Si, and Mg whereas C is present only in trace amounts. S is present in core and thus also in mantle-core boundary. P is so called siderophilic element meaning that it tends to avoid Si. It is theorized that during the formation of Earth from magma ocean

siderophilic elements including P separated from the mantle and went to core. In [41] ratio of concentrations of P in core and mantle was estimated to be $D(P) = 30$ but the article does not report the concentration of P on mantle. In [43] the phosphorus content of upper mantle is reported to be in the range 130-220 ppm which would give 3-7 percent in core. One can also imagine a formation of phosphate deposits in mantle core boundary: in absence of oxygen these kind of deposits are formed at sea floor. This kind of deposits might have formed at the top of the solid structures reported to exist at mantle core boundary [49] . These structures could themselves have formed as light elements from inner core has gradually diffused to the mantle core boundary and could include phosphate deposits. If so then mantle-core boundary could contain considerable amounts of P and the replacement C, N, O with Si, P, O or Si, P, S might make sense.

2. Water flow is not the only flow which could generate the self-organization patterns defining braidings as the analogs of tqc programs. Since O dominates in mantle water is however the first guess. It is known that lower mantle can contain water at least up to .2 weight per cent [42] . Water molecules are stable at the temperatures considered. The phase diagram of water [4] shows that water is in overcritical phase in the temperatures and pressures considered4000 K and 1.4 million atm and at the bottom of the mantle.

3. The replacement of O with S might be considered in the mantle-core boundary since S is present in liquid core. Water would be replaced with hydrogen sulfide H_2S (responsible for the smell of rotten eggs!) if it appears in liquid form H_2S at temperatures and pressures considered. H_2S could be also used as food. H_2S is used by some bacteria living in deep ocean volcanic vents as a nutrient and also in our own gut: chemically this means that H_2S acts as electron donor in primitive photosynthesis like process to give ATP . That sulphur is essential for growth and physical functioning of plants might be due to the fact that it preceded oxygen based life [2] . For instance, Cys and met containing sulphur are very important amino-acids.

4. The polymers should contain atoms acting as plugs for flux tubes acceptors flux tubes ($O =$ or $S =$) and terminal points of flux tubes identifiable as donors of hydrogen bonds. $S-H$ shows only very weak tendency for hydrogen bonding so that Si, P, O option looks more promising and is of course especially natural if IT life forms are considered. For instance, silicic acids [28] satisfying the formula $[SiO_x(OH)_{4-2x}]_n$ are candidates for polymers containing both $O =$:s and OH:s. The presence of PO_4 could have made possible the formation simple analogs of nucleotides and AMP, ADP , and ATP molecules. It might be possible to abstract nucleotides with a polymer consisting of four different simple molecules which are phosphorylized and attached to the backbone made of sugars.

5. One can continue the analogy with carbon life even further. The backbone could consist of the variants of riboses with carbon cycles replaced with Si cycles, the variants of aromatic rings with C and N replaced with P, and base pairing between $N - H$ and $O =$ replaced with $P - H$ and $O =$. In the case of amino-acids one can also consider the replacement of $C, N \to Si, P$. It is of course far from obvious that the possibly existing silicon analogs of organic polymers are stable enough against rapid burning to SiO_2 and water. One might hope that the higher mass of Si stabilizes them chemically at temperatures involved. Professional chemist could probably kill this kind of ideas without big effort.

Could one consider analogs of cell membrane and gel phase crucial for cellular life?

1. The first guess would be that gel like phase might have emerged only after these plasmoid like life-forms came in contact with water and induced the generation of structure water in presence of metabolic energy feed. On the other hand, it could well be that structured dater might form around charged polymers also at high temperatures and pressures as in the case of ordinary cell. Also silica (SiO_2) is known to form a gel. Also glass consists of SiO_2: the transparency of glass to visible light might be also relevant. A group of algae polymerize silicic acid to so called biogenic silica used to construct their cell walls.

2. Lipids forming cell membrane would be replaced with structures consisting of hydrosilicons with the silicon analog of carbon residue as its hydrophilic head and silicon analog of the hydrophobic

fat forming the tail of the lipid. The formation of these double layers would be an outcome of self-organization. The analogs of phospholipids having PO_4 at their hydrophilic tail would be needed for tqc.

3. Super-conductivity plays an essential role in the TGD based model for cell membrane. Large enough values of Planck constant in principle allow to have super-conductivity at magnetic flux tubes.

4. The requirement that the energy $E = ZeV$ associated with Josephson junctions over the cell membrane like structure is above thermal energy requires very strong electric field over the membrane unless the membrane is thick. In the case of ordinary cell membrane the energy is rather near to thermal energy at room temperature. Now the energy would be roughly ten times higher and correspond to about .5 eV. Whether this kind of strong electric field is realizable is not clear. One might hope that the densities of ions could be high enough in the dense environment.

Do metabolism and photosynthesis possess signatures telling about intra-terrestrial evolution?

Also the intra-terrestrial metabolism should rely on atomic/molecular "Karma's cycles". Assume that the protons and electrons can be modeled as free particles in box. This assumption might not be correct as the model for ATP- ADP involving Coulomb binding energy of proton with negatively charge ATP molecule reducing the size of metabolic energy quantum already demonstrated. In this case the wavelength would be roughly by a factor 1/2 longer than predicted meaning Coulombic binding energy of order .25 eV.

In any case, with this assumption the quanta saturating to $E_{max}(k) = [.5, 1, 2, 4, 8, 16]$ eV and wavelengths $\lambda_{min} = [1240, 620, 310, 155]$ nm could have been important. The maximal quanta $E_0(k)$ correspond to the dropping from space-time sheet labeled by $k = 137 - \Delta k$ (in the case of proton) to a very large space-time sheet. The size of the space-time sheets would be given by $L(k) = r \times 2^{(k-151)/2} \times L(151)$, $L(151) = 10$ nm and $r = \hbar/\hbar_0$ the ratio of the Planck constant in question to its standard value. Actually and entire spectrum of quanta given by the formula $E_n = (1 - 2^{-}n)E_0(k)$ saturating to $E_0(k)$ for large values of n. In [6] the presence of unidentified lines in the spectrum of UV,visible, and IR radiation from interstellar space has been shown to have a satisfactory explanation in terms of universal metabolic energy quanta.

The spectrum of diffuse interstellar medium exhibits three poorly understood structures [48] : Unidentified Infrared Bands (UIBs), Diffuse Interstellar Bands (DIBs) [27] , and Extended Red Emission (ERE) [206] allowing an interpretation in terms of dropping of protons or electrons (or their Cooper pairs) to larger space-time sheets. The model also suggests the interpretation of bio-photons in terms of generalizes EREs.

1. Unidentified infrared bands (UIBs) contain strong bands at $\lambda = 3300, 6200, 11, 300$ nm. Th

2. There are diffuse interstellar bands (DIBs) at wavelengths 578.0 and 579.7 nanometers and also at 628.4, 661.4 and 443.0 nm. The 443.0 nm DIB is particularly broad at about 1.2 nm across - typical intrinsic stellar absorption features are 0.1 nm [48] .

3. The Extended Red Emission (ERE) [48, 206] is a broad unstructured emission band with width about 80 nm and located between 540 and 900 nm. The large variety of peak wavelength of the band is its characteristic feature. In majority of cases the peak is observed in the range 650-750 nm but also the range 610-750 nm appears. This general vision can be compared with experimental facts.

The generalization ontogeny recapitulates phylogeny principle would suggest that the recent metabolism should have some features serving as telltale signatures of the IT past. The IT past could in turn reflect the primordial evolution in interstellar dust. The signatures of this period would be maxima of the action spectrum for wavelengths which correspond to both the universal metabolic energy quanta and transition energies for transitions of simple molecules present in the molecular dust. Visible and UV range are the most promising regions to consider.

1. There are two wave lengths of maximal effectiveness in the photosynthesis of plants and these correspond to what are called photo-system I and II (see p. 287 of [180]). Photo-system I is maximally activated at $\lambda = 680$ nm, corresponds to the chlorophyll a, and is not involved with the oxygen evolution. $k = 136$ corresponds to wavelength saturating to $\lambda_{min} = 620$ nm (1 eV). The model of ATP- ADP process suggests that Coulombic binding energy is increases the wavelength.

2. Photo-system II is activated by shorter wave lengths and maximum effectiveness is between 500-600 nm. Photo-system II utilizes second type of chlorophyll (b, c or d) plus some accessory pigments. All photosynthetic cells producing oxygen possess both photo-systems whereas bacteria which do not produce oxygen have only the photo-system I. Hence at least the photo-system I might derive from a very early intra-terrestrial period. The spectrum of metabolic energy quanta for $k = 135$ corresponds to the wave length range [620,413,354,..,310] nm. Coulombic binding energy could increase the wavelength from the 413 nm for $k = 135$ and $n = 2$.

3. The action and absorption spectra of green alga Ulva Taeniata, see p. 284 of [180] , have besides 680 nm maximum also a broad maximum in the range 400-500 nm peaked around 430 nm. The action spectrum has also a shoulder like structure around 600 nm. For $k = 135$ the first peak could correspond to $n = 1$ (620 nm) and second peak $n = 2$ (412 nm).

4. For some bacteria encountered in hot springs [83] the effective wave length range is in the near infrared range 700-1000 nm rather than in the range of visible frequencies dominating the sunlight. This looks strange since in general the evolution favors maximal metabolic economy. This leads to ask whether these bacteria might be kind of living fossils evolved in an intra-terrestrial environment. This range of wavelength corresponds in a reasonable approximation to that obtained by scaling the wave length range 400-500 nm in previous case and thus to $k = 136$.

5. DNA bases (A, G, T, C) strongly absorb UV light at around 260 nm. For $k = 16$ the nearest metabolic energy quanta correspond to $n = 2$ and $n = 3$ giving wavelengths 310 nm and 207 nm. For proton the p-adic length scale is below atomic size for $\hbar/\hbar_0 \geq 16$.

10.6.4 What about analogs of EEG?

It looks strange to mention EEG if one speaks about primordial life forms. These analogs of EEG have of course nothing to do with brains. The prediction is that the fractally scaled counterparts of EEG (in loose sense of course) provide the fundamental communication and control tool for the magnetic body. This analog of EEG is determined by the cyclotron energy spectrum nE_c of biologically important ions scaling like $\hbar$ and by the characteristic energy $E_J = ZeV$ associated with Josephson junctions assignable to membrane like structures and having no dependence on $\hbar$. The energies nE_c and the differences $nE_c \pm E_J$ define the harmonics of bands and their satellites. Alpha band corresponds to E_c and beta and theta bands to differences in the case of ordinary EEG.

Conditions from the thermal stability of the analog of EEG

The analogs of EEG and its scaled up variants are in a fundamental role in the control of biological body by magnetic body and this should hold true also for ITs. According to the model of EEG resulting as a special case of the model for the fractal hierarchy of EEGs and its generalizations [23] , the analog of EEG involves two components.

1. Cyclotron component

The first component corresponds to the harmonics of cyclotron frequencies of biologically important ions: many of them belong to the alpha band in the case of ordinary ions.

Since 10 Hz corresponds to a secondary p-adic time scale assignable to electron defining an inherent time scale of elementary particle in zero energy ontology, one can ask whether this frequency means breakdown of the fractality hypothesis and raises the frequency scale of ordinary EEG in special role. One can also wonder whether 10 Hz frequency could define a universal biorhythm.

Dark ions reside at magnetic flux sheets traversing DNA and cyclotron radiation affects directly DNA. Cyclotron frequencies are associated with motor control affecting directly DNA and inducing

gene expression among other things. The models leads naturally to the introduction of the notions of super genome and hyper genome [23] .

2. Josephson junction component

Josephson junctions assumed to be associated with cell membrane define second contribution to EEG as frequencies associated with coherent state of photons emitted by Josephson current. This component is present only if Josephson junctions, naturally assignable with a membrane like structure separating the plasmoid from environment, are present.

The frequencies are expressible as $f_{n,\pm} = nf_c \pm f_J$ and in the case of ordinary EEG alpha band and its harmonics split into counterparts of beta and theta band. Alpha band has scaled variant also in more general case and corresponds to ions which define alpha band for ordinary ions.

1. The essential condition is that cyclotron energy scale is above the thermal energy $E_{th} = 2.88T$ ($k_B = 1$ in the units used) . This fixes the minimal value of the integer k_d characterizing the level of dark matter hierarchy involved. For ordinary EEG frequency of order 1 Hz the minimal value of k_d is roughly $k_d = 44$. DNA cyclotron frequencies assuming that the charge of DNA is solely due to the phosphate groups PO_4^{2-} are around 1 Hz and just above the thermal threshold.

2. Second condition is that Josephson energy determined by the membrane voltage defines Josephson energy which is above thermal energy. This gives $Q_{em}eV \geq 2.88T$ for far from vacuum extremals. For almost vacuum extremals the classical Z^0 field proportional tothe classical em field contributes to the coupling and one must replace the charge Q_{em} of charge carrier with effect em charge Q_{eff} [23] : this increases the scale of Josephson energies roughly by a factor 10. For far from vacuum extremals Josephson energies are near thermal energies whereas for almost vacuum extremals they are in visible and UV region, and one can identify biophotons and EEG photons as decay products of dark Josephson photons.

3. Superconductivity prevails only below some critical temperature whereas vacuum extremal property is expected to be possible only above some critical temperature. This suggests that cell membrane functions properly only in a narrow temperature range. The range 36-37 C is suggested by the fact that the effects of ELF em fields on vertebrate brain are observed only in this range.

Josephson frequency f_J is inversely proportional to $\hbar$ and would scale in the case of EEG would scale as

$$f_J = \frac{T}{T_{room}} \times f_{J,room} \quad ,$$

where $f_{J,room} \simeq 5$ Hz holds true. Alpha band and its harmonics and also the widths of theta and beta bands would scale like B. The positions of theta and beta bands would scale like temperature, and one would have the formula

$$f_{n,\pm} = \frac{B}{B_E} nf_c \pm \frac{T}{T_{room}} f_J$$

for the frequencies in the generalized beta and theta bands, when $k_d = 44$ holds true also in the high-T environment.

It is illustrative to consider some examples.

1. *Mantle-core boundary*
   The temperature is $T = 4000$ K $\sim 13T_{room}$ at the mantle-core boundary. This temperature allows simple ordinary molecules like carbon monoxide and water (due to the high pressure). Thermal energy is still eV and below Josephson energy and super-conductivity is possible only if cyclotron energies are high enough. For 5 Hz cyclotron frequency $r = 47$ gives energy of order eV. One could thus consider the possibility that both the super-conductivity and criticality could be possible in scaled up temperature range.

2. *Sunspots*
   The average temperature of the solar photosphere is about 5800 K whereas the minimum temperature is $T_{min} = 4000$ K and same as the temperature at mantle-core boundary. Inside

sunspots the temperature varies in the range 3000-4800 K and sunspots, which are analogous to tornadoes, would be good candidates for the seats of solar life forms. Spectral analysis demonstrates the presence of water inside sunspots [3] . There is also evidence for a solid calcium ferrite surface at photosphere [8] .

The value of the sunspot magnetic field is between 1600-2500 Gauss and thus cyclotron frequency is about $3200 - 5000$ times higher than at the surface of Earth. Also in this case $k_d = 44$ level would correspond to thermally stable "EEG" photons with frequencies in the range of ordinary EEG.

What could the analog of EEG for IT look like?

In the following estimates for cyclotron frequencies are for the possibly existing dark companion $B_{end} = 2B_E/5$ of the Earth's magnetic field for which the effects of ELF fields on vertebrate brain provide a direct support.

If the sensory representations of IT life-forms are realized at the personal magnetic canvas and at magnetosphere in the same manner as ours, the cyclotron frequency of the representing ion at distance r_1 is must be same as the cyclotron frequency of the represented ion at distance r_0. Assuming that magnetic field strength scales like $1/r^3$, this gives cyclotron transitions at the distance of about

$$r_1(A) = (A/A_1)^{1/3} \times r_0 \ ,$$

giving

$$y(A, A_1) = (A/A_1)^{1/3} \times x \ .$$

Here $r_0 = xR$ is the radius associated with the life-form, and $r_1 = yR$ is the distance at which the sensory representation is realized. R denotes the radius of Earth and A the mass of the ion at r_0 associated with IT cyclotron transition and A_1 the mass of the ion at r_1 defining the cyclotron transitions associated with the sensory representation.

If the most important frequencies of generalized EEG correspond to cyclotron frequencies, if prebiotic live resides at the mantle-core and core-inner core boundaries, and if the magnetic field inside Earth behaves as dipole field in a reasonable approximation, one can deduce the EEG frequency range of aliens by scaling the human frequency range by the ratio

$$x^{-3} = (\frac{R}{r})^3 = \left[\frac{f_S(r)}{f_S(R)}\right]^3 \ ,$$

where r is the distance of the boundary region from the center of the Earth. The constraint that representation is realized in inner magnetosphere gives the bound $y \leq 6$ and the constraint that it is realized in ionosphere gives $y \simeq 1$.

1. Biosphere

In this case the basic equation is obtained by putting $x = 1$ in the general equation so that one has

$$y = (\frac{A}{A_1})^{1/3} \ .$$

For protonic representations with $A_1 = 1$ possible in entire inner magnetosphere the constraint $y \leq 6$ allows all possible values of A.

2. Mantle-core boundary

For mantle-core boundary the ratio is roughly $x^{-3} = 7.1$ so that the EEG frequency range $1.5 - 90$ Hz scales up to $107 - 639$ Hz. Sensory representations can in this case be realized as ionic transitions in atmosphere. The basic equation is

$$y = (\frac{A}{A_1})^{1/3} x \ ,$$

where A is the mass number of the ion in mantle-core boundary and A_1 is the mass number of representative ion. For protonic representation one has

$$y = 1.92A^{1/3} \quad .$$

The condition $y \leq 6$ guarantees that representation is realized in the inner magnetosphere and gives $A \leq 27$. This corresponds in ordinary EEG to frequencies $f \geq 11$ Hz. For $A_1 > 1$ also scaled up variants of alpha and theta frequencies are representable: note however that the densities of these ions are probably much smaller than in ionosphere.

One can consider also ionospheric ion representations satisfying $y \simeq 1$ for mantle-core boundary. Now the mass numbers of the ions involved are related by

$$\frac{A}{A_1} \simeq x^{-3} \simeq 7.1 \quad .$$

The biologically most interesting ions have $A > 7$ and are representable. One manner to realize this sensory representation is using cells or brains of various organisms and one might consider the possibility that we actually are life-forms which have developed as magnetospheric sensory representations of the life-forms at the mantle-core boundary.

3. Core-inner core boundary

For core-inner core boundary the ratio is roughly $x^{-3} = 263$ for $f_S(r) = 50$ Hz and $x^{-3} = 135$ for $f_S(r) = 40$ Hz. In this case only electronic sensory representations are possible and one has

$$y = (\frac{Am_p}{m_e})^{1/3}x \quad ,$$

1. For $x^{-3} = 263$ this gives

   $$y \simeq 1.98 \times A^{1/3} \quad .$$

   The range $[1, 6]$ for y corresponds to the inner magnetosphere and the upper bound $A \leq 27$ and to scaled up variants of cyclotron frequencies above 11 Hz in ordinary EEG. Only beta and gamma bands would be represented.

2. For $x^{-3} = 135$

   $$y \simeq 2.48 \times A^{1/3}$$

   The upper bound for A is $A \leq 14$ and to the scaled up variants of cyclotron frequencies above ~ 20 Hz in ordinary EEG.

4. Inner core-most inner core boundary

The boundary of the most inner core of radius 300 km could also be carrier of life-forms, perhaps plasmoid like life-forms. The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth, which would be constant and of order .2 Tesla below this distance if dipole approximation makes sense.

If important "EEG" frequencies correspond to cyclotron frequencies, part of the "EEG" would be scaled up by a factor $2^{169-157} = 2^{12} \simeq 4000$ so that EEG frequency range $.25-90$ Hz would be mapped to $1-360$ kHz. Ionic cyclotron frequencies would be in the MHz range with proton cyclotron frequency equal to 1.2 MHz. The cavity resonance frequency analogous to the lowest Schumann frequency for a structure with radius 300 km is 159 Hz.

If the sensory representations of IT life-forms possibly existing at at $r_0 = 300$ kilometers are realized as electronic cyclotron transitions one has

$$y \simeq .59 \times A^{1/3} \quad .$$

Ions with $A \geq 6$ would be represented above Earth's surface. All ionic representations would be realized in Earth's interior.

10.7 Comparison of McFadden's views with TGD

In his book Quantum Evolution [185] Johnjoe McFadden discusses the deep problems of molecular biology from quantum point of view and develops very interesting ideas about evolution and consciousness. Because of deep insights about what is not understood in biology, this discussion should provide new insights for any quantum consciousness theorist attempting to build a bridge between theory and biological reality. In the sequel McFadden's vision is compared with TGD view and some new ideas inspired by it in TGD framework are proposed.

10.7.1 General ideas

Before dwelling into concrete examples, it is good to compare McFadden's general starting points with those of TGD.

1. In accordance with most interpretations of quantum mechanics, McFadden assumes that the initial situation involved no de-coherence and that the biological evolution means basically the emergence of de-coherence, essentially the appearance of conscious observers performing quantum measurements.

   In TGD framework the situation is just the opposite: evolution means the emergence of effective macro–temporal quantum coherence meaning that the duration of sharp mental images (subselves) increased. During thee primordial stage typical lifetime of self was of order 10^4 Planck times and defined minimal de-coherence time. Dark matter hierarchy provides and hierarchy of Planck constants a concrete realization for a hierarchy of moments of consciousness with increasing geometric duration and quantum parallel dissipation which is second new element of TGD picture.

   The number theoretic generalization of Shannon entropy having negative values for rational and even algebraic entanglement is a further mathematical concept. Quantum computers are basic examples of systems possessing positive number theoretic negentropy, and this certainly conforms with the genuine information content of multi-verse states. It is not clear whether Negentropy Maximization is really consistent with the Second Law of thermodynamics and one must keep mind open for the possibility that Second Law is illusion created by the neglect of dark matter hierarchy meaning at the same time neglect of living life forms.

2. McFadden does not fix his views about quantum measurement theory but assumes that decoherence is an outcome of quantum measurements performed by environment or some subsystem of it. McFadden sees enzymatic action as a basic example of quantum measurement in which an amplification to a macroscopic phenomenon occurs.

   In TGD framework one can imagine two basic elements.

   (a) The emergence of symbolic representations as names of molecules made possible lock and key mechanism and "molecular sex". Once it is possible to name molecules, it becomes possible to regard bio-chemical pathways as analogs of computer programs proceeding rather deterministically. As already found, this idea has very concrete implications for understanding of bio-catalysis.

   (b) The most important bio-molecules could be seen as selves with especially long wake-up periods in a highly negentropic state of macro–temporal quantum coherence, and able to perform intentional actions applying the time mirror mechanism. The magnetic bodies of bio-structures are at the top of the intentional hierarchy.

3. McFadden sees quantum Zeno effect and its inverse as basic quantum control tools used by enzymes to increase reaction rates or induce mutations. Although the Zeno effect has also TGD counterpart, the intentional action of molecular magnetic bodies based on time mirror mechanism seems a more plausible option. Long ranged dark weak forces, in particular charge entanglement by W MEs, exotic ionization, and the control of the strength of the screening of the classical Z^0 force provides an additional mechanisms of enzyme control explaining chiral selection. Sol-gel transition inducing polymerization and its reverse allows to control the stability of bio-polymers. The leakage of particles between space-time sheets is a further control mechanism and involved with the time mirror mechanism.

4. McFadden assumes that the superpositions of peptide-environment product states involving different peptides with different neutron and proton numbers are possible so that the measurement involves also measurement of proton and neutron numbers. This option looks implausible because it is very difficult to think that states with different fermion numbers, masses, and charges would quantum superpose.

   In fact, it has become clear quite recently that TGD could in well-defined sense allow also quantum superpositions of different DNA molecules. This kind of superpositions are routinely assumed for coherent states of Cooper pairs in super-conductivity although they break conservation of charge, fermion number, and energy. The point is that in zero energy ontology [16] the total quantum numbers of physical states always vanish and the states decompose into positive energy part such that negative energy part located in its geometry future. Therefore it is possible to have quantum superpositions which in positive energy ontology, which is excellent approximation, would look like quantum superpositions of different DNA molecules. This possibility is not discussed in this chapter but it is needless to say that it could mean a revolution in the understanding of living matter. Even thermodynamics could be interpreted in a completely new manner since thermodynamical states which are "superpositions" of states with different values of conserved charged could have genuine quantal counterparts.

McFadden's view about biochemistry

McFadden represents a very general view about the essentials of bio-chemistry.

1. Protons associated with hydrogen bonds and electronic Cooper pairs serve as basic tools of quantum bio-control.

2. The localization of proton induces what McFadden interprets as a quantum measurement of proton's position.

In TGD framework the mechanism of catalytic action based on the temporary dropping of proton from the H_N-atom associated with catalyst or reactant, replaces this mechanism. Catalytic action could be seen as a short lasting period of "group sex" between catalyst and reacting molecules. Liberation of standard metabolic energy quantum is automatically involved with the process.

Important problems of quantum biology

The following list provides examples of problems that McFadden wants to understand in terms of quantum physics.

1. The extreme effectiveness of enzyme action.

2. The mechanism of mutations, in particular that of adaptive mutations and multiple mutations.

3. Evolution.
   i) The loss of complexity in computational models of evolution contra the increase of complexity in real evolution.
   ii) The emergence of the first self replicators.
   iii) The evolution of extremely complex reaction pathways, such as the one leading to the buildup of the ATP ase enzyme.

10.7.2 Enzyme action

Enzymes as quantum mouse traps is the metaphor introduced by McFadden. Typically enzyme catches the reactant molecules to a fixed conformation and fires a proton to the substrate molecule inducing in this manner a re-organization of some chemical bonds. The enzyme gains the lost proton later from a water molecule.

Mouse trap metaphor conforms completely with the TGD described view about catalytic action and also with the idea about enzyme as a quantum critical system.

1. Production of lactic acid from pyruvate

McFadden represents the production of the lactic acid from pyruvate, which is one of the last steps of catabolism, as a typical example of enzyme action. The process involves LDH, lactate dehydrogenase, catalyzing the transformation of the pyruvate to lactic acid, and NADH providing a proton and an electron pair. LDH donates the proton involved with the transformation of C=0 to C-O-H. NADH in turn provides proton and electron pair so that C=O is replaced with H-C-OH. NAD^+ receives proton and a compensating electron pair from water and LDH_- receives a proton from a water molecule.

2. Catabolism of lactose

Second example used my McFadden relates to the catabolism of lactose induced by the enzyme beta galactose. The rate of the process is trillion times higher than one might expect. McFadden proposes that the process involves a localization of proton in certain amino-acid of the beta galactose to a particular hydrogen bond. If the localization occurs to a correct hydrogen bond, the proton is injected to the lactose molecule and induces hydration. The suggestion is that a repeated quantum measurement of proton's position in beta galactose keeps the proton in the correct position so that the decay occurs with a much higher rate than it would occur otherwise.

It is not necessary to repeat how the catalysis could be understood in TGD framework. The decay of the lactose involves hydrolysis in which lactose molecule receives water H_N-O-H molecule from the environment and the loss of proton destabilizes the negatively charged molecule.

Hydrolysis could involve local gel-sol type transition transforming ordered water to ordinary water, which is able to provide the needed water molecule. The gel-sol transition could closely correlate with the non-standard localization of the proton inside enzyme. The process could involve an intentional action of a magnetic body of some system involved and thus negative energy topological light rays and charge entanglement by W MEs.

10.7.3 Quantum evolution

McFadden considers evolution from a quantum point of view. After the criticism of the RNA world paradigm McFadden poses several questions. How complexity could have emerged during the evolution? What was the first self-replicator? How the complex metabolic pathways could have evolved? What might be the quantum mechanisms of adapted and multiple mutations?

How evolution can create complexity?

McFadden pays attention to the fact that in the computational models of evolution final states tend to be less complex than the initial ones. This can be seen as a consequence of dissipation which leads to asymptotic self-organization patterns which are very simple. This is just the opposite of what is observed in Nature (note however the fact that the rapid extinction of new species after Cambrian explosion might be interpreted in terms of a loss of complexity).

In TGD framework the ability of living systems to circumvent the loss of complexity is due the facts that TGD Universe is quantum critical and p-adic cognition implies p-adic evolution predicting the emergence of systems characterized by increasing values of the p-adic prime and the integer characterizing the levels of dark matter hierarchy serving as their "intelligence quotients".

At the molecular level TGD allows to resolve this puzzle elegantly. During the pre-biotic exotic RNA period the predecessor of the genetic code is realized as many-to-one replication of exotic RNAs meaning a loss of information. This occurred for both singlet and doublet exotic RNA and for their composite forming a double helix with the size of the singlet helix being scaled up by a factor two. This however led to a dead alley involving only the RNAs representing the maximal invariant set of the RNA→RNA mapping as an asymptotic state. Final state was indeed simpler than the initial state.

At some stage the product code transformed to a code coding for RNA triplets, and amino-acids which originally catalyzed the mapping of RNA to RNA, took the role of the coded molecules. RNAs were mapped to DNAs by reverse transcriptase and the high error rate of the reverse transcription implied a rapid mutational rate. The many-to-one character of RNA→RNA replication implying the dead alley thus transformed from a curse to a blessing since it represented implicitly the protein-DNA genetic code.

Criticism of RNA world

McFadden represents severe critics against RNA world paradigm which is the dominating vision about pre-biotic evolution [168] . The basic objections are following.

1. In water environment bio-polymers become un-stable against depolymerization by hydration. This makes the idea of primordial sea implausible. The presence of the ordered water could resolve this problem even in the standard physics based models. In many-sheeted space-time the hypothesis that pre-biotic evolution occurred intra-terrestrially in the womb of the magnetic Mother Gaia makes sense and could resolve basic objections against the notion primordial sea.

2. Enzymatic action requires chiral selection. In TGD framework this can be interpreted as a strong indication for the necessity of the classical long ranged weak forces in the enzymatic control (say charge entanglement by W MEs).

3. McFadden lists several reasons for why RNA is implausible as a pre-biotic chemical. RNA consists of three components: RNA base, ribose, and phosphate. RNA bases and phosphate have been generated in the experiments trying to simulate pre-biotic evolution but the spontaneous emergence of ribose looks implausible. The problem is that a plethora of other sugars are produced.

   Some property of ribose should distinguish it from the other sugars. In TGD framework one might argue that for the ribose self "wake-up" periods or even periods of macro-temporal quantum coherence meaning sharp and non-entropic mental images are longer than for the other sugars. Quite generally, important bio-molecules could be identified as maximally autonomous systems able to "stay awake" and realize intentions.

   A more concrete explanation is based on stability.

   i) Both RNA, DNA and aminoacids are negatively charged and thus inherently unstable. The assignment of "names" to generalized hydrogen bonds represented by quark and antiquark at the ends of the magnetic flux tube to the basic building bricks of these polymers could make them stable and lead automatically to highly selective catalytic actions.

   ii) Suppose that the OH groups associated with the sugars have tendency to form a hydrogen bond with water molecules leading to ionization of the water molecule and liberation of proton dropping to a larger space-time sheet so that the polymer generates negative charge. If the number of O-H groups is too large the resulting negative charge can destabilize polymers formed by ribose, phosphate, and RNA nucleotides. Note that also the formation of double strand a liberates one proton per hydrogen bond which has a further de-stabilizing effect. This could explain why RNA with 4 O-H groups forms only short double strands whereas DNA having only 3 O-H groups forms very long double strands.

4. One can also wonder why just phosphate, ribose and RNA bases find each other and why the large number of other combinations are not realized. The naming based on flux tubes would restrict dramatically the possible combinations able to form spatially and temporally coherent systems bound together by flux tubes and automatically lead to a final state in which molecules having no braids with environment disappear from the system. Phosphate, ribose and RNA base could also find each other by tuning to common wave length by sending negative energy MEs entangling them with each other.

5. The presence of RNA bases, phosphate and ribose is not enough. McFadden finds it difficult to understand why only RNA molecules amongst many other reaction products of its three basic components are selected. In laboratory the activation of the RNA base allows to select RNA as a dominant reaction product. One possibility is that the liberation of activation energy helps to overcome the potential wall hindering the formation of RNA. This is could also due to the fact that the bound states of the activated RNA base with other two components are short-lived or decay to RNA in accordance with the idea RNA selves have especially long wake-up periods and is winner in the fight for survival. Magnetic body could be able to intentionally activate the RNA bases using universal metabolism present even without ATP ase machinery.

6. In the laboratory isolation, purification, and channeling of the reactants to the reaction volume are crucial parts of the process producing RNA and ribozymes, and almost-self-replicators. In the conventional chemistry framework it is very difficult to imagine how these processes could have occurred during pre-biotic evolution.

   The notion of magnetic body might come in rescue. Magnetic flux quanta could make possible highly controlled reaction network. A possible concrete toy model goes as follows. Suppose that quantum-classical correspondence holds true in the sense that the shape of the magnetic flux tube containing charged particles reacts to the presence of the charged particles so that it can be regarded as a classical orbit of a charged particle in the average magnetic field inducing Lorentz force. This makes sense only if a given magnetic flux tube contains particles with a fixed charge-to-mass ratio, and means that magnetic body indeed isolates and purifies the reactants to the magnetic flux tubes and allows them to react at the nodes of the magnetic web.

Evolution of metabolism

McFadden describes basic aspects of catabolism in an enjoyable manner. Catabolism can be seen as a process in which electrons from the orbitals of complex bio-molecules (in particular glucose) are gradually transferred to the orbitals of oxygen atoms. This process releases energy used as a metabolic energy in the form of ATP molecules.

In the standard chemistry framework the mechanisms behind $ADP \to ATP$ transformation seem miracle like. It is not easy to understand how an evolution based on mere chance and necessity could have led to the recent form of this machinery: intermediate steps seem to be simply absent. For instance, according to McFadden the reaction pathways generating the ATP ase enzyme catalyzing the generation of ATP involves 13 steps and all these steps are necessary. The probability that this pathway could have been generated by a random change is infinitesimally small and comparable to that for a monkey playing with a typewriter to compose Shakespeare's sonnets by accident.

1. Universal metabolic currencies

In TGD framework the predicted universal metabolic currencies remove partially the veil of mysteries surrounding the evolution of metabolism.

The dropping of a proton from atomic space-time sheet to a larger one generates a universal metabolic energy quantum. Thus metabolism would have been present already before the chemical storage of the metabolic energy. At the pre-biotic period the generation of negative energy topological light rays with photon energy $\sim .5$ eV could have induced the dropping of protons and remote utilization of the liberated energy. Indeed, the model for intra-terrestrial life led to the hypothesis that the infrared radiation corresponding to a temperature of about 4000 K near the mantle-core boundary could have provided the energy quanta of about .4 eV driving protons back to the atomic space-time sheets. The evolution of photosynthesis led later to the chemical storage of the metabolic energy.

The mitochondrial battery is kept at the potential of .15 eV by the metabolic energy feed. This process involves oxidation process in which electrons from the orbitals of molecules like glucose end down to the orbitals of oxygen atoms. The electron pairs are provided by NADH molecules in mitochondrial metabolism occurring in the water filled space between mitochondrial membranes. The energy liberated in this manner drives protons from the interior of the mitochondria to the space between the membranes. NAD^+ ion then receives the compensating electronic Cooper pair from water later.

The molecular battery provides the energy to generate ATP molecules serving as universal energy currencies. Three protons leaking back along the channel inside ATP ase molecule, which is analogous to the wire connecting the plus and minus poles of a battery, gain a net energy of $3 \times .15 = .45$ eV. This energy they donate to a proton, which uses it to get back to the atomic space-time sheet of the ATP molecule.

2. Does metabolism generate cell level qualia?

In a philosophical mood one could wonder the purpose of the endless ATP Karma's cycle: why not just the primitive metabolism involving only .5 eV photons? A partial explanation is the possibility to store metabolic energy chemically so that system becomes less dependent on environment. A

connection with the TGD based model of sensory receptor as a quantum capacitor suggests a deeper interpretation. The dielectric breakdown of the quantum capacitor gives rise to qualia which correspond to the increments of the total quantum numbers at either electrode when the dielectric breakdown occurs. ATPase could be seen as generating local di-electrical breakdown inducing primitive protonic qualia as a side product.

3. Molecular intentionality

The basic challenge of the bio-chemistry based approach to evolution is to understand how simple reaction steps coherently integrate to long multi-step reaction pathways. The assumption of molecular intentionality simplifies dramatically this task. Indeed, the best manner to understand and plan a complex electronic instrument is to know its purpose. The manual provides explanation of the purpose and magnetic body serves as the manual of the bio-logical body. For instance, it is much easier to understand how the reaction pathway leading to ATP ase has developed if one knows that the function of this pathway is to liberate universal metabolic energy quanta from mitochondrial battery besides possibly producing protonic qualia.

The fact the number of steps is 13 suggests 13-adicity and it would be interesting to see whether various reaction pathways tend to have a prime number of steps. It deserves to be noticed that $k = 169 = 13^2$ defines the p-adic prime associated with the magnetic flux tubes of the Earth's magnetic field and its possible dark companion $B_{end} = 2B_E/5$, and that the micro-tubular surface defines naturally cognitive code with $k = 13^2$ bits consisting of 13 13-bit sequences defined by tubuline conformations for a full 2π twist around micro-tubule.

Biological evolution could be seen as being induced by the evolution of cognition and of intentional actions. By the properties of the p-adic topology it proceeds from long time and length scales to shorter ones (p-adically short corresponds to something long in the real sense since rational space-time points are common to real and p-adic sectors of the imbedding space). This would suggest that the evolution of bio-logical functions is induced by the evolution of the intentional actions of the magnetic bodies, which were initially like rough sketches and gradually became more and more refined. Also motor skills develop in the same manner.

4. The emergence of molecular pathways

The emergence of names attached to molecules makes possible generation of computer program like dynamics in which programs call corresponds to association of molecules with names conjugate to some name of catalyst molecule to clusters so that catalytic action leading to a particular final state becomes possible.

The names of molecules could dictate the dynamics to a high degree. Situation could be like in the human society: knowing that person carries the label "physics teacher" allows to make amazingly precise long term predictions about the daily behavior of the person whereas the knowledge of all imaginable chemical and physical data about the person would not allow to predict anything interesting about the activities of the person in time scales longer than few seconds.

Quantum mechanism of mutations

McFadden suggests the reduction of the superposition of normal and enol configurations of T nucleotide to a tautomeric enol configuration as a quantum mechanism of mutation. The position measurement of the proton can locate it to the second nitrogenic hydrogen bond and thus transform T nucleotide to the isomeric but short-lived enol configuration having only two hydrogen bonds connecting it to the complementary base. In the enol state DNA replication assigns G instead of A with T.

Zeno effect could allow to effectively freeze T to this configuration and thus increase the rate of mutations. The same mechanism could work also at the level DNA→ mRNA transcription and protein translation and assign lys instead of glu to the enol configuration.

The mechanism poses an additional condition to the proposal that DNA nucleotides correspond to quarks and antiquarks. The question is what determines which quark or antiquark corresponds to a given nucleotide and the mechanism of mutation based on disappearance of hydrogen bond suggests that the number of hydrogen bonds (2 or 3) determines this so that one would have correlation with with the weak isospin of quark (u or d) and number of hydrogen bonds (3 or 2).

1. Adaptive mutations of E. coli

In adaptive mutations the bacterium E. coli unable to catabolize lactose to get metabolic energy develops a mutation allowing it to generate beta galactose inducing the decay of the lactose. This mutation occurs with a probability which is higher than predicted by randomness. McFadden poses the question how the information about the presence of the lactose is communicated from the environment to the DNA level.

If life would be mere quantum chemistry, the only possibility would be that the information transfer sequence DNA→mRNA→ proteins of Central Dogma is somehow reversed. What McFadden suggests is DNA-mRNA-betagalactoce-lactose entanglement such that DNA appears as a superposition of ordinary and enol configurations. Lactose would take the role of quantum measurer of the proton's position inside T nucleotide, and Zeno effect would increase the rate of the mutation.

In TGD Universe the bacterial magnetic body receives information about the presence of lactose and its intention to "eat" lactose is transformed to a desire represented by a negative energy ME entangling directly with DNA. The intention of the magnetic body of E. coli would be to push the DNA to enol configuration by kicking the proton to the abnormal position. Negative W ME could induce long lasting entanglement with normal and enol configurations of T nucleotide so that the enol configuration would appear with a higher probability than in the absence of quantum entanglement and mutated DNA results more often in the replication. The alternative option is that magnetic body induces the gel-sol transition inducing mutation in the manner already described.

Quite generally, feeding of dark protons to atomic space-time sheets and gel-sol transition would serve as switches used by the cellular magnetic body to realize its desires. This mechanism could be seen as a refined form of remote metabolism providing metabolic energy for the starving bacterium.

2. Multiple mutations of TB bacteria

TB (tubercle bacillus) bacteria are able to develop a simultaneous resistance against several drugs [185] . This occurs for bacteria which have only brief growth periods followed by long dormant periods. McFadden interprets dormant periods in terms of entanglement with the environment. When this period ends even multiple mutations could result in the quantum measurement at DNA level.

In the TGD framework the magnetic body of TB population would receive information about the fates of various members of the population in the multi-drug environment and would have a strong desire to develop multi-drug resistance. The long dormant periods of bacteria allowing them to survive bring in mind the sleeping periods of higher life forms, and suggests the entanglement of the bacteria with the other members of the population, also those living in the geometric past and already deceased as victims of the drugs. This kind of entanglement would allow the magnetic body to manipulate the genomes of the still-living bacteria so that they have better changes to survive in the multi-drug environment. McFadden does not discuss whether the simple mechanism of mutations working in the case of E. coli might be enough in the case of TB bacteria.

Note that the notion of hyper-genome allows to understand bacterial colonies as systems analogous to multi-cellulars controlled by genes expressed collectively.

3. Mutations and intronic DNA

The TGD based view about pre-biotic evolution allows to imagine more effective mechanisms of mutations replacing the simple mechanism utilized by E. coli and working in case of eukaryotes.

In the TGD Universe reverse transcriptase plays a key role in the pre-biotic evolution as a generator of the genetic variation. The variation is due to the high error rate of the reverse transcription. For instance, the amazing ability of the HIV virus (retro-virus) to adapt is based on the reverse transcription of HIV RNA to DNA. It would be strange if this ability would have been lost during the sub-sequent evolution. Perhaps fragments of DNA are transformed to mRNA also during dormant, "inwards directed" periods. mRNA fragments are however not translated to proteins now but transformed back to DNA fragments by reverse transcriptase replacing the previous DNA fragment in DNA with a new one. This mechanism might work at least in case of eukaryotes having cell nucleus and mean that mRNA is not transferred outside the nucleus. The replacement of DNA fragment need not occur immediately. mRNA fragments would thus act like retro-viruses to produce the needed genetic variation. In this framework ordinary retro-viruses such as HIV might be seen as kind of fallen angels.

This kind of activity in which collective selves of populations modify the genomes of their members might be present in all eukaryotes during sleeping (or more generally, dormant) periods. The generation of mutations might be one of the fundamental purposes of sleep and explain why sleep is so important for healing.

This mechanism of mutations might be still too primitive for eukaryotes. In TGD framework the intronic portion of DNA expresses itself as temporal field patterns using p-adic cognitive codes, in particular memetic code. Introns play the role of the computer software whereas genes take the role of the hardware. In this picture introns would be naturally involved with the control of the adaptive mutations of higher organisms. In the modern home computers hardware is becoming more and more dynamical, and computer metaphor suggest that the passive DNA could contain segments representing kind of computer store containing variants of various genes taken in use if required. Transposons might represent these new pieces of the hardware.

This replacement need not involve the removal of the old gene fragment and could be only functional. Computer metaphor inspires the idea that the intronic portion of DNA represents a given gene as a dynamical list of addresses, kind of links or program calls, specifying which portions of DNA contribute to the gene, and that this list characterizes how the splicing of mRNA occurs. Therefore the mutation could occur at the intronic software level as a mere updating of the list representing the gene.

The challenge is to understand how this addressing might be realized physically. For instance, addressing might involve simply common fragments of DNA in meme and corresponding portions of gene serving as addresses making possible a "tuning to a common wave length". Alternatively, magnetic flux tubes might serve as space-time correlates of the links. They could be generated intentionally as wormhole magnetic fields consisting of pairs of positive and negative energy magnetic flux tubes parallel to DNA strand. The generation of wormhole magnetic fields identified as the basic motor activity of the magnetic body could also explain the appearance and disappearance of EEG bands. By the p-adic fractality similar mechanism could be at work also in DNA length scale.

4. Could zero energy ontology be relevant for living matter?

Zero energy ontology [7, 16] emerged originally from the observation that Robertson-Walker cosmologies correspond in TGD framework to vacuum extremals for which all conserved classical charges vanish (the non-conserved gravitational mass density does is non-vanishing). The construction of S-matrix led to a precise formulation of zero energy ontology.

Zero energy ontology states that physical states have vanishing net quantum numbers and consist of positive energy states at boundaries of future directed light-cones in the geometric past ("not so big bang") and negative energy states at the boundaries of past directed light cones in the geometric future ("not so big crunch") assignable to arguments of N-point function.

Due to the fact that conformal weights are complex it is possible to distinguish between positive energy particles propagating to the geometric future and negative energy particle propagating to geometric past. Phase conjugate laser photons contra ordinary laser photons represent basic empirical example about this distinction.

In the construction of S-matrix identified as unitary entanglement coefficients between these tow kinds of states (this notion makes sense for hyper-finite factors of type II_1) these states represent incoming and outgoing states of particle reaction so that measurement of reaction rates is basically quantum measurement in which time-like entanglement is reduced instead of space-like entanglement [16] .

A rather strong argument in favor of zero energy ontology comes from superconductivity [12] . The models super-conductivity utilize formally the notion of coherent state of Cooper pairs involving quantum superposition of arbitrary numbers of Cooper pairs. This is in conflict with various conservation laws in standard ontology but in zero ontology it is quite possible to consider quantum superposition of zero energy states with various values of quantum numbers for positive energy states.

This opens the gates for rather fascinating speculations. Time-like charge entanglement would allow to imagine a time-like variant of the capacitor model of sensory receptor. For instance, sensory qualia could result in the reduction of coherent state of Cooper pairs to a state with a well defined charge.

Also different DNA sequences with different masses and charges might appear in quantum superpositions for time like entanglement and this might be relevant for evolution of genetic code. In particular, the model of McFadden for mutations might generalize dramatically. As a matter fact, the proposed identification of S-matrix (or rather its generalization M-matrix which need not be unitary) as time-like entanglement coefficients assumes the presence of all pairs of initial and final states appearing in the S-matrix in the superposition so that this possibility could be seen as a prediction.

10.8 Great vision about biological evolution and evolution of brain

The following great vision about evolution and is not perhaps strictly about hierarchy of EEGs. The hierarchy of dark matter and EEGs however leads to this vision naturally. The first part of vision relates to biological evolution. Second part is about the evolution of brain. Here the key thread is evolution of two kinds of intelligences, the ordinary fast intelligence evolving via the emergence of fast computation type activities and emotional slow intelligence developing via the emergence of higher levels of dark matter hierarchy. The latter intelligence is what distinguishes us from animals.

10.8.1 Basic assumptions

The great vision about evolution and brain relies on two several new notions and ideas.

1. Life as something in the intersection of real and p-adic worlds making possible negentropic entanglement- both space-like and time-like. This makes possible to understand what conscious intelligence is and NMP reduces evolution to a generation of negentropic entanglement. DNA as topological quantum computer hypothesis [26] finds also a justification.

2. The notion of many-sheeted space-time implying a universal hierarchy of metabolic energy quanta, and the notion of magnetic body.

3. Communication and control based on Josephson radiation and cyclotron transitions crucial for understanding biophotons and EEG and its fractal generalization as a key element of bio-communications.

4. Zero energy ontology and the closely related notion of causal diamond (CD) assigning a hierarchy of macroscopic time scales to elementary particles coming as octaves of the basic time scale and justifying p-adic length scale hypothesis. Zero energy energy ontology also justifies the vision about memory and intentional action and the idea that motor action can be seen as time reversal of sensory perception.

5. The hierarchy of Planck constants and the identification of the fundamental evolutionary step as an increase of Planck constant. Evolutionary steps mean migration to the pages of the Big Book labeled by larger values of Planck constant and living system can be regarded as a collection of pages of the Big Book such that a transfer of matter and energy between the pages is taking place all the time. The change of the Planck constant implies either reduction or increase of the quantum scales-this leads to a model for biocatalysis and a model of cognitive representations as scaled down or scaled up "stories" mimicking the real time evolution.

6. A resonant like interaction between hierarchy of Planck constants and p-adic length scale hierarchy favoring the values of Planck constant proportional to powers of two, and idea that weak and color interactions are especially important in the length scales which correspond to Mersenne primes and Gaussian Mersennes. The simplest option is that weak bosons have their standard masses but appear as massless below their Compton length which scales up like $\hbar$ and preferred p-adic length scales correspond to Mersenne primes. Also copies of weak bosons and gluons with ordinary value of Planck constant and reduced mass scale can (and will) be considered.

How to identify the preferred values of Planck constant?

The basic problem is to identify the preferred values of Planck constant and here one can only make theoretical experimentation and all what follows must be taken in this spirit. One can consider assumptions which become increasingly stronger.

1. If only singular coverings of CD and CP_2 are possible Planck constant is a product of integers. Algebraic simplicity of algebraic extensions of rationals favors ruler and compass integers (Appendix).

2. A resonant interaction between the dark length scales and p-adic length scales with ordinary value of Planck constant favors Planck constants coming as powers of two.

3. An even stronger assumption would be that p-adic length scales coming as Mersennes and Gaussian Mersennes are especially interesting.

   (a) If weak bosons can appear with the ordinary value of Planck constant only in the p-adic length scale $k = 89$, one obtains the condition

   $$k_d = k - 89 \quad , \quad k \in \{89, 107, 113, 127, 151, 157, 163, 167\} \tag{10.8.1}$$

   for the values of of $r = 2^{k_d}$ allowing dark weak bosons in p-adic length scales assignable to Mersennes. These values of k_d assign to electrons and quarks dark p-adic length scales $L(k_{eff}) = \sqrt{r}L(k)$, $r \equiv \hbar/\hbar_0 = 2^{k_d}$. The scales could correspond to size scales of basic units of living systems.

   (b) If weak bosons and possibily also gluons with ordinary value of Planck constant are possible in all p-adic length scales $L(k)$, $k \in \{89, 107, 113, 127, 151, 157, 163, 167\}$, one obtains much richer structure. This hierarchy defines defines secondary dark matter hierarchies from the condition that the scaling the p-adic length scale $L(k_1)$ in this set by $\sqrt{r}$, $r \equiv \hbar/\hbar_0 = 2^{k_d}$, gives a p-adic length scale equal to another p-adic length scale $L(k_2)$ in this set. This requires $k_d + k_1 = k_2$ so that the values

   $$k_d = k_2 - k_1 \tag{10.8.2}$$

   are favored for the scaling of $\hbar$. In this case the hierarchy of dark scales assignable to quarks and leptons is much richer. The tables below demonstrate that electron appears as its dark variant for all Mersennes and also in atomic length scales $k = 137, 139$ so that this option puts electron in a completely unique position.

4. Also other scales are possible. For instance, $r = 2^{47}$ required by 5 Hz Josephson frequency gives dark weak scale which corresponds $k = 136$ as a p-adic scale. The stages of sleep can be understood in terms of scaling of $\hbar$ by factor 2 and 4 so that also the atomic length scale $k = 137$ and the scale $k = 138$ are involved.

Since the experimental input is rather meager, one is forced to do theoretical experimentation with various hypothesis. The quantitative experimental tests are rather primitive but basically quantal.

1. The time scales assignable to CDs of leptons and quarks and their scaled up counterparts for the preferred values of Planck constant should define biologically important time scales. One might even speak about evolutionary level of electron. These time scales could define fundamental biorhythms and also time scales of long term memory and planned action.

2. Josephson frequencies and cyclotron frequencies scaling like $1/\hbar$ (if magnetic field scales down like $1/\hbar$) charactering biologically important ions and elementary particles. In accordance with the quantum criticality of living matter it is assumed that cell membrane corresponds to almost vacuum extremal so that classical Z^0 force is an essential element of the model. Also these frequencies should define fundamental bio-rhythms and characterize the evolutionary level of cell. Experimentally of special importance are the cyclotron frequencies assignable to Ca^{++} ions.

3. The amplitude windows for electric field scaling like $\hbar$ for a particular cyclotron frequency define a basic prediction.

Tables about predicted time and length scales

The following tables summarize various predictions for time scales and length scales. They correspond to the most general assumption that exotic bosons with the ordinary value of Planck constant are possible in all length scales associated with Mersennes and Gaussian Mersennes.

k_d	p_1	p_2		k_d	p_1	p_2
4	163	167		38	**89**	127
6	107	113		38	113	151
6	151	157		40	127	167
6	157	163		44	107	151
10	157	167		44	113	157
12	151	163		50	107	157
14	113	127		50	113	163
16	151	167		54	113	167
18	**89**	107		56	107	163
20	107	127		60	107	167
24	**89**	113		62	**89**	151
24	127	151		68	**89**	157
30	127	157		74	**89**	163
36	127	163		78	**89**	167

Table 5. The integers k_d characterizing the preferred values of $r = \hbar/\hbar_0 = 2^{k_d}$ identified from the condition that the dark variant of p-adic length scale $L(p_1)$ corresponding to some ordinary p-adic length scale defined by Mersenne prime M_p or Gaussian Mersenne $M_{G,p}$, $p \in \{89, 107, 113, 127, 151, 157, 163, 167\}$ corresponds to similar p-adic length scale $L(p_2)$. If one assumes that weak bosons can appear with ordinary value of Planck constant only in the p-adic length scale $k = 89$, only the rows with $p_1 = 89$ of the table are possible: in these cases p_1 is in boldface and the row has double underline. The corresponding values of k_d are in the set $\{18, 24, 38, 62, 68, 74, 78\}$.

Note that the table above include only the dark length scales associated with $k = 89$ gauge bosons.

Z, W	d	u	e	k_d
89	120	124	127	**0**
93	124	127	131	4
95	126	129	133	6
99	130	133	137	10
101	132	135	139	12
103	134	137	141	14
105	136	139	143	16
107	138	141	145	**18**
109	140	143	147	20
113	144	147	151	**24**
119	150	153	157	30
125	156	159	163	36
127	158	161	165	**38**
129	160	163	167	40
133	164	167	171	44
139	170	173	177	50
143	174	177	181	54
145	176	179	183	56
149	180	183	187	60
151	182	185	189	**62**
157	188	191	195	**68**
163	194	197	201	**74**
167	198	201	205	**78**

Table 6. The dark p-adic length scales $\sqrt{r}L(k) = L(k_{eff})$, $k_{eff} = k + k_d$, of intermediate gauge bosons Z, W, d and u quarks, and electron for the values $r = 2^{k_d}$ of Planck constant defined in Table

5. The uppermost row gives the integers characterizing the p-adic length scales of the particles for the standard value of Planck constant. k_{eff} characterizes also the CD times scale through the formula $T(CD, k_{eff}) = 2^{k_{eff}-127} \times .1$ seconds. The rows which correspond to the less general option for which only M_{89} corresponds to weak bosons with ordinary value of Planck constants have double underline and the corresponding values of k_d are in boldface.

k_1	k_M		k_1	k_M		k_1	k_M		k_1	k_M
113	89		113	107		163	127		163	157
127	89		119	107		167	127		169	157
151	89		123	107		133	127		173	157
157	89		113	107		139	127		163	157
163	89		117	107		143	127		167	157
167	89		111	107		133	127		161	157
95	89		175	113		137	127		169	163
109	89		181	113		131	127		183	163
133	89		187	113		225	151		207	163
139	89		191	113		229	151		213	163
145	89		119	113		157	151		219	163
149	89		133	113		171	151		223	163
103	89		157	113		195	151		177	163
127	89		163	113		201	151		201	163
133	89		169	113		207	151		207	163
139	89		173	113		211	151		213	163
143	89		127	113		165	151		217	163
113	89		151	113		189	151		187	163
119	89		157	113		195	151		193	163
125	89		163	113		201	151		199	163
129	89		167	113		205	151		203	163
95	89		137	113		175	151		169	163
101	89		143	113		181	151		175	163
105	89		149	113		187	151		179	163
95	89		153	113		191	151		169	163
99	89		119	113		157	151		173	163
93	89		125	113		163	151		167	163
145	107		129	113		167	151		187	167
169	107		119	113		157	151		211	167
175	107		123	113		161	151		217	167
181	107		117	113		155	151		223	167
185	107		195	127		235	157		227	167
113	107		201	127		163	157		181	167
127	107		205	127		177	157		205	167
151	107		133	127		201	157		211	167
157	107		147	127		207	157		217	167
163	107		171	127		213	157		221	167
167	107		177	127		217	157		191	167
121	107		183	127		171	157		197	167
145	107		187	127		195	157		203	167
151	107		141	127		201	157		207	167
157	107		165	127		207	157		173	167
161	107		171	127		211	157		179	167
131	107		177	127		181	157		183	167
137	107		181	127		187	157		173	167
143	107		151	127		193	157		177	167
147	107		157	127		197	157		171	167

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Table 9. The table gives all weak boson length scales -both non-dark and dark implied by the assumption that all Mersennes primes and their Gaussian counterparts and their dark counterparts defined $k_d = k_i - k_j$ them are possible.

particle	Z, W	d	u	e
k	89	120	123	127
f(CD)/Hz	2.7488×10^{12}	1280	160	10

Table 8. The fundamental frequencies associated with the CDs of intermediate gauge bosons Z, W, d and u quarks, and electron. Note that for intermediate gauge bosons the frequency of CDs corresponds to energy $E = 1.13 \times 10^{-2}$ eV and wavelength $\lambda = 1.01 \times 10^{-4}$ m (size of a large neuron).

Z, W	d	u	e	k_d
3.64e-13	7.81e-04	6.25e-03	1.00e-01	**0**
5.821e-12	1.25e-02	1.00e-01	1.60e+00	4
2.31e-11	5.00e-02	4.00e-01	6.40e+00	6
3.73e-10	8.00e-01	6.40e+00	1.02e+02	10
1.49e-09	3.20e+00	2.56e+01	4.10e+02	12
5.97e-09	1.28e+01	1.02e+02	1.65e+03	14
2.38e-08	5.12e+01	4.10e+02	6.55e+03	16
9.54e-08	2.05e+02	1.64e+03	2.62e+04	**18**
3.81e-07	8.19e+02	6.55e+03	1.05e+05	20
6.10e-06	1.31e+04	1.05e+05	1.68e+06	**24**
3.91e-04	8.39e+05	6.71e+06	1.07e+08	30
2.50e-02	5.37e+07	4.30e+08	6.87e+09	36
1.00e-01	2.15e+08	1.72e+09	2.75e+10	**38**
4.00e-01	8.59e+08	6.87e+09	1.10e+11	40
6.40e+00	1.37e+10	1.10e+11	1.76e+12	44
4.10e+02	8.80e+11	7.04e+12	1.12e+14	50
6.55e+03	1.41e+13	1.13e+14	1.80e+15	54
2.62e+04	5.63e+13	4.50e+14	7.21e+15	56
4.19e+05	9.01e+14	7.21e+15	1.15e+17	60
1.68e+06	3.60e+15	2.88e+16	4.61e+17	**62**
1.07e+08	2.31e+17	1.84e+18	2.95e+19	**64**
6.87e+09	1.48e+19	1.18e+20	1.89e+21	**74**
1.10e+11	2.36e+20	1.89e+21	3.02e+22	**78**

Table 9. The $\hbar$-scaled fundamental time scales $T(CD, k_{eff}) = 2^{k_{eff}-127} \times .1$ seconds associated with the CDs of intermediate gauge bosons Z, W, d and u quarks, and electron for the values $\hbar/\hbar_0 = 2^{k_d}$ of Planck constant defined in Table 5. The scales are expressed in seconds. The uppermost row gives the time scales of CDs for the standard value of Planck constant. The rows which correspond to the less general option for which only M_{89} corresponds to weak bosons with ordinary value of Planck constants have double underline and the corresponding values of k_d are in boldface.

Electron and u quark are different

Before continuing an important observation is in order. Electron is exceptional when compared to quarks. It appears as a dark particle in all p-adic length scales defined by biologically important Gaussian Mersennes and also in atomic length scales $k = 137$ and $k = 139$. The reason is trivial: by the basic assumptions electron must appear at same length scales as weak bosons above $k = 127$ since

it corresponds to Mersenne prime. Also for the less general option (exotic intermediate gauge bosons are possible only as the dark variants of the standard ones) it appears at cell membrane length scale $k = 151$, which is due to the fact that one has $113 - 89 = 151 - 127 = 24$. Also u quark can appear with $k_{eff} = 137, 139, 163, 167$ and also this is an accident. The light invariants of intermediate gauge bosons appearing in long p-adic length scales would naturally correspond to almost vacuum extremals making possible the criticality as the basic aspect of life. One must of course be very cautious about the masses of exotic counterparts of u and d quark: one can also consider the possibility that masses are identical.

10.8.2 Dark matter hierarchy and big leaps in evolution

Dark matter hierarchy leads to an amazingly concrete picture about evolutionary hierarchy allowing to identify the counterparts for concepts like mineral, plant, and animal kingdom that we learned during schooldays and ceased to take seriously as students of theoretical physics as we learned that other sciences are just taxonomy. Even more, a view about what distinguishes between prokaryotes, eukaryotes, animal cells, neurons, EEG, and even about what makes cultural evolution, becomes possible. This view is also very useful when one tries to understand the role of microtubules.

The appearance of CDs scaled up in size by $r = \hbar/\hbar_0$ and space-time sheets scaled up in size by $\sqrt{r}$ means the emergence of new levels of structure and it is natural to identify big leaps in evolution in terms of emergence of new larger matter carrying space-time sheet magnetic flux sheets and corresponding magnetic bodies. If magnetic flux quanta are scaled by r magnetic flux quantization conditions remain unaffected if magnetic field strengths scale down by $1/r$ so that the energies of cyclotron photons are not affected. The thickness of flux tubes can remain unchanged if the currents running at the boundaries of the flux quantum cancel the magnetic flux. As already found, this mechanism must be at work inside living organisms wheras in far away region flux quanta are scaled up in size.

The attractive hypothesis is that the leaps in evolution correspond to the emergence of dark variants of weak and possibly also color interactions in dark p-adic length scales which correspond to ordinary p-adic length scales characterized by Mersenne primes. These leaps would be quantum leaps but in different sense as thought usually. The emergence of higher dark matter levels would basically mean the integration of existing structures to larger structures. A good metaphor are text lines at the pages of book formed by magnetic flux sheets whose width is scaled up by r as the new level of dark matter hierarchy emerges. The big leaps can occur both at the level of organism and population and organisms with rather low individual dark matter level can form societies with high dark matter levels and high collective intelligence (honeybees and ants are good example in this respect).

Certainly also other scalings of Planck constant than those summarized in tables are possible but these scalings are of primary interest. This intuition is supported by the observation that electron is completely exceptional in this framework. Electron's dark p-adic length scales corresponds to p-adic length scales $L(k)$, $k = 167, 169$, assignable to atomic and molecular physics and to the Gaussian Mersennes $M_{G,k} = (1+i)^k - 1$, $k \in \{151, 157, 163, 167\}$, assignable to the length scale range between cell membrane thickness 10 nm and nucleus size 2.58 μm. The corresponding p-adic length scales, the number of which is 23, are excellent candidates for the scales of basic building brickes of living matter and vary from electron's p-adic length scale up to 1.25 m ($k = 167$ defining the largest Gaussian Mersenne in cell length scale range) and defining the size scale of human body. The corresponding p-adic time scales are also highly interesting and vary from .1 seconds for electron defining the fundamental biorhythm to 9.6×10^{14} years which is by 4-5 orders longer than the age of the observed Universe. For $k = 167$ the time scale is 1.1×10^{11} years and is by one order of magnitude longer than the age of the observed Universe estimated to be 1.37×10^{10} years [1] .

This conceptual framework gives rather strong guidelines for the identification of the levels of evolutionary hierarchy in terms of dark matter hierarchy. The outcome is a more detailed vision about big evolutionary leaps. Note that in the sequel only the general option is considered: the justification for this is that for this option electron appears as a dark particle for all length scales defined by Gaussian Mersennes as well as in atomic length scales. The basic vision in nutshell is that evolution means the emergence of dark weak and gluonic physics in both dark and ordinary length scales and that the size scales of the basic biostructures correspond to Mersenne primes and their Gaussian variants.

A sketch about basic steps in evolution

The vision about evolution depends on what one assumes about the initial state.

1. If one assumes that weak bosons with ordinary value of Planck constant were present in the begining, evolution would mean a steady growth of k_d. The problem is that small values of $k_d = k_1 - k_2$ correspond to the Gaussian Mersennes defining cellular length scales. If these exotic weak physics were present from the beginning, large parity breaking in cellular length scales would have been present all the time.

2. An alternative and perhaps more realistic view is that the evolution means the emergence of exotic weak physics corresponding almost vacuum extremals in increasingly longer length scales. A possible mechanism could have been the induction of exotic $\hbar_0$ variant of weak physics at the nearest Mersenne length scale k_{next} by the dark variant of weak physics at level k so that one would have $k_d = k_{next} - k$. The simplest induction sequence would have been $89 \to 107 \to 113 \to 127 \to 151 \to 157 \to 163 \to 167$ corresponding to $k_d \in \{18, 6, 14, 24, 6, 6, 4\}$. A possible interpretation of exotic $\hbar_0$ physics is in terms of almost vacuum extremals and non-standard value of Weinberg angle: also weak bosons of this physics would be light. This sequence defines the minimal values for k_d but also larger values of k_d are possible and would correspond to steps between neighbours which are not nearest ones.

The following sketch about the basic steps of evolution relies on the latter option.

1. Elementary particle level

Magnetic bodies with size scale defined by the sizes of CDs assignable to quarks and leptons and possibly also weak bosons (already now the size of big neuron emerges) corresponds to the lowest level of hierarchy with the sizes of the basic material structures corresponding to the Compton lengths of elementary particles. The fundamental bio-rhythms corresponding to frequencies 10, 160, and 1280 Hz appear already at this level in zero energy ontology which suggests that elementary particles play a central and hitherto unkown role in the functioning of living matter.

2. $89 \to 107$ *step with* $k_d = 18$

The first step would have been the emergence of $k_{eff} = 107$ weak bosons inducing $\hbar_0$ weak physics in $k = 107$ length scale characterizing also ordinary hadrons. This in turn would have led to the emergence of exotic nucleons possibly corresponding to almost vacuum extremals. The reduction of the model for the vertebrate genetic code to dark hadron physics [78] is one of the most unexpected predictions of quantum TGD and assumes the existence of exotic- possibly dark- nucleons whose states with a given charge correspond to DNA, RNA, mRNA, and tRNA. The $\hbar_0$ variants of these nucleons would interact via weak bosons with hadronic mass scale. The exotic variants of the ordinary $k = 113$ nuclei would correspond to the nuclear strings consisting of exotic nucleons [18, 78] and define nuclear counterparts for DNA sequences. Their dark counterparts could define counterparts of DNA sequences in atomic physics length scales. Therefore a justification for the previous observation that genetic code could be realized at the level of hadron physics and that chemical realization would be higher level realization finds justification. The anomalous properties of water could be also partly due to the presence of dark nucleons and the proposal was that the presence of exotic nuclei is involved with water memory [34] . The possible existence of the the analog of DNA-RNA transcription between ordinary DNA and its nuclear counterpart would have dramatic implications. For instance, one can imagine a mechanism of homeopathy based on this kind of transription process which would also allow a modification of genome by using dark nuclei to communicate the DNA sequences through the cell membrane to the target nuclei.

3. $107 \to 113$ *step with* $k_d = 6$

The next step would have been the emergence of $k_{eff} = 113$ weak bosons inducing $\hbar_0$ weak physics in $k = 113$ length scale characterizing also ordinary hadrons. Exotic variants of the ordinary nuclei possibly corresponding to almost vacuum extremals could have emerged interacting weakly (or actually relatively strongly!) via the exchange of weak bosons with mass scale of order 100 MeV. Also dark variants of the exotic $k = 107$ nucleons could have have emerged and formed exotic nuclei of size scale $k = 119$.

4. $113 \to 127$ *step with* $k_d = 14$

At this step weak bosons in electron mass scale would have emerged. Whether these weak bosons could have induced large parity breakings in atomic and molecular length scales is not clear. Viruses, which do not yet possess cell membrane could correspond to this level of hierarchy.

5. $127 \to 151$ *step with* $k_d = 24$

This step would have been fundamental since weak bosons in cell membrane length scale would have appeared. Note that by $113 - 89 = 24$ this step also leads from $k = 89$ weak bosons to $k = 113$ weak bosons. The weak bosons assignal to $k = 151$ could correspond to the weak interactions associated with almost vacuum extremals and $sin^2(\theta_W) = .0295$ could correspond to the weak physics in question.

$k_d = 24$ step for $k = 113$ $\hbar_0$ weak bosons would have produced them in $k_{eff} = 137$ atomic length scale with $L(137) \simeq .78$ Angstrom This could have naturally led to large parity breaking effects and chiral selection.

Dark $k_{eff} = 151$ electrons appearing in the TGD inspired model of high T_c super-conductivity would have been a by-product of this step. Whether dark electrons could have transformed to light $\hbar_0$ electrons (of mass .25 keV) with a common mass scale of order 10^2 eV with exotic weak bosons is an interesting question. The model of high T_c super-conductivity predicts the presence of structures analogous to cell membrane. This would suggest that cell membranes emerged and chiral selection emerged at this step so that one could not distinguish the emergence of molecular life as a predecessor for the emergence of cell membrane like structures. This would conform with the fact that DNA molecules are stable only inside cell nucleus. Note that for $k_{eff} = 151$ electron's CD has time scale $2^{24} \times .1$ seconds -that is 19.419 days (day=24 hours).

The smallest nanobes [64] appearing in rocks have size 20 nm and could have emerged at this step. The size of the viruses [101] is between 10-300 nm covers the entire reange of length scales assignable to Gaussian Mersennes, which suggests that smallest viruses could have emerged at this step. Also the smallest [63] [63] , which by definition have size smaller than 300 nm could have appeared at this stage.

6. The remaining steps

The remaining steps $k = 151 \to 157 \to 163 \to 167$ could relate to the emergence of coiling structure DNA and other structures inside cell nucleus. $k = 167$ would correspond to $k_d = 167 - 89 = 68$ to be compared with the value $k_d = 47$ required by 5 Hz Josephson frequency for the neuronal membrane for -70 mV resting potential. Note that $k_d = 48$ (state 1-2 of deep sleep) corresponds to $k = 163$.

By their smallness also double and triple steps defined by $k_d = k_{i+n} - k_i$, $n > 1$, are expected to be probable. As a consequence, electrons can appear as dark electrons at all the Gaussian Mersenne levels. At these steps the dark electrons corresponding to primes $k_{eff} = 137, 139$ would appear. For $k = 137$ dark electron appears with CD time scale equal to 128 seconds- rather precisely two minutes. The model for EEG suggests that the exotic weak bosons appear in the scales $k_{eff} = 136, 137, 138$.

Further multisteps from the lower levels of hierarchy would give structures with size scales above the size of cell nucleus possibly assignable to organs and structural units of brain. The dark levels assignable to electron are expected to be of special interest. It is encouraging that the longest scale assignable to electron in this manner corresponds to $k = 205$ and length scale of 1.28 m defining body size. As a consequence dark electrons are predicted at levels $k = 137, 139, 141, 143, 145, 147$ coming as octaves.

Prokaryotic cells (bacteria, archea) without cell nucleus for which cell membrane is responsible for metabolic functions and genome is scattered around the cell could have emerged at this step. This would mean that the emergence of the cell membrane thickness as a fundamental scale is not enough: also the size scale of membrane must appear as p-adic length scale. The sizes of most prokaryotes vary between 1 μm and 10 μm: the lower bound would require $k = 163$. There also prokaryotes with sizes between .2 μm ($k = 157$ corresponds to .08 μm) and 750 μm. Cell nuclei, mitochondria, and other membrane bounded cell nuclei would have evolved from prokaryotes in this framework. The sizes of eukaryote cells are above 10 μm and the fact that multicellular organisms are in question strongly suggests that the higher multisteps giving rise to weak bosons and dark electrons in length scales above $L(167)$ are responsible for multi-cellular structures.

This scenario leaves a lot of questions unanswered. In particular, one should understand in more detail the weak physics at various length scales as well as various exotic nuclear physics defined by dark nucleons and dark variants of nuclei.

Division of the evolution to that of biological body and magnetic body

Electron's Mersenne prime M_{127} is the highest Mersenne prime, which does not correspond to a completely super-astrophysical p-adic length scale. In the case of Gaussian Mersennes $M_{G,k}$ one has besides those defined by k in $\{113, 151, 157, 163, 167, \}$ also the ones defined by k in $\{239, 241, 283, 353, 367, 379, 457, 997\}$ [2] . The appropriately extended model for evolution allows to distinguish between three kinds of values of k_{eff}.

1. The values of k_{eff} for which electron can appear as dark particle and thus satisfying $k_{eff} \leq 205$ (Table 5). These levels would correspond to structures with size below 1.25 m defined roughly by human body size and it is natural to assign the evolution of super-nuclear structures to the levels $167 < k_{eff} \leq 205$.

2. The values of of k_{eff} for which dark gauge bosons are possible in the model. This gives the condition $k_{eff} \leq 235$. These levels correspond to structures in the range 1.25 m-40 km. The identification as parts of the magnetic body can be considered.

3. The values of k_{eff} obtained by adding to the system also the Gaussian Mersenne pair $k \in \{239, 241\}$ allowing also the dark electrons. The lower size scale for these structures is 640 km.

4. The higher levels corresponding to k_{eff} in $\{283, 353, 367, ...\}$. The lower size scale for these structures is 3 AU (AU is the distance from Earth to Sun).

$k_{eff} > 205$ levels would correspond to the emergence of structures having typically size larger than that of the biological body and not directly visible as biological evolution. This evolution could be hidden neuronal evolution meaning the emergence of extremely low Josephson frequencies of the neurons modulating higher frequency patterns and being also responsible for the communication of long term memories.

Biological evolution

In principle the proposed model allowing multisteps between hierarchy levels defined by Mersenne primes and their Gaussian counterparts could explain the size scales of the basic structures below the size scale 1.25 m identified in terms of the $k_{eff} \leq 205$ levels of the hierarchy.

1. The emergence of cells having organelles

The appearance of the structures with $k_{eff} > 167$ (possibly idetifiable as magnetic body parts) should correlate with the emergence of simple eukaryotic cells and organisms, in particular plant cells for which size is larger than 10 μm, which could correspond to $k_{eff} = 171$ for electron and dark variants of weak gauge bosons. $k_{eff} = 177$ is the next dark electron level and corresponds to 80 μm scale. It seems natural to assume that these dark weak bosons do not transform to their $\hbar_0$ counterparts at these space-time sheets.

Cell nucleus would be the brain of the cell, mitochondria would be the energy plant, and centrioles generating microtubules would define the logistic system. Also other organelles such as Golgi apparatus, ribosomes, lysosomes, endoplasmic reticulum, and vacuoles would be present. These organelles would live in symbiosis by topologically condensing to $k_{eff} \geq 171$ magnetic body controlling their collective behavior. Centrosomes associated with animal cells would not be present yet but microtubule organizing centers would already be there.

The recent observations show that centrioles are not always in the characteristic T shaped conformation. Daughter centrioles resulting during the replication of mother centriole use first ours of their lifetime to roam around the cell before becoming mature to replicate. A possible interpretation is that they are also life forms and that magnetic body utilizes daughter centrioles to perform some control functions crucial for the future development of the cell. For instance, centrioles visit the place where axonal growth in neurons starts.

Cytoskeleton would act as a counterpart of a central nervous system besides being responsible for various logistic functions such as transfer of proteins along microtobuli. Centrioles give also rise to basal bodies and corresponding cilia/flagella used by simple cells to move or control movement of air or liquid past them. Centriole pair would be also used by the magnetic body to control cell division.

The logistic functions are the most obvious functions of microtubules. Magnetic body would control cell membrane via signals sent through the cell nucleus and communicated to the cell membrane along microtubuli. Basal bodies below the cell membrane and corresponding cilia/flagella would serve as motor organs making possible cell motion. Tubulin conformations representing bits would allow microtubule surface to represent the instructions of the magnetic body communicated via via cell nucleus to various proteins moving along the microtubular surface so that they could perform their functions.

TGD based view about long memory recall as communication with geometric past allows also the realization of cellular declarative memories in terms of the conformational patterns. Memory recall corresponds to a communication with geometric past using phase conjugate bosons with negative energies reflected back as positive energy bosons and thus representing an "image" of microtubular conformation just like ordinary reflected light represents ordinary physical object. There would be no need for a static memory storage which in TGD framework would mean taking again and again a new copy of the same file.

Receptor proteins would communicate cell level sensory input to the magnetic body via MEs parallel to magnetic flux tubes connecting them to the magnetic body. We ourselves would be in an abstract sense fractally scaled up counterparts of receptor proteins and associated with dark matter iono-lito Josephson junction connecting the parts of magnetosphere below litosphere and above magnetosphere. The communication would be based on Josephson radiation consisting of photons, weak bosons, and gluons defining the counterpart of EEG associated with the level of the dark matter hierarchy in question.

3. The emergence of organs and animals

The emergence of magnetic bodies with k_{eff} in the range $(177, 181, 183, 187,\ 189, 195, 201, 205)$ allowing both dark electron and weak bosons could accompany the emergence of multicellular animals. Magnetic body at this level could give rise to super-genome making possible genetic coding of organs not yet possessed by plant cells separated by walls from each other. The super structures formed from centrosomes and corresponding microtubuli make possible complex patterns of motion requiring quantum coherence in the scale of organs as well as memories about them at the level of organs.

4. The emergence of nervous system

k_{eff} in the range $(187, 189, 195, 201, 205)$ allowing dark electrons and weak bosons gives size scales $(.25, .5, 4, 32, 128)$ cm, which could correspond to the scales of basic units of central nervous system. What would be of special interest would be the possibility of charged entanglement based on classical W fields in macroscopic length scales. The emergence of the new level means also the integration of axonal microtobuli to "text lines" at the magnetic flux sheets making possible logistic control at the multineuronal level. The conformational patterns of the microtubular surface would code nerve pulse patterns to bit patterns representing declarative long term memories. An interesting question is whether the reverse coding occurs during memory recall.

The evolution of magnetic body

For mammals with body size below 1.25 m the levels $k_{eff} > 205$ cannot correspond to biological body and the identification in terms of magnetic body is suggestive. The identification of EEG in terms of Josephson frequencies suggests the assignment of EEG with these levels.

1. The emergence of EEG

EEG in the standard sense of the word is possessed only by vertebrates and one should understand why this is the case. The value of Josephson frequency equal to 5 Hz requires only $k_d = 47$ so that something else must be involved. A possible explanation in the framework of the proposed model comes from the following observations.

1. Besides the maximal p-adic scale $k = 205$ for which electron and weak bosons appears as dark variants the model allows also levels at which only gauge bosons appear as dark particles. From

Table 9 one finds that levels $k \in \{207, 211, 213, 217, 219, 221, 223, 225, 229, 235\}$ are allowed. Could it be that these levels and possibly some highest levels containing both electrons and gauge bosons as dark particles are a prerequisite for EEG as we define it. Its variants at higher frequency scales would be present also for invertebrates. The lowest Josephson frequency coded by the largest value of $\hbar$ in the cell membrane system determins the Josephson frequency.

2. The membrane potentials -55 mV (criticality against firing) correspond to ionic Josephson energies somewhat above 2 eV energy ((2.20,2.74,3.07,2.31) eV, see Table 1). For 2 eV the wavelength 620 nm is near to $L(163) = 640$ nm. Therefore the Josephson energies of ions can correspond to the p-adic length scale $k = 163$ if one assumes that a given p-adic mass scale corresponds to masses half octave above the p-adic mass scale so that the opposite would hold true at space-time level by Uncertainty Principle. Josephson frequencies $f_J \in \{5, 10, 20, 40, 80, 160\}$ Hz correspond to $k_d \in \{47, 46, 45, 44, 43, 42\}$ giving $k_{eff} \in \{210, 209, 208, 207, 206, 205\}$.

   (a) Cerebellar resonance frequency 160 Hz would correspond to $k = 205$ -the highest level for for which model allows dark electrons (also 200 Hz resonance frequency can be understood since several ions are involved and membrane potential can vary).

   (b) The 80 Hz resonance frequency of retina would correspond to $k_{eff} = 206$ -for this level dark electrons would not be present anymore.

   (c) 40 Hz thalamocortical frequency would correspond to $k_{eff} = 207$.

   (d) For EKG frequencies are EEG frequencies below 20 Hz 12.5 and heart beat corresponds to .6-1.2 second cycle (the average .8 s corresponds to $k_{eff} = 212$).

3. Even values of k_{eff} are not predicted by the model based on Mersenne primes allowing only odd values of k_{eff} so that the model does not seem to be the the whole truth. The conclusion which however suggests itself strongly is that EEG and its variants identified as something in the range 1-100 Hz, are associated with the levels in at which only dark weak bosons are possible in the proposed model. Note that the size scales involved with EEG would be above the size scale of human body so that we would have some kind of continuation of the biological body to be distinguished from the magnetic body. The time scales assignable to the dark CDs would be huge: for instance, $k = 205$ would correspond to $T = 2^{42} \times .1$s making about 1395 years for electron.

2. Does magnetic body correspond to the space-time sheets carrying dark weak bosons?

The layers of the magnetic body relevant for EEG have have size of order Earth size. Natural time scale for the moment of sensory consciousness is measured as a fraction of second and the basic building blocks of our sensory experience corresponds to a fundamental period of .1 seconds. This scale appears already at $\hbar_0$ level for electron CD. The natural question concerns the relationship of the magnetic body to the $k > 205$ space-time sheets carrying only gauge bosons in the model and having size scale larger than that of biological body. Do they correspond to an extension of biological body or should they be regarded as parts of the magnetic body? The following observations suggest that they could correspond to layers of the magnetic body responsible for the fractal variant of EEG.

1. The primary p-adic time scales (Compton times) $T(239)$ and $T(241)$ correspond to frequencies, which are $2^{\pm 1/2}$ kHz. The geometric average $k = 240$ corresponds to kHz frequency. Is the appearance of kHz scale a mere accident or do the frequencies assignable to the quark CDs correspond to Compton times $\propto \sqrt{2^{k_{eff}/2}}$?

2. One can apply scalings by 2^{k_d} to the triplet $(239, 240, 241)$ to get a triplet $(239 + k_d, 240 + k_d, 241 + k_d)$. The results are summarized in Table 10. Clearly the frequencies in question cover also the EEG range. Note that these frequencies scale as $\sqrt{1/r}$ whereas Josephson frequencies scale as $1/r$.

k_d	f_1/Hz	f_2/Hz	f_3/Hz
0	707	1000	1412
4	177	250	354
6	89	1250	177
10	22.1	31.3	44.2
12	11.1	15.6	22.1
14	5.5	7.8	11.1
16	2.8	3.9	5.5
18	1.4	2.0	2.8
20	0.7	1.0	1.4
24	0.2	0.2	0.3

Table 10. The Compton frequencies obtained by scaling $2^{k_d/2}$ from the basic triplet $k_{eff} = (239, 240, 241)$. The values of k_d correspond to those predicted by the model based on Mersenne primes.

Also ZEG and WEG would appear but in much shorter scales dictated by k_{eff} and might accompany EEG. Somehow it seems that the effective masslessness of weak bosons below given scale is highly relevant for life. One can of course ask whether some larger Gaussian Mersenne could change the situation. There is a large gap in the distribution of Gaussian Mersennes after $k = 167$ and the next ones correspond to $M_{G,k}$, with k in $(239, 241, 283, 353, 367, 379, 457, 997)$ [2] . The twin pair $k = (239, 241)$ corresponds to a length scales $(1.6, 3.2) \times 10^2$ km and the minimum value for k_d are (72,74) ($167 \to (239, 241)$ transition).

3. Long term memory and ultralow Josephson frequencies

What determines the time scale associated with long term memory is a crucial question if one really wants to understand the basic aspects of consciousness.

1. Does the time scale correspond to the size scale of CD assignable to electron scaled by $r = \hbar/\hbar_0$? In this case relatively small values of r would be enough and $r = 2^{47}$ would give time scale of 10^{13} s for for electron's CD, which is about 3×10^5 years. This does not make sense.

2. Does Josephson frequency define the relevant time scale? In this case the long term memory would require the analog of EEG in the time scale of memory span. $k_{eff} = 205$ would give 6 ms time scale for memory from the assigment of $k_{eff} = 163$ to the Josephson photons at V=-50 mV implying $k_d = 42$. Minute scale would require $k_{eff} = 217$. The highest level $k_{eff} = 235$ allowed by the model involving only Gaussian Mersennes with $k \leq 167$ would correspond to a time scale of 77.67 days (day is 24 hours). For Gaussian Mersennes defined by $k_{eff} = (239, 241)$ the time scales become about (41.4,82.8) months (3.4 and 6.8 years). These scales should also define important biorhythms. The claimed 7 years rhythm of human life could relate to the latter rhythm: note that the precise value of the period depends on the membrane potential and thus varies. The presence of the scaled up variants of the by $k_d \leq 78$ allows longer time spans of long term memory and the scaling defined by $k_d = 167 - 163 = 4$ scales up the span of long term memories to (54.4,108.8) years.

4. Cultural evolution

Higher levels in the hierarchy would correspond mostly to the evolution of hyper-genome coding for culture and social structures. Introns are good candidate for the nucleodes involved. The development of speech faculty is certainly a necessary prerequisite for this breakthrough. Already EEG seems to correspond to dark layers of biological body larger than biological body so that one can cask whether the weak bosons and dark electrons in the length scales $k = 239, 241, 283, 353, 367, ...$ could be relevant for the collective aspect of consciousness and cultural evolution. Maybe the size scales $(175, 330)$ km and their scaled up variants by $k_d \leq 78$ might have something to do with the spatial scale of some typical social structure (not city: the area of New York is only 790 km^2).

10.8.3 Could insect colonies have "EEG"?

Only vertebrates can have EEG in 1-100 Hz range. According to the proposed model this means the presence of the $k > 205$ levels which can be regardd as a continuation of the biological body carrying dark weak bosons and having size scales larger than 1.25 m. That only vertebrates have EEG conforms with the empirical findings about the effects of ELF em fields on vertebrate brain.

This does not however imply that one could not assign EEG to the collective levels of consciousness. For instance, in the case of social insects forming colonies some kind of collective EEG might exist and explain the ability of the colony to behave like single organism. Indeed, ELF magnetic field and magnetic fields affect the behavior of honeybees just as ELF em fields affect the behavior of vertebrates [175] : the model for this findings led to a model for the fractal hierarchy of EEGs.

One could argue that insect brain is so simple (in the case of honeybee the number of neurons 1/1000 of number of neurons in human retina) that it is not possible to assign "personal" EEG to honeybee. The fact that a honeybee isolated from colony dies just as does the cell separated from organism, suggests that the relationship of insect to colony is like that of a cell to organism. Hence one could test whether colonies of social insects or their sub-colonies might possess an analog of ordinary EEG. What this would mean that ant colonies have sufficiently complex hyper-genome making possible collective variants of memory, sensory input, and intelligence, as well as the ability to realize collective motor actions. Even bacterium colonies have intricate social structures [203] so that one must remain open minded.

An objection against this line of thinking is that even in the case of collective EEG the proposed model assigns the Josephson frequencies with neurons. One might imagine Josephson frequencies at EEG range even in case of insects- say the queen of the nest. Since dark photons are in question the fields are very weak. I do not know whether any-one has got the crazy idea about checking whether beehive has EEG -certainly not any routine measurement! One an also imagine a fractal counterpart of EEG at the level of some individuals- say queen of the nest- at very low frequencies making possible long term memory.

Do honeybees have long term memory?

The realization that insect colonies rather than insects might correspond to higher $k_{eff} > 205$ levels of the dark matter hierarchy came via an indirect route. The article "Why honeybees never forget a face?" of New Scientist [106] described evidence supporting the view that that honeybees might possess long term memory in the time scale of days.

Adrian Dyer of the University of Cambridge and colleagues trained honeybees to associate a sucrose drink with a photograph of a particular face. The insects were then tested on their memory and recognition skills by being presented with the picture of this face and the pictures of three other faces not associated with any reward. Of the seven bees tested, two lost interest in the trial and flew away. But the five remaining bees correctly identified the target face in more than 80 per cent of trials, even though the reward had been removed. Moreover, some bees remembered the face two days later, indicating that they had formed a long-term memory of it.

1. The conservative explanation is that the achievement is due to keeping the face-honey association intact in the absence of the stimulus which created it in a time scale of days. For this option the ability of honeybee to express the distance and orientation to the food source could be hardwired involving no conscious memory about the flight. Also the interpretation of the honeybee dance telling the distance and orientation of food source to advices where to fly would be completely "instinctive"- whatever this means.

2. A more radical option is that honeybee hive rather than honeybee has long term memories in the sense as long term memories are interpreted in TGD framework: that is as communications with the geometric past. In this case the span of long term memories is determined by the level of dark matter hierarchy as time scale defined by Josephson frequency assignable to level of dark matter hierarchy in question and a span of few days for long term memories forces the conclusion $k_d \geq 63$: the upper bound is $k_d = 78$ (see Table 5), when one allows only $k \leq 167$ Mersennes and this corresponds to 87.6 years.

One can ask whether the ability of honey bee queen to found a new honeybee colony could involve long term memory in the time scale of year. If this were the case, the queen would not face her

formidable challenge alone: the former colony in the geometric past still exists as a conscious entity and could communicate advices to the queen. The magnetic body of the former colony could exist also in the geometric now, being physically associated with the queen. This magnetic body could serve as the conscious entity communicating to the queen the advices and commands making possible to construct the beehive. A more conservative explanation is that these activities are genetically hardwired and instinctive (leaving open what 'instinctive' really means if it actually means anything).

The distinguished social position and anatomy of queen are consistent with the hypothesis that queen has more massive connections than other bees with the magnetic body of beehive. For instance, it is known that the new hive is oriented in exactly the similar manner as the old. Either long term memory or passive magnetic coding of the orientation of the hive with respect to Earth's magnetic field made possible by the magnetite in the abdomen of queen could explain this. The neurons of queen could correspond to a very large value of $\hbar$ giving rise to the required low Josephson frequencies.

The colony would have sensory resolution in a time scale of a fraction of second and short term memory in minute time scale. The counterpart of EEG at the level of hive is highly suggestive and conforms with the finding that ELF magnetic fields with strengths in the range .1-1 mT ($2B_E - 20B_E$ affect honeybee dance [175] as does also the absence of Earth's magnetic field. Interestingly, 1-2 mT DC field causes epileptiform activity in the case of humans [137] (the change of the DC field used seems to be more important that the period it is applied). Could the beehive suffer a kind of epileptic seizure!

The intentional actions of the honeybee colony would be realized via magnetic flux sheets traversing the super-genes of the insects participating to the action in question. Workers, soldiers, etc.. would act to some extent as organs of the colony being connected by hyper-genes of hyper-genome to larger units. Queen could act as the analog of a complex Grand Mother neuron in brain or a leader in human society.

This view can be criticized. Honeybee dance [56] is performed by forager bees and the dance represents among other things the angle between the lines connecting hive to the food source and sun as the angle between movement of bee and vertical direction (also other options are possible). The intricate pattern of the dance in turn codes for the distance to the food source. If beehive is a conscious entity using bees as its cells, why is honeybee dance needed at all? TGD based vision about the evolution of modern human society from a bicameral society in which individuals received advice and commands from "God" [63, 64] , suggests an answer to this criticism. The society able to survive must be maximally flexible and allow maximal individual intelligence and maximal freedom of individual actions consistent with the overall goals. This requires delegation of simple tasks to lower levels meaning also that communications between individuals become necessary (the development of language and other communications parallels the transition from bicamerality to modern society in the case of humans). The communication itself might however involve also the beehive. Foreagers could be like the prophets of the bicameral society communicating in semitrance the advices of God to the colony.

It should be noticed in passing that honeybees have already earlier made a visit to TGD inspired theory of consciousness [31] . As discovered by topologist Barbara Shipman [30] , honeybee dance has a mathematical description in terms of a construct assignable to color group SU(3) of gauge interactions between quarks and gluons. This led her to propose that color interactions might have some deep role in living matter. This is in a sharp contrast to the fact that color interactions as establishment knows them are completely invisible above the length scale of 10^{-15} meters. The TGD based prediction that there exists an entire hierarchy of scaled up copies of QCD, in particular QCDs with confinement length scale of order cell size, changes completely the situation.

Honeybees as magneto-receptors of the beehive or magnetic cells as magneto-receptors of bee?

Earth's magnetic field has a crucial status in the model of living systems even at the lowest levels of dark matter hierarchy so that Earth's magnetic field is expected to play a role in the functioning of all cells, also bees and ants. This is indeed the case.

It is known that that bees have two navigation systems. The first system is based on the direction of sun and polarization of solar light but does not work on cloudy days. The second navigation system uses Earth's magnetic field and is used in cloudy days. Bees have in their abdomen magnetite (Fe_3O_4) particles of size about 30 nm and iron storage protein ferritin which correspond 10 to nm

sized super-paramagnetic particles [144] . Magnetite particles and ferritin in principle make possible magneto-reception instead of a mere passive compass behavior.

The minimum option is that honeybee itself does not receive any neural information about the magnetic field but acts as a passive magneto-receptor of the bee colony or sub-colony (such as workers flying to the food source) and that the information contained by the receptor grid allows the sub-colony to deduce its position in the varying magnetic field. "BEEG" would mediate this information to the magnetic body of the (sub-)colony and the general mechanism based on Josephson currents does not require nerve pulse patterns to achieve this.

Since foreagers seem to act as individuals able to navigate in the magnetic field of Earth, it would seem that some cells of the honeybee could act as magneto-receptors so that the reaction of the magnetic particles would be coded to a neural signal. It has been proposed that the changes in the shape of the configurations formed by magnetite particles in a varying magnetic field induce changes in the shape of neuron and in this manner can induce neural signal. This mechanism could also induce the voltage perturbations coding the information to the Josephson current giving rise to the sensory part of EEG as a state of coherent ELF photons. Perhaps the genes expressing these neurons are activated only in foragers and ferritin makes possible the magneto-reception in this sense.

Social bacteria and magneto-tactic bacteria

Magneto-tactic behavior of bacteria [120] was discovered for 30 years ago by microbiologist Richard P. Blakemore and means that certain motile, aquatic bacteria orient and migrate along magnetic field lines. This ability could be purely passive compass mechanism made possible by the magnetite detected in the bacteria.

During last years we have learned that bacteria are not simple creatures having only single goal: to multiply and fill the Earth. Bacteria are able to communicate and act co-operatively [203] . This raises the question whether hyper-genes could appear already at this level and whether bacteria acting as a colony they individual bacteria could act as magneto-receptors of colony allowing it to detect even variations of the magnetic field much like individual cells in the brain of vertebrates or perhaps even in the abdomen of honeybee are believed to serve as magneto-receptors.

Great leaps in evolution as emergence of higher levels of dark matter hierarchy at level of individuals

The vision about great leaps in evolution led to the view that the emergence of EEG corresponds to the emergence of $k_{eff} > 205$ levels of dark matter hierarchy. On the other hand, the time scale of gene translation corresponds to that associated with the ordinary EEG, which forces to ask whether these levels are present already in the lowest life forms. Perhaps a more plausible option is that the .1 second time scale of electronic CD defines the time scale of gene translation and corresponds therefore to the standard value of $\hbar_0$. The findings about honeybees however support the view that $k_{eff} > 205$ levels are present but are associated with the honeybee colony rather than individuals. This however requires that the these levels have neuronal realization in terms of Josephson frequencies.

Therefore a more precise formulation of the hypothesis about great leaps in evolution would be that great leaps in evolution correspond to the emergence of a new dark matter level at the level of individual organism. If this view is correct then $k_{eff} > 205$ levels would correspond to a collective level of consciousness in the case of invertebrates down to bacteria, which are indeed found to form societies [203] . This conforms also with the fact that the genome of invertebrates is too small to allow realization of $k_{eff} > 205$ flux sheets as genes or even super-genes. The somewhat unexpected conclusion would be that all activities of invertebrates involving gene expression would be controlled by collective levels of consciousness: invertebrates would not be individuals in this sense. Viruses do not possess DNA translation machinery which is consistent with the absence of also collective $k_{eff} > 205$ levels. One can of course ask whether the queen of honeybee could be an exception to this rule.

If one believes that the time scale of gene expression corresponds to Josephson frequency then the explanation for the universality of the genetic code could be that $k_{eff} > 205$ levels controls gene expression: for $k_{eff} > 205$ wave length scale indeed corresponds to the length scale assignable to the magnetosphere of Earth. One could of course counter argue that it is more reasonable form magnetic

Mother Gaia to delegate this kind of duties to the lower levels and that the CDs of electron and quarks are ideal for this purpose.

10.8.4 Dark matter hierarchy, hierarchical structure of nervous system, and hierarchy of emotions

One can ask how the structural and functional hierarchy of CNS and the hierarchy of emotions relates to the dark matter hierarchy. The basic picture wherefrom one can start is following.

1. The emergence of nervous system corresponds to the emergence of $k_{eff} < 205$ levels of dark matter hierarchy above $k_{eff} < 167$. For instance, worms and insects would correspond to this level.

2. Vertebrates have EEG and thus the most primitive vertebrates (reptiles) should correspond to $k_{eff} \geq 205$.

3. The emergence of new structures need not mean the emergence of new levels of dark matter hierarchy. Rather, the most reasonable criterion for the presence of these levels is the emergence of behaviors involving long term goals and the magnetic bodies of the parts of brain assignable to the control of this kind of behaviors would correspond to higher values of k_{eff}. Also the maximum span of memories at given level should be characterized by the value of k_{eff} associated with the brain structures involved (hippocampus, mammillary bodies). This picture conforms with the fact that already insects possess neurons, ganglia, and head containing the predecessor of cerebrum but correspond to $k_{eff} \leq 205$ most naturally.

For goal related emotions the maximal time scale assignable to the achievement of the goal might allow to identify the time scale characterizing corresponding level of dark matter hierarchy. The lowest level emotions would be "primitive" emotions not related to any goal and one can as whether they could be assigned to organs consisting of ordinary cells and correspond to $k_{eff} \leq 205$.

1. The time scale of planned behavior and of long term memories makes possible to estimate upper bounds for the values of k_{eff} assuming Josephson frequency hypothesis. $k_{eff} \leq 205$ would give the upper bound of 6 ms which corresponds to cerebellar resonance frequency 160 Hz. This time scale looks too short even for the simplest vertebrates and one must be very cautious here.

2. An alternative interpretation is as the shortest possible span for short term memory whose time scale is known to vary.

3. Cerebellar rhythm could be analogous to hippocampal theta rhythm and involved with the crebella memory storage and therefore would not tell anything about the span of the memory but would characterize the time resolution of memories and planned actions. The role of cerebellum in the fine coordination of motor actions indeed requires high time resolution.

Brain has anatomic division into midbrain, hindbrain, and forebrain [41] . Midbrain and hindbrain (sometimes both are included in brain stem) is possessed by even the most primitive vertebrates and its emergence could therefore correspond to the emergence of $k_{eff} \geq 205$ levels and EEG. The emergence of these levels relates naturally to the emergence of long term planning of motor actions in motor areas. The emergence of limbic brain, which defines the most primitive forebrain, could mean the emergence of the Gaussian Mersenne defined by $k_{eff} = 239$ containing dark electron condensates level and goal related emotions. This conforms with the fact that for mammals forebrain and cerebral hemispheres dominate whereas for other vertebrates hindbrain and cerebellum are in the dominant role.

Reptilian brain as $k_{eff} \leq 205$ system?

Reptilian brain contains only the structures corresponding to brain stem (midbrain and hind brain, in particular cerebellum) and as far structures are considered would correspond to $k_{eff} \leq 205$ levels of the hierarchy. Cerebellum is not believed to contribute directly to our consciousness. The absence of higher looks however an unrealistic assumption since reptiles certainly have long term memories.

Simplest emotions correspond to emotions involving no goal. Moods like excitement, feeling good/bad/tired/strong, etc.. could represent examples of such emotions and could be experienced already by reptilians. Of course, the scaled up variants of these emotions could appear at higher levels of hierarchy and would relate to the states of magnetic bodies (degree of the quantum coherence of Bose-Einstein condensates!).

Limbic system

Limbic system is not possessed by reptiles [4] . It is responsible for emotions, control of emotions, and also emotional intelligence. Limbic system corresponds to the brain of the most mammals. The limbic brain includes the amygdala, anterior thalamic nucleus, cingulate gyrus, fornix, hippocampus, hypothalamus, mammillary bodies, medial forebrain bundle, prefrontal lobes, septal nuclei, and other areas and pathways of the brain.

1. The sub-cortical part of the limbic system involves amygdalar and septal divisions. According to [4] amygdalar division promotes feeding, food-search, angry, and defensive behaviors related to obtaining food. Septal division promotes sexual pleasure, genital swelling, grooming, courtship, and maternal behavior. These divisions are emotional mirror images of each other hand could correspond to $205 < k_{eff} < 239$.

2. The cortical part of the limbic system contains cingulate gyrus which is the newest part of the limbic system and belongs to thalamo-cingulate division which promotes play, vocalization (e.g., the separation cry), and maternal behavior. The time scale of memories would be shorter than 3.4 at this level.

3. Frontal lobes [2] are often regarded as the organ of volition. The frontal lobes are involved in motor function, problem solving, spontaneity, memory, language, initiation, judgement, impulse control, and social and sexual behavior. Prefrontal lobes representing the extreme front part of frontal lobes belong also to the limbic system and are responsible for motivation and ability to pose long term goals. This ability distinguishes humans from other primates. For these reasons frontal lobes, in particular prefrontal lobes, could involve the highest levels of dark matter hierarchy in the case of humans. The Gaussian Mersenne levels $k_{eff} = (239, 241)$ could be assigned as lowest level in this hierarchy. The time scale of long term memories would be longer than 3.4 years at these levels.

Cortico-striatal emotions like sadness, hate, fear anger, surprise, embarrassment, happiness, contentment, and joy involve goal structures and failure or success to achieve the goal in essential manner and would involve prefrontal lobes.

These levels would naturally relate to collective levels of consciousness coded by hyper genes. Hence these emotions could also relate to goals not directly related to the fate of biological body. Mirror neurons are a crucial prerequisite of a social behavior (autistic children seem to lack them), which suggests that hyper genes are involved at least with them.

Social emotions (feeling embarrassed, ashamed, guilty, loved, accepted, ...) could be induced by the collective levels of dark matter hierarchy as punishments or rewards for social behavior very much like neurotransmitters are believed to provide rewards and punishments at neuronal level.

Neocortex and two kinds of intelligences

Neocortex is often assumed to be superior ("neomammalian") part of the brain and makes the majority of brain hemispheres. The species which are considered to be highly intelligent, such as humans and dolphins, tend to have large amounts of neocortex. The amount of neocortex is roughly proportional to the brain size for primates.

Neocortex cannot correspond to $k_{eff} \geq 239$ (defining Gaussian Mersenne) as a whole. The decomposition of sensory areas to layers is consistent with the presence of lower levels since it is time resolution which matters in the case of sensory representations. Same conclusion applies to sensory association areas. The fine tuning of the motor control performed by cerebellum is consistent with $k_{eff} \leq 205$. Intelligence understood in the conventional sense of the word is accurate, works fast, and is computer like. The part of neocortex responsible for ordinary intelligence would be a rapid

and accurate processor of sensory and cognitive representations. Hence $k_{eff} < 239$ would naturally characterize sensory areas, secondary and primary motor areas, to hippocampal representation of declarative memories, and all association areas except dorsolateral prefrontal sensory-motor association cortex where short term memories are represented.

Emotional intelligence works slowly and is responsible for visions and holistic views and would thus correspond to higher levels of dark matter hierarchy. Limbic system is involved with emotions, motivation and long term planning and would thus be responsible for emotional intelligence. Indeed, the damage to frontal lobes [2] need not affect ordinary intelligence but affects emotional intelligence.

The levels of dark matter hierarchy associated with short and long term memory

The first thing to ask is of course whether the notions of short and long term memory make sense in TGD framework. Indeed, it would seem that it is more natural to speak about hierarchy of memories with characteristic time scales coming as selected powers of two.

1. According to [8] , the span of other than visual short term memories is 30-45 seconds. This requires $k_{eff} \in \{217, 218\}$.

2. Visual short term memories [1] representing selected features of visual field are reported to have time span of few seconds. This suggests $k_{eff} \in \{213, 214, 215\}$.

3. Iconic visual memories representing entire visual field have much shorter time span of order 1 s: $k_{eff} \in \{211, 212\}$ would be appropriate for them,

4. Long term memories would correspond to $k_{eff} > 218$.

Hippocampus and mammillary bodies involved with long term memory recall are part of the limbic system. The hippocampal theta rhythm 4-12 Hz , which could corresponds roughly to $k_{eff} \in \{163, 162, 161\}$ has nothing to do with the span of long term memories but would define the time resolution of the memories: the moment of sensory experience indeed corresponds to 10 Hz frequency. The frequencies responsible for memory storage need not have anything to do with the ultralow frequencies characterizing the temporal distance of the past event associated with the memory recall and hippocampus could just build a kind of bit sequence which during memory recall is communicated from the geometric past to some part of the future brain or magnetic body.

Anterograde amnesia means an inability to restore long term memories. The damage of hippocampus or of mammillary bodies can induce anterograde amnesia. In the usual conceptual framework the explanation would be the inability to store new long memories. In TGD framework this would be inability to construct those cognitive representations which are communicated to the geometric future in long term memory recall. Retrograde amnesia seems to involve almost always anterograde amnesia and means loss of memories for some time span before the injury. A possible explanation is that injury can propagate also to the geometric past of the brain quantum jump by quantum jump.

During ageing memories tend to be lost but the memories of childhood are the most stable ones. A possible interpretation is that faster rhythms of the generalized EEG tend to disappear: kind of scaled up variant for the process of falling into sleep accompanied by silencing of higher EEG bands could be in question.

What about transpersonal levels of consciousness?

$k_{eff} > 245$ levels of dark matter hierarchy correspond to time span longer than 109 years and cannot relate to the biological body alone. They could relate to higher collective levels of the dark matter hierarchy and evolution of social structures. The memories extending over personal life span claimed by meditators could have interpretation in terms of $k_{eff} > 245$ transpersonal levels of consciousness. Also the "god module" located to temporal lobes could correspond to this kind of levels of dark matter hierarchy. If it corresponds to Gaussian Mersenne with $k_{eff} = 283$ the time scale of memories becomes huge: about 10^{14} years so that the notion of "god module" is indeed appropriate.

10.9 Oil drops in water solution as a primitive life form?

The origin of life is one the most fascinating problems of biology. The classic was carried out almost 60 years ago. In the experiment sparks were shot through primordial atmosphere consisting of methane, ammonia, hydrogen and water and the outcome was many of the aminoacids essential for life. The findings raised the optimism that the key to the understanding of the origins of life. After Miller's death 2007 scientists re-examined sealed test tubes from the experiment using modern methods found that well over 20 aminoacids - more than the 20 occurring in life - were produced in the experiments.

The Urey-Miller experiments have yielded also another surprise: the black tar consisting mostly of hydrogen cyanide polymer produced in the experiments has turned out to be much more interesting than originally thought and suggests a direction where the candidates for precursors of living cells might be found. In the earlier experiments nitrobenzene droplets doped with oleic anhydride exghibited some signatures of life. The droplets were capable to metabolism using oleic anhydride as "fuel" making it possible for the droplet to move. Droplets sensed each other's presence and reacted to it and also demonstrated rudimentary memory.

In the sequel a model for the oil droplets as primitive life form is developed using as a constraint the TGD inspired quantum model for living matter. The key ingredients are the notions of magnetic body, the assignment of dark matter identified a hierarchy of macroscopic quantum phases to a hierarchy of Planck constants, zero energy ontology, the model for DNA-cell membrane system as topological quantum computer, and Negentropy Maximization Principle combined with the notion of number theoretic entropy. This entropy can be negative for rational and even algebraic entanglement probabilities, which inspires the vision about life as something in the intersection of real and p-adic worlds.

The basic objection against the identification of oil droplets as a primitive life form is that droplets have no genetic code and do not replicate. The TGD inspired model for dark nucleons however predicts that the states of dark nucleon are in one-one correspondence with DNA, RNA, tRNA, and aminoacid molecules and that vertebrate genetic code is naturally realized. The question is whether the realization of the genetic code in terms of dark nucleon strings might provide the system with genetic code and whether the replication could take place at the level of dark nucleon strings rather than droplets. TGD inspired quantum model of biology leads to a model for oil droplets as a primitive life form. In particular, a proposal for how dark genes could couple to chemistry of oil droplets is developed.

10.9.1 Intelligent oil droplets

New Scientist tells about a new twist related to the Urey-Miller experiment. Martin Hanczyc and his colleagues of University of Southern Denmark in Odense are doing research with a rather ambitious goal: the discovery of the recipe of life. The highly demanding challenge is to find candidates for the protocell that preceded the recent cell. What makes the task so difficult that it is not even clear what one should be searching for. For instance, what basic characteristics distinguishing living matter from inanimate systems protocell is expected to have before one can speak about primitive life form? And if one accepts the dogmas of standard biology, one encounters also the nasty hen-egg question which came first: metabolism or the genetic machinery.

Hanczyc and his colleagues have been experimenting with simple candidates for primitive life forms: oily nitrobenzene [68] droplets doped with oleic anhydride [72] immersed in alkaline aqueous solution (alkalinity is by definition an ability to reduce acidicity). They have found that these systems have some attributes generally associated with life. The recent experiments replaced oleic anhydrite with the black tar consisting of complex branched and fractal looking hydrogen cyanide (HCN) polymer [41] produced by Urey-Miller experiments and found that also now the droplets exhibit lifelike behavior: they sense and respond their neighbors and move towards "food" sources.

The earlier experiments using nitrobenzene droplets doped with oleic anhydridge immersed in alkaline solution began immediately to move along straight lines. What happened that the oleic anhydride at the surface of the droplet reacted with the water splitting to two oleic acid molecules [71] by hydration. This dropped the surface tension of the droplet and by a kind of spontaneous symmetry breaking the reaction rate had maximum at some point of the droplet and a "hot spot" was generated drawing oleic anhydride from the interior of the droplet and generating a convective flow. A pH gradient develops along the surface. The oleic acid in turn moved along the droplet surface from the hot spot to

the diametrically opposite side of the droplet (http://pubs.acs.org/doi/abs/10.1021/ja806689p) [145]. The net effect was a linear motion. pH gradient is claimed to be essential for the generation of motion but I must admit that I do not quite understand this point. A primitive metabolism liberating energy is obviously in question. By momentum conservation the total momentum for the convective flow and flow of oleic acid was compensated by a center of mass motion of the droplet.

One could claim that this process belongs to the same class of self-organization processes as the generation of convection patterns as one heats liquid from below. Other researchers have however discovered that the oil droplets can also travel along chemical gradients, something known as chemotaxis used by many bacteria to find food and void threats. One oil droplet managed even to solve" a complex maze containing "food" at its other end [129]. Whether this kind of behavior can be regarded as a mere chemistry is far from obvious to me. To me this a achievement look like a genuinely goal directed intentional behavior.

Hanczyc has also found that when the oil droplets approach each other they change course to avoid collision, or can circle each other-like partners in Viennese waltz! Oil droplets seem to have even memory. By videoing the paths of oil droplets Hanczyc found that the decision to stop or continue was not random but the behavior at any point of orbits was affected by the earlier behavior. This is by the way an elegant experimental manner to show that non-deterministic behavior is not just randomness. The experiments have been also carried using instead of oleic anhydride mineral oil consisting of a mixture of alkanes having as building block polymers from from CH_4 by dropping two hydrogen from each C as also lipids have (methane CH_4 is the simplest alkane). What distinguishes mineral oil molecules from the oleic anhydride molecules are the oxygen atoms in the middle of the reflection symmetric linear molecule. Also now the droplets move although the process takes place with a slower rate.

The basic objections against the identification of the oil droplets as a life form is that they do not replicate and there is no genetic code. One must be however very cautious with this kind of statements. Maybe the primary life forms are not the droplets and the behavior of droplets reflects the control actions of these life forms on droplets. Perhaps also genetic code could be realized at at totally different level. The recent findings of the group of HIV Nobelist Montagnier [178] indeed suggest a new realization of genetic code in water closely related to to water memory and TGD suggests a concrete realization of this code [34].

10.9.2 Some key ideas of TGD inspired quantum biology

Before proposing a model for intelligent oil droplets as a primitive life form its good to list some of the basic ideas of TGD inspired quantum biology.,

1. The basic hypothesis is that the dark matter at the magnetic flux tubes of the magnetic body assignable to any physical system serves as an intentional agent controlling the behavior of the ordinary matter [22]. Dark matter can correspond to just the ordinary particles- at least electrons and protons- in a phase with non-standard large value of Planck constant forming macroscopic quantum phases. Also biologically important ions could form this kind of phases. TGD inspired nuclear physics [1] allows also the bosonic counterparts of fermionic with same nuclear charge so that every fermionic ion could be accompanied by exotic bosonic ion so that Bose-Einstein condensates could become possible.

2. The model for dark nucleons [1, 34] as entangled triplets of three quarks leads to the identification of the counterparts DNA, RNA, tRNA, and aminoacids as three-quark states and one can identify also vertebrate genetic code. DNA sequences correspond to dark nucleon sequences - dark nuclei - in this correspondence. The proposal is that dark proton sequences in water form dark nucleons with so large a Planck constant that nucleon size corresponds to size of singe DNA codon. There is indeed evidence that in attosecond time scale (time scale for corresponding causal diamonds) water obeys effective chemical formula $H_{1.5}O$ as far as scattering of electrons and neutrons is considered [6, 8, 23]. This would suggest that 1/4 of protons are in dark large Planck constant phase in the experimental situation. This proportion is expected to depend on temperature and pressure and should explain the rich spectrum of anomalies of water [7] by regarding it as a two phase system [24]. Perhaps these protons could form dark nucleon sequences realizing genetic code. These sequences could replicate and evolve and could define at least the analog of DNA or RNA. Maybe even DNA-mRNa-aminoacids translation processing

could take place. If a translation machinery transforming exotic DNA to ordinary has developed during evolution, this fundamental realization of genetic machinery might make possible kind of Research & Development making possible to experiment with different genomes. Evolution would not be a random process anymore [34].

3. The proposal is that the ordered water layers associated with polar molecules dissolved in water are attached to the magnetic body of the molecule induced in water environment and that this magnetic body mimicking ithe original molecule is an essential element of this primitive life [34]. The self-organization processes of these layers induced by external perturbations could be the predecessor of processes like protein folding and de-folding. The mechanism of water memory could be based on dropping of the magnetic bodies of molecules as a result of repeated shaking involved with homeopathic procedure inducing a sequence of catastrophes driving the evolution of these primitive life forms. One can also ask whether these magnetic bodies could define the analog of proteins providing one realization of dark matter genetic code.

4. If dark nucleons have been the predecessors of chemical life forms, one can circumvent the hen-egg question about whether the genetic code or metabolism came first. In zero energy ontology negative energy signals propagating in the direction of geometric past would in turn provide fundamental mechanism of intentional action, metabolism, and memory. If this is the case, evolution would have only led to a refinement of the fundamental mechanisms of life already existing: there would be no need to pull anything out of hat. The mechanisms for chemical storage and utilization of energy are needed and moving oil droplets would provide a primitive realization of these mechanisms.

5. The notion of negentropic entanglement makes sense if one accepts the role of p-adic number fields and the vision about life as something residing in the intersection of real and p-adic worlds [44]. Entanglement probabilities for negentropic entanglement must be rational or algebraic numbers in the algebraic extension of p-adic numbers involved and there is unique prime for which this entanglement entropy is maximally negative. Negentropic entanglement makes possible new kind of many particle states analogous to bound states but with negative binding energy. The reason is that negentropic entanglement is stable against state function reduction if Negentropy Maximization Principle determines its dynamics also in the case of negentropic entanglement. The proposal is that the mysterious high energy phosphate bond corresponds to negentropic entanglement and carries both metabolic energy and information [6]. In this framework ATP-ADP cycle has also information theoretic interpretation as a transfer of conscious information.

The model for DNA as topological quantum computer [26, 78] led among other things to an identification of magnetic flux tubes connecting bio-molecules as a basic building bricks of living matter.

1. Flux tubes are assumed to connect DNA nucleotides to lipids of the nuclear and cell membranes. Flux tubes could begin from =O in the double bonds R=O or from negatively charged oxygens. In the case of DNA R would correspond to the basic unit in phosphate deoxiribose backbone consisting of aromatic 5-cycle and PO_4 containing one =O and one O^- [29]. The lipid end would contain =O and -OH and the flux tube could end to either of these or possibly -OH ionized to $-O^-$ by a transformation of proton to dark proton.

2. The braiding of flux tubes makes topological quantum computation like processes possible [26]. The contractions and expansions of flux tubes induced by phase transitions changing the value of Planck constant would be a basic control mechanism allowing to understand how two biomolecules (say DNA and its conjugate) can find each other in the thick soup of organic molecules. The reconnections of the magnetic flux tubes would be second basic control mechanism and ATP $\rightarrow$ADP process [5] involving splitting of phosphate group and liberating metabolic energy and its reverse would represent standardized reconnection process and its reversal.

3. The flux tube ends would contain quark and antiquark (u,d and their antiquarks are involved) coding for the four DNA letters A,T,C,G so that also dark quarks and their antiquarks would provide an elementary particle level realization for the codons. Note that topological quantum

computation does not necessitate genetic code and therefore also the repeating DNA sequences regarded as junk could be used for topological quantum computations.

10.9.3 General ideas about oil droplets as a primitive life form

It is interesting to see what one obtains if one takes the dark nucleon realization of genetic code, the mechanism of water memory realized as magnetic bodies attached to the ordered water layers associated with polar molecules, the model for DNA as topological quantum computer, and the ideas about magnetic body with dark matter as fundamental bio-control as basic ingredients of the model of intelligent oil droplets.

1. The formation of hot spot on the oil droplet resembles spontaneous symmetry breaking. The interpretation as a generation of magnetic body of approximately dipolar magnetic field is attractive. The magnetic body would control the droplet. The change of the direction of the motion of the oil droplet would correspond to the change of the orientation of the magnetic body and would thus reduce to a motor action of the magnetic body.

2. The flux tubes of the magnetic body would be most naturally parallel to the direction of the nitrobenzene polymer strands. Oleic anhydride molecules and the hydrogen cyanid polymers would be transferred along the magnetic flux tubes of an approximately dipolar magnetic field entering to the hot spot from interior and the oleic acid molecules could move along the flux tubes continuing along the surface of the droplet to the diametrically opposite point. The migration of birds along magnetic field lines is a direct analogy for this.

3. The dark matter at the magnetic body would give the oil drop its "intelligence". The dark nuclear genome could be realized at the magnetic body and the magnetic bodies might define the replicating life form as in the TGD based model of water memory for which the magnetic bodies represent molecules as far as low frequency electromagnetic fields characterized by cyclotron frequencies are considered. One could see intelligent oil droplets as manifestation of control actions of a life form defined by dark matter at magnetic flux tubes and the first step in the process eventually leading to a complex control and coordination of the behavior of ordinary matter.

4. The ability of droplets to react to the presence of other droplets would be due to the communications between magnetic bodies based on low frequency photons at cyclotron frequencies but having energy above thermal energy if the value of Planck constant is large enough.

At least oleic anhydrite, hydrogen cyanide, and mineral oil can serve as a fuel of oil droplets and this raises the question what might be the common property shared by them. Certainly this property must relate to metabolism and the model for ordinary metabolism suggests that this property is shared also by the high energy phosphate bond.

1. Oleic anhydrite is a lipid formed by as a fusion of two oleic acids consisting of a sequence of CH_2 units and the characteristic (C=O)-(O-H) group at its end. The burning of the molecule splits it to two oleic acids by hydration meaning utilizing one water molecule. The formation of oleic acid in turn involves dehydration so that the burning process is analogous to depolymerization of DNA or aminoacid sequence by hydration.

2. Mineral oil is also a lipid and looks like oleic anhydride locally. In the ideal case however the crucial ..(C=O)-O-(C=O)-.. portions are lacking. Oxygenation could however produce this kind of defects to the mineral oil molecules so that the mechanism of burning would remain the same.

3. Hydrogen cyanide HCN involves valence bond of valence 3 between C and N. The polymers are constructed from H-C-N sequences with single valence bond between both C:s and N:s of two subsequent horizontal H-C-N units, which one can think of as being obtained from (H-C)-(H-C)... sequence and ..N-N-N... sequences with each N and C connected by horizontal valence bond. This polymer replaces oleic acid as a "fuel" reacting with water and liberating metabolic energy. These polymers - which would serve as primitive analogs of proteins- would be transferred along the magnetic flux tubes and burned at the hot spot by hydration. HCN has

been proposed to have been a primitive precursor of both amino acids and nuclei acids. With motivations coming from the general vision about quantum biology, it will be proposed that also hydrogen cyanide polymers contain in their C-backbone ..(C=O)-O-(C=O)-.. portions as local defects due to oxygenation so that the burning would occur via hydration in all three cases.

10.9.4 What are the prerequisites for metabolism and topological quantum computation like processes?

The basic question is whether metabolism interpreted in TGD framework as negentropy transfer and thus requiring the analogs of high energy phosphate bond and ATP-ADP cycle is possible. The high energy phosphate bonds make also possible flux tube structures serving as a prerequisite for topological quantum computation like process. Both oleic anhydride, hydrogen cyanide and mineral oil can serve as a metabolic source and one should identify the common property of them making. This property should be the analog of high energy phosphate bond.

1. High energy phosphate bond carries metabolic energy. This bond is poorly understood and I have proposed that high energy phosphate bond carries negentropic entanglement which identified in TGD framework as the basic characteristic of life [44]. In the middle of oleic anhydride there (C=O)-O-(C=O) structure and its splitting in hydration liberates energy. This suggests that this structure also now carries the negentropic entanglement and the metabolic energy. The splitting process of oleic anhydrite occurring at the hotspot would be analogous to ATP→ADP process involving splitting of PO_4 molecule from ATP.

2. Oleic acid is a lipid containing at its second end the characteristic (C=O)-OH group assumed to serve as a terminal for the magnetic flux tubes in the model of DNA-cell membrane system as quantum computer. In the presence energy feed one could imagine that the inverse process transforming oleic acid to oleic anhydride takes place and a primitive version of the metabolic cycle involving photosynthesis and cellular breathing can be imagined. Metabolic and quantum information processing would be very intimately related. By DNA as topological quantum computer analogy the magnetic flux tubes connecting oleic anhydride molecules would make be responsible for primitive topological quantum computation if present in the system.

3. Also when the tar from Urey-Miller experiment replaces oleic anhydrite small amount of oleic anhydride was used to build a film around oil droplet to lower surface tension. This suggests that the oleic anhydride has a deeper purpose and defines the analog of cell membrane and make possible for the magnetic flux tubes from the interior of the droplet to attach to the lipids? This could occur at least in the hot spot and at point opposite to it so that magnetic flux tubes would connect the diametrically opposite points of the droplet Oleic anhydride would therefore serve a dual purpose serving both as a metabolic resource and a building brick of the protocell membrane: metabolic energy would be accompanied by information. Also in real life lipids -about which fats are a special case- have this double role.

4. The process occurs also both for hydrogen cyanide and mineral oil and and this raises obvious objections since the energy and information carrying (C=O)-O-(C=O) structures making also possible the flux tube connects are not present in the ideal situation. One must however remember that the situation in real life is far from ideal and the most obvious idea is that the polymers as such are not enough: oxygen is the basic metabolic resource and oxygenation serving as the loading of metabolic batteries might be the crucial element.

   (a) The backbone of both oleic acid, oleic anhydride, and of mineral oil polymers is CH_2 sequence common to all lipids. If some fraction of mineral oil polymers contain (C=O)-O -(C=O):s serving as carriers of metabolic energy and information the situation reduces to that for oleic anhydride apart from effects caused by the fact that the density of metabolic energy per volume is expected to be lower, which would explain why the motion is slower.

   (b) Also in the case of hydrogen cyanide polymers one can imagine the presence of similar defect structures due to oxygenation. A portion of ...(H-C)-(H-C)-(H-C).... sequence would be replaced with ....(H-C)-(C=O)-O-(C=O)-(H-C)... with three carbons lacking. The nitrogen sequence ...N-N-N-N-N.. would split to ...N-OH and OH-N... so that three nitrogens would be lacking. The total number of hydrogens would remain the same.

Under these assumptions the model explains all three cases using hydration as the basic mechanism of metabolism as well as the conditions required by DNA as topological quantum computer model. Note that the process consumes oxygen just as the ordinary breathing.

10.9.5 What about genetic code and counterpart of DNA?

Consider next the possible realization of the genetic code. The first thing to notice is that even in the case that genetic code is not realized the braiding would make possible topological quantum computation like processes and a realization of memory in terms of braiding patterns. Furthermore, chemical realization of the genetric code is not possible so that dark nucleons remain the only possibility in TGD framework. The challenge is to try imagine whether DNA like structures having flux tube connections with the counterparts of lipids in the cell membrane could exist. The following suggestion is a product of free imagination based on analogies and reflects my amateurish skills in biochemistry.

1. Aromatic rings [7] are an essential element of both phosphate deoxiribose backbone of DNA and of DNA letters itself. Nitrobenzene molecule obeys chemical formula (C_6H-5)-NO_2 and contains benzene ring to which NO_2 nitro group is attached. The oily character is due to the benzene ring. Benzene rings could serve as a counterpart for the hydrocarbon 5-cycles appearing in phosphate deoxiribose backbone. Note however that in deoxiribose ring one carbon is replaced with O and two hydrogens with OH. Moreover, single benzene molecule would correspond to the counterpart of DNA triplet rather than single nucleoside. One could however argue that only a backbone is in question so that the differences might not matter.

2. One would naively expect that both nitrogen and phosphorus have same valence equal to three. In PO_4 phosporus has 5 valence bonds as a rule and the interpretation is that phosphorus tends to donate its valence electrons to get empty shell. This kind of states are known as oxidation states and are possible also for nitrogen: hydroxylamine NO_2H is one example of this kind of state. In fact, from the from structural formula of nitrobenzene (see Fig. 10.3) one finds that nitrogen gives one electron to second oxygen so that also this state can be regarded as an oxidation state. This inspires the idea that nitrogen takes the role of phosphorus at least partially.

3. If one does not allow oxidation states, the simplest manner to construct the analog of phosphate deoxiribose backbone is as structure ...X-X-X..., with X= R-O- (R_1-N)-O, where R denotes oleic anhydride and R_1 is for benzene residue. The bridges connecting benzene rings would be reflection symmetric. The breaking of reflection symmetry is however essential since it determines the reading direction of DNA.

4. If one accepts oxidation states, the simplest option is that in benzene-NO_2 complex NO_2 is replaced with (N=0)-O and the counterpart of phosphate deoxiribose backbone would have the structure ...X-X-X—, X=R- (R_1-N=0)-O with R denoting oleic anhydride and R_1 benzene. Oleic anhydride has valence bond to N so that N has 5 valence bonds as phosphorus in phosphate. Also the crucial =O is present. The units connecting subsequent benzene rings are not reflection symmetric anymore as indeed required. There is however no charged oxygen as in the case of ordinary DNA. Note that the analogs for AMP, ADP, ATP make sense since one can single replace P by N phosphate PO_4.

5. An interesting question is whether the nitrogen based metabolism could be realized as a primordial metabolism. Nitroglycerin is analogous to tri-phosphate although the nitrates are not arrranged linearly as in ATP and is used as both heart medicine and as an active incredient of explosives. The latter use conforms with the idea about the presence of high energy nitrate bond in NO_4.

6. The two mirror image branches of oleic anhydride molecule consist of 15 carbon atoms and the structure is rather long as compared to the basic unit of phosphate deoxiribose backbone so that the distance between subsequent benzene units would be rather long- of order 10 Angstroms. On the other hand, 10 DNA codons correspond to 10 nm length in a good accuracy so that one codon would take 1 nm length also in this case. If double strand is formed, twisting is possible so that the scales could be the same. The size scale of the dark nucleon representing single DNA

codon should correspond to the size scale of single oleic anhydride molecule and the required value of Planck constant would be of order 10^6 as the ratio of this scale and nucleon size of order 10^{-15} meters.

7. The counterparts of DNA nucleotides forming a linear structure should join to the benzene rings. Dark nucleon sequences remain the only possibility if one wants a realization of genetic code. Each dark codon represented by dark nucleon would be connected by three flux tubes with quark and antiquark at their ends to single unit of the proposed structure. There would be three =O:s per single benzene ring. Since single benzene ring corresponds to single DNA codon three =O:s are indeed expected. Therefore =O:s could indeed correspond to terminals for flux tubes coming from single dark nucleon representing single DNA codon.

8. The division of oil droplet would be the analog of cell replication and would involve at the deeper level the replication of dark nucleon sequences. This requires the analog of DNA double strand and the analogs of DNA codons would be dark nucleons. Genetic codons could be realized in terms of flux tubes connecting dark nucleon sequences to the oleic acids or oleic anhydrides at the surface of the droplet. It remains to be seen whether the division can be achieve in real world.

To sum up, the proposed model is rather direct application of TGD based vision about life and the killer test is whether the mineral oil oil molecules and hydrogen cyanide molecules are not ideal but actually contain the (C=O)-O-(C= O) pieces carrying energy and information and serve as terminals for the magnetic flux tubes.

10.9.6 Another approach to protocell

Also the group led by Jack. W. Szostak, who was the 2009 Nobel Prize winner in physiology or medicine - has carried out beautiful experiments in which they are able to create a candidate for protocell satisfying many of the basic requirements [139].

One such condition is the ability of protocell to transfer various nutrient molecules through the protocell membrane. In modern cell pumps and channels consisting of proteins are believed to serve that purpose (for a different view see the remark below). Genetically coded proteins were however absent during the primordial era. Therefore the membrane is constructed of branching lipids believed to exists during prebiotic era allowing sugars which are basic building bricks of DNA to permeate to the protocell. Given the DNA template , the basic building bricks of DNA molecule assemble to a copy of DNA in this protocell.

What is still lacking is the generation of the template strand of DNA itself and also the replication of protocell. If dark DNA in the form of dark nucleon strings is really there, the template could result as the assembly of the basic bricks of DNA around it and above a proposal for the analog of this kind of process is suggested. The replication of the dark genes would have been also present from the beginning and would have preceded the replication of genes and protocell. Biological evolution could be seen as a migration from dark space-time sheets to ordinary ones and somewhat analogous to the migration of life from sea to land.

Remark: There are puzzling experimental findings about quantal currents through cell membrane even in absence of metabolic sources. In many-sheeted space-time [57] one could interpret these currents as various kinds of Josephson currents running between cell interior and exterior along current carrying space-time shees. Pumps and channels would be more like a diagnostic tool allowing cell to measure the concentrations of various important biomolecules and ions.

At first sight the approaches of Szostak and Martin Hanczyc look very different. These approaches have however a lot of common at deeper level if one accepts TGD based view as DNA-cell membrane system or its more primitive version as a topological quantum computer like system relying on the braiding of magnetic flux tubes connecting the counterpart of DNA nucleotides to the lipids of protocell membrane and on the prebiotic realization of genetic code at the level of dark nuclear physics.

One could also argue that the protocell of Hanczyk represents oil based life as opposed to life as we know it. In TGD framework this is a mis-interpretation. The protocells of Hanczyk live in an aqueous environment. Nitrobenzene oil is an aromatic compound as also sugars and contains nitrogen taking in the proposed scenario same role as phosphorus in ordinary life. Oleic anhydride is lipid and- would provide basic building brick for a particular variant of DNA like structure half-way between dark and

completely chemical realization. Oleic anhydride would provide also the building bricks of protocell membrane and serve as a nutrient just like fat molecules- also lipids- serve in "real life".

10.10 Figures

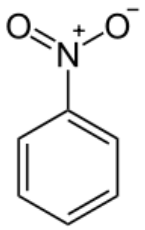

Figure 10.3: Nitrobenzene

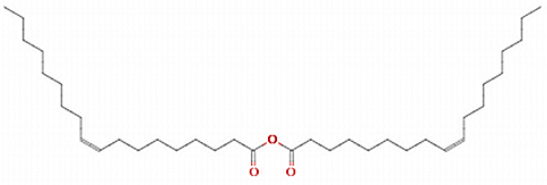

Figure 10.4: Oleic anhydride

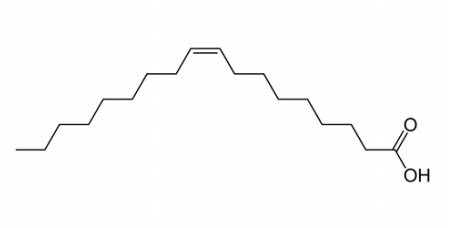

Figure 10.5: Oleic acid

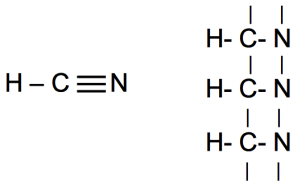

Figure 10.6: Hydrogen cyanide and hydrogen cyanide polymer.

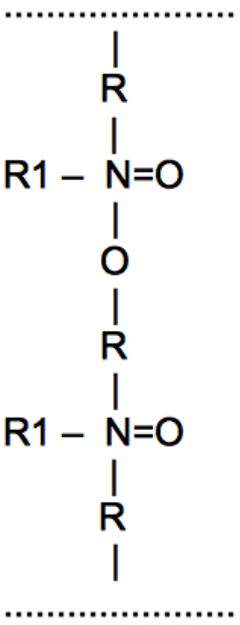

Figure 10.7: The analog of the deoxiribose phosphate backbone. R denotes oleic anhydride containing two =O:s and R1 benzene ring.

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Chapter 11

Expanding Earth Model and Pre-Cambrian Evolution of Continents, Climate, and Life

11.1 Introduction

TGD inspired quantum cosmology [66, 65] predicts that astrophysical objects do not follow cosmic expansion except in jerk-wise quantum leaps increasing the gigantic value of the gravitational Planck constant characterizing space-time mediating gravitational interactions between two masses or gravitational self interactions. This assumption provides explanation for the apparent cosmological constant.

Also planets are predicted to expand in a stepwise manner. This provides a new version of Expanding Earth theory originally postulated to explain the intriguing findings suggesting that continents have once formed a connected continent covering almost the entire surface of Earth but with radius which was one half of the recent one [65] .

This leads also to a rather fascinating vision about biology. The mysterious Cambrian Explosion [14] in which a large number of new species emerged suddenly (realized already Darwin as the strongest objection against his theory) could be understood if the life would have gone to underground lakes and seas formed during the expansion period as fractures were formed and the underground cavities expanded and were filled with water. This would have allowed the life to escape cosmic radiation, meteoric bombardment, and the extremely cold climate during Proterozoic period preceding the Cambrian Explosion and migrate back as highly developed life forms as the period of glaciations ended.

Before the Proterozoic era the radius of Earth would have been one half of its recent value and started to grow with gradually accelerating rate. This forces to rewrite the entire geological and climate history of Earth during the Proterozoic period.

1. The postulated physically implausible cyclic appearance of single connected super-continent containing all land mass can be given up and replaced with a single continent containing large inland seas. There is no need to postulate the existence of series of super-oceans whose ocean floor would have subduced totally so that no direct information about them would exist nowadays.

2. The dominating model for pre-Cambrian climate is so called Snowball Earth model [29] inspired by the finding that signatures of glaciations have been found at regions of Earth, which should have been near Equator during the Proterozoic. Snowball model has several difficulties: in particular, there is a lot of evidence that a series of ordinary glaciations was in question. For $R/2$ option the regions located to Equator would have actually been near North Pole so that the glaciations would have indeed been ordinary glaciations proceeding from the poles. A killer prediction is the existence of non-glaciated regions at apparent southern latitudes around about 45 degrees and there is evidence for these indeed exists [39] ! The model makes also testable paleomagnetic killer predictions. In particular, during periods when the magnetic dipole in the direction of rotation axis the directions of the magnetic fields for $R/2$ model are predicted to be same at South Pole and apparent Equator and opposite for the standard option.

11.2 Experimental evidence for accelerated expansion is consistent with TGD based model

There are several pieces of evidence for accelerated expansion, which need not mean cosmological constant, although this is the interpretation adopted in [4] . It is interesting to see whether this evidence is indeed consistent with TGD based interpretation.

11.2.1 The four pieces of evidence for accelerated expansion

Supernovas of type Ia

Supernovas of type Ia define standard candles since their luminosity varies in an oscillatory manner and the period is proportional to the luminosity. The period gives luminosity and from this the distance can be deduced by using Hubble's law: $d = cz/H_0$, H_0 Hubble's constant. The observation was that the farther the supernova was the more dimmer it was as it should have been. In other words, Hubble's constant increased with distance and the cosmic expansion was accelerating rather than decelerating as predicted by the standard matter dominated and radiation dominated cosmologies.

Mass density is critical and 3-space is flat

It is known that the contribution of ordinary and dark matter explaining the constant velocity of distance stars rotating around galaxy is about 25 per cent from the critical density. Could it be that total mass density is critical?

From the anisotropy of cosmic microwave background one can deduce that this is the case. What criticality means geometrically is that 3-space defined as surface with constant value of cosmic time is flat. This reflects in the spectrum of microwave radiation. The spots representing small anisotropies in the microwave background temperature is 1 degree and this correspond to flat 3-space. If one had dark matter instead of dark energy the size of spot would be .5 degrees!

Thus in a cosmology based on general relativity cosmological constant remains the only viable option. The situation is different in TGD based quantum cosmology based on sub-manifold gravity and hierarchy of gravitational Planck constants.

The energy density of vacuum is constant in the size scale of big voids

It was observed that the density of dark energy would be constant in the scale of 10^8 light years. This length scale corresponds to the size of big voids containing galaxies at their boundaries.

Integrated Sachs-Wolf effect

Also so called integrated Integrated Sachs-Wolf effect supports accelerated expansion. Very slow variations of mass density are considered. These correspond to gravitational potentials. Cosmic expansion tends to flatten them but mass accretion to form structures compensates this effect so that gravitational potentials are unaffected and there is no effect of CMB. Situation changes if dark matter is replaced with dark energy the accelerated expansion flattening the gravitational potentials wins the tendency of mass accretion to make them deeper. Hence if photon passes by an over-dense region, it receives a little energy. Similarly, photon loses energy when passing by an under-dense region. This effect has been observed.

11.2.2 Comparison with TGD

The minimum TGD based explanation for accelerated expansion involves only the fact that the imbeddings of critical cosmologies correspond to accelerated expansion. A more detailed model allows to understand why the critical cosmology appears during some periods.

Accelerated expansion in classical TGD

The first observation is that critical cosmologies (flat 3-space) imbeddable to 8-D imbedding space H correspond to negative pressure cosmologies and thus to accelerating expansion. The negativity

of the counterpart of pressure in Einstein tensor is due to the fact that space-time sheet is forced to be a 4-D surface in 8-D imbedding space. This condition is analogous to a force forcing a particle at the surface of 2-sphere and gives rise to what could be called constraint force. Gravitation in TGD is sub-manifold gravitation whereas in GRT it is manifold gravitation. This would be minimum interpretation involving no assumptions about what mechanism gives rise to the critical periods.

Accelerated expansion and hierarchy of Planck constants

One can go one step further and introduce the hierarchy of Planck constants. The basic difference between TGD and GRT based cosmologies is that TGD cosmology is quantum cosmology. Smooth cosmic expansion is replaced by an expansion occurring in discrete jerks corresponding to the increase of gravitational Planck constant. At space-time level this means the replacement of 8-D imbedding space H with a book like structure containing almost-copies of H with various values of Planck constant as pages glued together along critical manifold through which space-time sheet can leak between sectors with different values of $\hbar$. This process is the geometric correlate for the the phase transition changing the value of Planck constant.

During these phase transition periods critical cosmology applies and predicts automatically accelerated expansion. Neither genuine negative pressure due to "quintessence" nor cosmological constant is needed. Note that quantum criticality replaces inflationary cosmology and predicts a unique cosmology apart from single parameter. Criticality also explains the fluctuations in microwave temperature as long range fluctuations characterizing criticality.

Accelerated expansion and flatness of 3-cosmology

Observations 1) and 2) about super-novae and critical cosmology (flat 3-space) are consistent with this cosmology. In TGD dark energy must be replaced with dark matter because the mass density is critical during the phase transition. This does not lead to wrong sized spots since it is the increase of Planck constant which induces the accelerated expansion understandable also as a constraint force due to imbedding to H.

The size of large voids is the characteristic scale

The TGD based model in its simplest form model assigns the critical periods of expansion to large voids of size 10^8 ly. Also larger and smaller regions can express similar periods and dark space-time sheets are expected to obey same universal "cosmology" apart from a parameter characterizing the duration of the phase transition. Observation 3) that just this length scale defines the scale below which dark energy density is constant is consistent with TGD based model.

The basic prediction is jerkwise cosmic expansion with jerks analogous to quantum transitions between states of atom increasing the size of atom. The discovery of large voids with size of order 10^8 ly but age much longer than the age of galactic large voids conforms with this prediction. One the other hand, it is known that the size of galactic clusters has not remained constant in very long time scale so that jerkwise expansion indeed seems to occur.

Do cosmic strings with negative gravitational mass cause the phase transition inducing accelerated expansion

Quantum classical correspondence is the basic principle of quantum TGD and suggest that the effective antigravity manifested by accelerated expansion might have some kind of concrete space-time correlate. A possible correlate is super heavy cosmic string like objects at the center of large voids which have negative gravitational mass under very general assumptions. The repulsive gravitational force created by these objects would drive galaxies to the boundaries of large voids. At some state the pressure of galaxies would become too strong and induce a quantum phase transition forcing the increase of gravitational Planck constant and expansion of the void taking place much faster than the outward drift of the galaxies. This process would repeat itself. In the average sense the cosmic expansion would not be accelerating.

11.3 Quantum version of Expanding Earth theory

TGD predicts that cosmic expansion at the level of individual astrophysical systems does not take place continuously as in classical gravitation but through discrete quantum phase transitions increasing gravitational Planck constant and thus various quantum length and time scales. The reason would be that stationary quantum states for dark matter in astrophysical length scales cannot expand. One would have the analog of atomic physics in cosmic scales. Increases of $\hbar$ by a power of two are favored in these transitions but also other scalings are possible.

This has quite far reaching implications.

1. These periods have a highly unique description in terms of a critical cosmology for the expanding space-time sheet. The expansion is accelerating. The accelerating cosmic expansion can be assigned to this kind of phase transition in some length scale (TGD Universe is fractal). There is no need to introduce cosmological constant and dark energy would be actually dark matter.

2. The recently observed void which has same size of about 10^8 light years as large voids having galaxies near their boundaries but having an age which is much higher than that of the large voids, would represent one example of jerk-wise expansion.

3. This picture applies also to solar system and planets might be perhaps seen as having once been parts of a more or less connected system, the primordial Sun. The Bohr orbits for inner and outer planets correspond to gravitational Planck constant which is 5 times larger for outer planets. This suggests that the space-time sheet of outer planets has suffered a phase transition increasing the size scale by a factor of 5. Earth can be regarded either as n=1 orbit for Planck constant associated with outer planets or n= 5 orbit for inner planetary system. This might have something to do with the very special position of Earth in planetary system. One could even consider the possibility that both orbits are present as dark matter structures. The phase transition would also explain why n=1 and n=2 Bohr orbits are absent and one only n=3,4, and 5 are present.

4. Also planets should have experienced this kind of phase transitions increasing the radius: the increase by a factor two would be the simplest situation.

The obvious question - that I did not ask - is whether this kind of phase transition might have occurred for Earth and led from a completely granite covered Earth - Pangeia without seas - to the recent Earth. Neither it did not occur to me to check whether there is any support for a rapid expansion of Earth during some period of its history.

Situation changed when my son visited me and told me about a Youtube video [36] by Neal Adams, an American comic book and commercial artist who has also produced animations for geologists. We looked the amazing video a couple of times and I looked it again yesterday. The video is very impressive artwork but in the lack of references skeptic probably cannot avoid the feeling that Neal Adams might use his highly developed animation skills to cheat you. I found also a polemic article [1] of Adams but again the references were lacking. Perhaps the reason of polemic tone was that the concrete animation models make the expanding Earth hypothesis very convincing but geologists refuse to consider seriously arguments by a layman without a formal academic background.

11.3.1 The claims of Adams

The basic claims of Adams were following.

1. The radius of Earth has increased during last 185 million years (dinosaurs [28] appeared for about 230 million years ago) by about factor 2. If this is assumed all continents have formed at that time a single super-continent, Pangeia, filling the entire Earth surface rather than only 1/4 of it since the total area would have grown by a factor of 4. The basic argument was that it is very difficult to imagine Earth with 1/4 of surface containing granite and 3/4 covered by basalt. If the initial situation was covering by mere granite -as would look natural- it is very difficult for a believer in thermodynamics to imagine how the granite would have gathered to a single connected continent.

2. Adams claims that Earth has grown by keeping its density constant, rather than expanded, so that the mass of Earth has grown linearly with radius. Gravitational acceleration would have thus doubled and could provide a partial explanation for the disappearance of dinosaurs: it is difficult to cope in evolving environment when you get slower all the time.

3. Most of the sea floor is very young and the areas covered by the youngest basalt are the largest ones. This Adams interprets this by saying that the expansion of Earth is accelerating. The alternative interpretation is that the flow rate of the magma slows down as it recedes from the ridge where it erupts. The upper bound of 185 million years for the age of sea floor requires that the expansion period - if it is already over - lasted about 185 million years after which the flow increasing the area of the sea floor transformed to a convective flow with subduction so that the area is not increasing anymore.

4. The fact that the continents fit together - not only at the Atlantic side - but also at the Pacific side gives strong support for the idea that the entire planet was once covered by the super-continent. After the emergence of subduction theory this evidence as been dismissed.

5. I am not sure whether Adams mentions the following objections [6] . Subduction only occurs on the other side of the subduction zone so that the other side should show evidence of being much older in the case that oceanic subduction zones are in question. This is definitely not the case. This is explained in plate tectonics as a change of the subduction direction. My explanation would be that by the symmetry of the situation both oceanic plates bend down so that this would represent new type of boundary not assumed in the tectonic plate theory.

6. As a master visualizer Adams notices that Africa and South-America do not actually fit together in absence of expansion unless one assumes that these continents have suffered a deformation. Continents are not easily deformable stuff. The assumption of expansion implies a perfect fit of *all* continents without deformation.

Knowing that the devil is in the details, I must admit that these arguments look rather convincing to me and what I learned from Wikipedia articles supports this picture.

11.3.2 The critic of Adams of the subduction mechanism

The prevailing tectonic plate theory [24] has been compared to the Copernican revolution in geology. The theory explains the young age of the seafloor in terms of the decomposition of the litosphere to tectonic plates and the convective flow of magma to which oceanic tectonic plates participate. The magma emerges from the crests of the mid ocean ridges representing a boundary of two plates and leads to the expansion of sea floor. The variations of the polarity of Earth's magnetic field coded in sea floor provide a strong support for the hypothesis that magma emerges from the crests.

The flow back to would take place at so called oceanic trenches [17] near continents which represent the deepest parts of ocean. This process is known as subduction. In subduction oceanic tectonic plate bends and penetrates below the continental tectonic plate, the material in the oceanic plate gets denser and sinks into the magma. In this manner the oceanic tectonic plate suffers a metamorphosis returning back to the magma: everything which comes from Earth's interior returns back. Subduction mechanism explains elegantly formation of mountains [18] (orogeny), earth quake zones, and associated zones of volcanic activity [34] .

Adams is very polemic about the notion of subduction, in particular about the assumption that it generates steady convective cycle. The basic objections of Adams against subduction are following.

1. There are not enough subduction zones to allow a steady situation. According to Adams, the situation resembles that for a flow in a tube which becomes narrower. In a steady situation the flow should accelerate as it approaches subduction zones rather than slow down. Subduction zones should be surrounded by large areas of sea floor with constant age. Just the opposite is suggested by the fact that the youngest portion of sea-floor near the ridges is largest. The presence of zones at which both ocean plates bend down could improve the situation. Also jamming of the flow could occur so that the thickness of oceanic plate increases with the distance from the eruption ridge. Jamming could increase also the density of the oceanic plate and thus the effectiveness of subduction.

2. There is no clear evidence that subduction has occurred at other planets. The usual defense is that the presence of sea is essential for the subduction mechanism.

3. One can also wonder what is the mechanism that led to the formation of single super continent Pangeia covering 1/4 of Earth's surface. How probable the gathering of all separate continents to form single cluster is? The later events would suggest that just the opposite should have occurred from the beginning.

11.3.3 Expanding Earth theories are not new

After I had decided to check the claims of Adams, the first thing that I learned is that Expanding Earth theory [6] , whose existence Adams actually mentions, is by no means new. There are actually many of them.

The general reason why these theories were rejected by the main stream community was the absence of a convincing physical mechanism of expansion or of growth in which the density of Earth remains constant.

1. 1888 Yarkovski postulated some sort of aether absorbed by Earth and transforming to chemical elements (TGD version of aether could be dark matter). 1909 Mantovani postulated thermal expansion but no growth of the Earth's mass [26] .

2. Paul Dirac's idea about changing Planck constant led Pascual Jordan in 1964 to a modification of general relativity predicting slow expansion of planets. The recent measurement of the gravitational constant imply that the upper bound for the relative change of gravitational constant is 10 time too small to produce large enough rate of expansion. Also many other theories have been proposed but they are in general conflict with modern physics.

3. The most modern version of Expanding Earth theory is by Australian geologist Samuel W. Carey. He calculated that in Cambrian period (about 500 million years ago) all continents were stuck together and covered the entire Earth. Deep seas began to evolve then.

11.3.4 Summary of TGD based theory of Expanding Earth

TGD based model differs from the tectonic plate model but allows subduction which cannot imply considerable back-flow of magma. Let us sum up the basic assumptions and implications.

1. The expansion is or was due to a quantum phase transition increasing the value of gravitational Planck constant and forced by the cosmic expansion in the average sense.

2. Tectonic plates do not participate to the expansion and therefore new plate must be formed and the flow of magma from the crests of mid ocean ridges is needed. The decomposition of a single plate covering the entire planet to plates to create the mid ocean ridges is necessary for the generation of new tectonic plate. The decomposition into tectonic plates is thus prediction rather than assumption.

3. The expansion forced the decomposition of Pangeia super-continent covering entire Earth for about 530 million years ago to split into tectonic plates which began to recede as new non-expanding tectonic plate was generated at the ridges creating expanding sea floor. The initiation of the phase transition generated formation of deep seas.

4. The eruption of plasma from the crests of ocean ridges generated oceanic tectonic plates which did not participate to the expansion by density reduction but by growing in size. This led to a reduction of density in the interior of the Earth roughly by a factor 1/8. From the upper bound for the age of the seafloor one can conclude that the period lasted for about 185 million years after which it transformed to convective flow in which the material returned back to the Earth interior. Subduction at continent-ocean floor boundaries and downwards double bending of tectonic plates at the boundaries between two ocean floors were the mechanisms. Thus tectonic plate theory would be more or less the correct description for the recent situation.

5. One can consider the possibility that the subducted tectonic plate does not transform to magma but is fused to the tectonic layer below continent so that it grows to an iceberg like structure. This need not lead to a loss of the successful predictions of plate tectonics explaining the generation of mountains, earthquake zones, zones of volcanic activity, etc...

6. From the video of Adams it becomes clear that the tectonic flow is East-West asymmetric in the sense that the western side is more irregular at large distances from the ocean ridge at the western side. If the magma rotates with slightly lower velocity than the surface of Earth (like liquid in a rotating vessel), the erupting magma would rotate slightly slower than the tectonic plate and asymmetry would be generated.

7. If the planet has not experienced a phase transition increasing the value of Planck constant, there is no need for the decomposition to tectonic plates and one can understand why there is no clear evidence for tectonic plates and subduction in other planets. The conductive flow of magma could occur below this plate and remain invisible.

The biological implications might provide a possibility to test the hypothesis.

1. Great steps of progress in biological evolution are associated with catastrophic geological events generating new evolutionary pressures forcing new solutions to cope in the new situation. Cambrian explosion indeed occurred about 530 years ago (the book "Wonderful Life" of Stephen Gould [161] explains this revolution in detail) and led to the emergence of multicellular creatures, and generated huge number of new life forms living in seas. Later most of them suffered extinction: large number of phylae and groups emerged which are not present nowadays.

   Thus Cambrian explosion is completely exceptional as compared to all other dramatic events in the evolution in the sense that it created something totally new rather than only making more complex something which already existed. Gould also emphasizes the failure to identify any great change in the environment as a fundamental puzzle of Cambrian explosion. Cambrian explosion is also regarded in many quantum theories of consciousness (including TGD) as a revolution in the evolution of consciousness: for instance, micro-tubuli emerged at this time. The periods of expansion might be necessary for the emergence of multicellular life forms on planets and the fact that they unavoidably occur sooner or later suggests that also life develops unavoidably.

2. TGD predicts a decrease of the surface gravity by a factor 1/4 during this period. The reduction of the surface gravity would have naturally led to the emergence of dinosaurs 230 million years ago as a response coming 45 million years after the accelerated expansion ceased. Other reasons led then to the decline and eventual catastrophic disappearance of the dinosaurs. The reduction of gravity might have had some gradually increasing effects on the shape of organisms also at microscopic level and manifest itself in the evolution of genome during expansion period.

3. A possibly testable prediction following from angular momentum conservation ($\omega R^2 = constant$) is that the duration of day has increased gradually and was four times shorter during the Cambrian era. For instance, genetically coded bio-clocks of simple organisms during the expansion period could have followed the increase of the length of day with certain lag or failed to follow it completely. The simplest known circadian clock is that of the prokaryotic cyanobacteria. Recent research has demonstrated that the circadian clock of Synechococcus elongatus can be reconstituted in vitro with just the three proteins of their central oscillator. This clock has been shown to sustain a 22 hour rhythm over several days upon the addition of ATP: the rhythm is indeed faster than the circadian rhythm. For humans the average innate circadian rhythm is however 24 hours 11 minutes and thus conforms with the fact that human genome has evolved much later than the expansion ceased.

4. Scientists have found a fossil of a sea scorpion with size of 2.5 meters [200] , which has lived for about 10 million years for 400 million years ago in Germany. The gigantic size would conform nicely with the much smaller value of surface gravity at that time. The finding would conform nicely with the much smaller value of surface gravity at that time. Also the emergence of trees could be understood in terms of a gradual growth of the maximum plant size as the surface gravity was reduced. The fact that the oldest known tree fossil is 385 million years old [189] conforms with this picture.

11.3.5 Did intra-terrestrial life burst to the surface of Earth during Cambrian expansion?

Intra-terrestrial hypothesis [29] is one of the craziest TGD inspired ideas about the evolution of life and it is quite possible that in its strongest form the hypothesis is unrealistic. One can however try to find what one obtains from the combination of the IT hypothesis with the idea of pre-Cambrian granite Earth. Could the harsh pre-Cambrian conditions have allowed only intra-terrestrial multicellular life? Could the Cambrian explosion correspond to the moment of birth for this life in the very concrete sense that the magma flow brought it into the day-light?

1. Gould emphasizes the mysterious fact that very many life forms of Cambrian explosion looked like final products of a long evolutionary process. Could the eruption of magma from the Earth interior have induced a burst of intra-terrestrial life forms to the Earth's surface? This might make sense: the life forms living at the bottom of sea do not need direct solar light so that they could have had intra-terrestrial origin. It is quite possible that Earth's mantle contained low temperature water pockets, where the complex life forms might have evolved in an environment shielded from meteoric bombardment and UV radiation.

2. Sea water is salty. It is often claimed that the average salt concentration inside cell is that of the primordial sea: I do not know whether this claim can be really justified. If the claim is true, the cellular salt concentration should reflect the salt concentration of the water inside the pockets. The water inside water pockets could have been salty due to the diffusion of the salt from ground but need not have been same as that for the ocean water (higher than for cell interior and for obvious reasons). Indeed, the water in the underground reservoirs in arid regions such as Sahara is salty, which is the reason for why agriculture is absent in these regions. Note also that the cells of marine invertebrates are osmoconformers able to cope with the changing salinity of the environment so that the Cambrian revolutionaries could have survived the change in the salt concentration of environment.

3. What applies to Earth should apply also to other similar planets and Mars [2] is very similar to Earth. The radius is .533 times that for Earth so that after quantum leap doubling the radius and thus Schumann frequency scale (7.8 Hz would be the lowest Schumann frequency) would be essentially same as for Earth now. Mass is .131 times that for Earth so that surface gravity would be .532 of that for Earth now and would be reduced to .131 meaning quite big dinosaurs! have learned that Mars probably contains large water reservoirs in it's interior and that there is an un-identified source of methane gas usually assigned with the presence of life. Could it be that Mother Mars is pregnant and just waiting for the great quantum leap when it starts to expand and gives rise to a birth of multicellular life forms. Or expressing freely how Bible describes the moment of birth: in the beginning there was only darkness and water and then God saidLet the light come!

To sum up, TGD would not only provide the long sought mechanism of expansion of Earth but also a possible connection with the biological evolution. It would be indeed fascinating if Planck constant changing quantum phase transitions in planetary scale would have profoundly affected the biosphere.

11.4 Implications of Expanding Earth model for the pre-Cambrian evolution of continents, of climate, and of life

Expanding Earth hypothesis is by no means not new. It was proposed by Mantovani and I learned about it from the video animations of [36, 1] demonstrating that the continents fit nicely to form a single continent covering entire Earth if the radius is one half of the recent radius. What TGD has to give is a new physics justification for Expanding Earth hypothesis: cosmic expansion is replaced with a sequence of fast expansion periods increasing the value of Planck constant and these transitions occur in all scales.

If Expanding Earth hypothesis is correct it forces to modify dramatically the view about pre-Cambrian period. The super-continent theory could be replaced by much simpler theory and it might be possible to give up the assumption about hypothetical super continents and super oceans. The

view about glaciations [8] must be modified dramatically. Concerning the evolution of life the natural hypothesis is that it escaped to the underground seas formed as a consequence of expansion during pre-Cambrian era and returned back to the surface in Cambrian Explosion. In this section super-continent and super-ocean theory is discussed from TGD point of view. A model for glaciations based on the assumption that the radius of Earth was in good approximation one half of the recent radius during pre-Cambrian era is developed and shown to reduce to a sequence of ordinary glaciations initiated at pole caps. Snowball theory serves as a convenient reference. Expanding Earth theory is discussed also from paleomagnetic point of view and some experimental signatures of $R/2$ scenario differentiating it from standard scenarios are developed. Finally the hypothesis about underground evolution is discussed.

11.4.1 Super-continent theory

Super-continent theory assumes a cyclic formation of hypothetical super continents [30] . Rodinia [27] , Pannotia [22] , and Pangea [21] might have preceded by earlier super-continents. The period would be roughly 250 Myr.

1. The super-continent Rodinia [27] is assumed to have existed during interval: 1100-750 Myr. 750 Myr ago Rodinia rifted into three continents: Proto-Laurasia which broke up and eventually reformed to form Laurasia (North America and Asia), the continental craton of Congo (part of Africa), and Gondwana (now southern hemisphere plus India).

2. Pannotia [22] existed during time interval 600-540 Myr. Pannotia rifted in the beginning of Cambrian era to Laurentia (North America), Baltica, Siberia and Gondwana. See the illustration of Pannotia at [11] .

3. Wegener [3] ended up to postulate that super-continent Pangea should have existed about 250 Myr ago [21] . The support for its existence is rather strong since tectonic plate model and paleo-magnetic methods allows to trace the drift of the tectonic plates.

One can criticize the cyclic model. The concentration of land mass to Southern Hemisphere during Rodinia period does not look very probable event. The cyclically occurring formation of connected land mass surrounded by much larger ocean looks even less probable unless one can develop some very good physical mechanism forcing this. The basic motivation for super-continent theory are various correlations between distant parts of Earth which would cannot be understood otherwise. In $R/2$ model the the continents would have been quite near to each other during the expansion and the notion of cyclic formation of super-continents becomes un-necessary since land bridges between the continents could explain the correlations. There would have been just single super-continent all the time.

11.4.2 Standard view about oceans

In the standard model the total area covered by oceans has reduced since pre-Cambrian era due to the increase of the continental cover, which is nowadays 29 per cent. Oceans cover the remaining 71 per cent with Antarctica and Arctica included. The evolution of Oceans in standard model requires the introduction of hypothetical oceans which left no trace about their existence (subduction mechanism provides perhaps too convenient trash bin for hypothetical theoretical constructs).

1. Proto-Atlantic Ocean was introduced to explain some contradictions with Wegener's Pangea model allowing to conclude which parts at opposite sides of Atlantic Ocean had been in contact. Proto-Atlantic Ocean closed as Pangea formed and opened again in slightly different manner to form Atlantic Ocean. This process implied mixing of older pieces of the continents and explained the contradictions. Large inland sea is a natural counterpart of the Proto-Atlantic Ocean in $R/2$ option.

2. Mirovia [15] was the super-ocean surrounding Rodinia. It transformed to Pan-African Ocean surrounding Pannotia. Pan-African ocean was then closed so that the ocean floor of Mirovia disappeared by subduction and left no signs about its existence.

3. In the rifting [25] of Pannotia Panthalassic ocean [23] emerged and was the predecessor of the Pacific ocean.

The presence of super-oceans is forced by the assumption that the radius of Earth was the recent one during the pre-Cambrian era plus the local data related to the evolution of continents. The questionable aspect is that these oceans did not leave any direct trace about their existence. In $R/2$ model there is no need for these super-oceans except possibly the counterpart of Panthalassic Ocean [23] .

11.4.3 Glaciations during Neoproterozoic period

Glaciations dominated the Neoproterozoic period [16] between 1-.542 billion years. The period is divided into Tonian [33] , Cryogenian [4] , and Ediacaran periods [5] . The most severe glaciations occurred during Cryogenian period.

It is believed that during Cryogenian period [4] two worldwide glaciations -Sturtian and Marinoan glaciations- took place. This involves extrapolation of continental drift model and plate tectonics theory. Also hypothesis about hypothetical super-continents is needed so that one must take these beliefs with some skepticism. In $R/2$ model the world wide glaciations are replaced with ordinary glaciations proceeding from poles.

1. Sturtian glaciation occurred 750-700 Myr. The breakup of Rodinia is believed to have occurred at this time. One can wonder whether there is a correlation between these events. $R/2$ model suggest that the energy needed to compensate the reduction of gravitational energy in expansion could have caused the cooling.

2. Marinoan (Varanger) glaciation ended around 635 Myr ago.

Deposits of glacial tillites [32] at low latitudes serve as support for the claim that these glaciations were world wide. In $R/2$ model Equator corresponds to North pole in TGD framework where Rodinia covered entire Earth and the interpretation would as ordinary glaciations.

After the end of Marinoan glaciation followed Ediacaran period during 635-542 Myr [5] . The first multicellular fossils appeared at this time. Their relationship to Cambrian fossils is unclear. The standard interpretation for the small number of fossils in pre-Cambrian period is that hard shells needed for fossilization were not yet developed. The problem is that these shells should have developed almost instantaneously in Cambrian explosion.

11.4.4 Snowball Earth model for the glaciation during pre-Cambrian era

Snowball Earth [47, 46, 29] is recently the leading model for the glaciations [9] during Proterozoic era. The term is actually somewhat misleading: Iceball Earth would more to the point. Slushball earth [44] is a variant of Snowball Earth which does not assume total freezing near equator.

The history behind the Snowball Earth concept is roughly following [29] .

1. Mawson studied the Neoproterozoic stratigraphy of South Australia and identified extensive glacial sediments and speculated with the possibility of global glaciation. He did not know anything about continental drift hypothesis and plate tectonic theory and thought that the ancient position of Australia was the same as it is today. Continent drifting hypothesis however explained the finding as sediments deposited at the higher latitudes the hypothesis was forgotten.

2. Later Harland suggested on basis of geomagnetic data that glacial tillites [32] in Svalbard and Greenland were deposited at tropical latitudes. In TGD framework with with $R \to R/2$ these tillites would have been at higher latitudes towards North Pole.

3. The facts are that Sun was 6 per cent fainter at that time and glaciations are known to occur. The question is whether they were global and long-lasting or a sequence of short-lasting possibly local glaciations. The Russian climatologist Budyko constructed a model based on energy balance and found that it is possible to have a global glaciation if the ice sheets proceeded enough from polar regions (to about 30 degree latitude). The model was based on the increased reflectiveness (albedo) of the Earth's surface due to the ice covering giving rise to positive feedback loop.

Budyko did not believe that global glaciation had occurred since the model offered no way to escape eternal glaciation.

4. Kirschwink introduced the term Snowball Earth, which is actually misleading. Iceball Earth would be more to to the point. He found that the so called banded iron formations are consistent with a global glaciation. He also proposed a mechanism for melting the snowball. The accumulation of CO_2 from volcanoes would have caused ultra-greenhouse effect causing warming of the atmosphere and melting of the ice.

5. Slushball Earth [44] differs from Snowball Earth in that that only a thin ice cover or even its absence near equator is assumed. The model allows to explain various findings in conflict with Snowball Earth, such as the evidence for the presence of melt-water basins.

6. Zipper rift model [48] assumes that there was a sequence of glaciations rather similar to the glaciations that have occurred later. The model assumes that the rifts [25] of the super-continent Rodinia occurred simultaneously with glaciations. The associated tectonic uplift led to the formation of high plateaus hosting the glaciers. The iron band formation can be be assigned with inland seas allowing complex chemistries and anoxicity near the sea floor.

The basic ideas of the Snowball Earth model

Snowball Earth [47, 46, 29] differs from ordinary glaciations in that only oceans are frozen whereas in the ordinary glaciation land mass is covered by ice. The basic ideas of the snowball Earth relate to the mechanism initiating the global freezing and melting.

1. The glaciation would have been initiated by some event, say a creation of super-volcano. Also astrophysical mechanism might be involved. Somewhat paradoxically, tropical continents during cryogenian period [4] are needed for the initiation because they reflect the solar radiation more effectively than tropical oceans.

2. The positive ice-albedo feedback is an essential concept: the more ice the larger the fraction of the radiation reflected back so that the more ice is generated. If the glaciation proceeds over a critical latitude about 30 degrees positive feedback forces a global glaciation.

3. The problem of the model is how to get rid of the glaciation. The proposal of Kirschvink was that the accumulation of CO_2 from volcanoes could have led to a global super-warming. The time scale for CO_2 emissions is measured in millions of years. The needed atmospheric concentration of CO_2 is by a factor 350 higher than the recent concentration. Due the ice cover the CO_2 could not be absorbed to the siliceous rocks and concentration would increase. The melting of the ice meant higher absorbtion of heat by uncovered land. Positive feedback loop was at work again but in different direction.

Evidence for and objections against Snowball Earth

Wikipedia article about Snowball Earth [29] discusses both evidence for and objections against Snowball Earth. Low latitude sediments at tropical latitudes and tropical tillites at Equatorial latitudes provide strong piece of evidence for Snowball Earth. Calcium carbonate deposits having ^{13}C signature (per cent for the depletion of ^{13} isotope and large for organic material) consistent with that for mantle meaning abiotic origin is second evidence. Iridium anomaly located at the base of Calcium Carbonate deposits is third piece of evidence. The evidence for Snowball Earth will be discussed in more detail later since it is convenient to relate the evidence to $R/2$ model for glaciations.

1. Paleomagnetic data [20] used to the dating of sediments assuming tectonic plane theory and super-continent drifting might be misleading. No pole wandering maps exist and the polarity of the magnetic field must be deduced by statistical methods. The primary magnetization could have been reset and the orientation of the magnetic minerals could have changed from the original one. It is also possible that magnetic field patterns were not dipolar. Also the assumption of hypothetical super-continents and oceans brings in uncertainties. In $R/2$ model of course the determination of the positions changes completely.

2. Carbon isotope ratios are not what they should be. There are rapid variations of $^{12}C/^{13}C$ ratio with organic origin. Suggests that freezing and melting followed each other in rapid succession. In standard framework this would suggest Slushball Earth meaning ice-free and ice-thin regions around the equator and hydrological cycles. In $R/2$ model the regions at Equator are near North Pole and the explanation would be in terms of ordinary glaciations.

3. The distribution of isotopes of element Boron suggest variations of pH of oceans. The explanation is in terms of buildup of carbon dioxide in atmosphere dissolved into oceans/seas. In $R/2$ model a sequence of glaciations would explain the findings.

4. Banded iron formations providing support for the model are actually rather rare and absent during Marinoan glaciation.

5. Wave-formed ripples, far-traveled ice-rafted debris and indicators of photosynthetic activity, can be found throughout sediments dating from the 'Snowball Earth' periods. This serves a evidence open-water deposits. In snow-ball model these could be 'oases' of melt-water but computer simulations suggest that large areas of oceans would have left ice-free. in $R/2$ model these would be signatures of ordinary glaciations.

6. Paleomagnetic data have led to the conclusion that Australia was at Equator. In $R/2$ model it would have been near North Pole. Namibia was also thought to be near Equator [31] . Indirect arguments forced the conclusion that it at 75 degree Southern latitude. In $R/2$ model this corresponds to 60 degrees Southern latitude and ordinary glaciation proceeding from South Pole is a natural explanation and ordinary glaciation would be in question in both cases.

7. There is evidence for the continental ice cover does not fit with Snowball Earth predicts that there should be no continental ice-cover. The reason is that freezing of the ocean means that there is no evaporation from oceans and no water circulation so that ice-cover cannot develop on continents. There is considerable evidence that continents were covered by thick ice [29] . This suggests ordinary glaciations possible in $R/2$ model.

11.4.5 TGD point of view about pre-Cambrian period

What is new in TGD based view about pre-Cambrian period is basically due to the $R/2$ hypothesis.

TGD view about evolution of continents

The hypothesis about the existence of the super-continent Pangea [21] was inspired by the work of Wegener [3] . The hypothesis about the existence of former super-continents were forced by the correlations with fossil records suggesting connected continent. This is not necessary if the gigantic ocean was absent during $R/2$ era. The continent Rodinia [27] could look much like the Rodinia of standard geology except that they formed single connected region with radius $R/2$.

1. It is possible that there was only single super-continent with widening inland seas all the time until 250 billion Myr. The first option is R increased slowly and that inland lake formed. Rifts could have got wider gradually during this era. If there were land bridges between the continents there would be no need for postulating the cyclic re-formation of super-continent.

2. One can pose many questions about the character of the expansion.

   (a) What was the duration of the expansion? Could the expansion have occurred in the time period 750-100 Myr (100 Myr corresponds to the age of dinosaurs with large body size made possible by the reduced gravitation and oxygenation of the atmosphere)? Duration would have been about 650 Myr in this case. Or did it began already at the beginning of Neoproterozoic period [16] when super-continent Rodinia began to break up? In this case the duration would be about 1 Myr. The estimate based on the quantum model of gravitational radiation predicts that the transition lasted for about 1.1 Gy so that the latter option would be more plausible in this framework.

(b) Did the expansion accelerate as does also cosmic expansion in TGD based universal model for the expansion periods containing only the duration of the expansion period as a parameter [66] and applying in alls scales? It seems that accelerated expansion is the only sensible option since around 540 Myr the size of Earth should have been rather near to $R/2$ (perhaps so even at the period of Pangea around 250 My) unless one assumes that super-continent re-formed again.

3. One can also consider the possibility that the continents indeed broke up and reformed again during Cambrian era. One should however have a good physical reason for why this happened. Something must have connected the pieces together and created correlations. Gravitational magnetic flux tubes and phase transitions increasing and reducing Planck constant? Or could it be that the bridges connecting the continents acted like strings inducing oscillation of the distance between continents so that Pangea was surrounded by a large ocean?

4. The formation of the rift [25] feeding magma from core to the surface would be due to the expansion leading to the formation of fractures. The induced local elevations would be like mountains. As in zipper-rift model ice could have covered these plateaus because the temperature was lower. This is not however essential for TGD based model of glaciations.

5. TGD based variant of Expanding Earth allows subduction but its role could have been small before the Pangeia period if the expansion was accelerating and led only to a relatively small increase of the radius before the Mesozoic period [14] and continued with an accelerating rate during Mesozoic from 250 Myr to 65 Myr. It is interesting that Mesozoic period begins with the most intensice known extinction of history- so called Permian-Triassic extinction event [74] - known as Great Dying. About 95 of marine species and 70 percent of terrestrial species became extinct. Maybe genetically determined bio-rhythms could not follow the rapidly changing circadian rhythm. Another explanation for the extinction is the warming of the climate. For this there is indeed support: there is evidence that Antarctica was climate refuge during the extinction [112] . Perhaps both factors were involved and were not independent of each other since rapid expansion might have generated massive methane leakages from underground seas and lakes.

TGD based view about evolution of oceans

Continents would have covered most of the area during $R/2$ era and the covered fraction was slightly smaller than 1/4 of the recent area of Earth. This depends on the area taken by inland seas and polar caps. Nowadays the area covered by continents and inland seas is about 31 per cent so that continental area has increased and would be due to the expansion in vertical direction and deepening of the oceans. The area covered by oceans has increased from a small value to about 70 per cent. Only a small fraction of ocean floor would be subduced in Expanding Earth model. The Proto-Atlantic would have been only a small inland sea. Panthalassic Ocean was inland sea, which expanded to Pacific Ocean during expansion. Pacific Ocean could contain data about ancient ice ages if it was frozen. It however seems that data are consistent with the absence of global glaciation.

Model for glaciations

In TGD framework single super continent covering most of Earth becomes the counterpart of Rodinia [27] . The hypothetical oceans are replaced with inland seas and polar caps. The super-continent covering most of Earth absorbs less solar heat than tropical oceans so that glaciations become more probable. Snowball Earth is replaced with a series of ordinary glaciations proceeding from poles since the places at Equator were near North Pole. There is no need for the glaciations to progress to the equator. The rifting for the counterpart of Rodinia is consistent with the formation of fractures due to the expansion of Earth. The reduction of gravitational binding energy due to the increase of the radius requires feed of energy and this could be one reason for the cooling and initiation of the glaciation.

There are several questions which must be answered if one wants to gain a more detailed understanding.

1. How does $R/2$ model modify the view about glaciations? Very probably there was a frozen polar cap. Snowball Earth could be replaced with ordinary glaciations proceeding from North and South Pole.

2. How does the predicted 3+3 hour diurnal cycle modify the ordinary picture? Certainly 3-hour day reduces the amplitude of the diurnal temperature variations. Could this period have left genetic traces to the mono-cellulars, say biological clocks with this period?

3. How does the predicted four times stronger surface gravity affect the glaciation process? Could strong gravity leave detectable signatures such as anomalously strong effects on the shape of surface of Earth or deeper signatures about the motion of ice.

There are also questions related to the energetics of the expansion.

1. The expansion required energy and could have induce glaciations in this manner. Energy conservation would hold for the total mechanical and gravitational energy of Earth given by

$$E = \frac{L^2}{2I} - k\frac{GM^2}{R} < 0 \ . \tag{11.4.1}$$

   Here L is the conserved angular momentum of order $L \simeq I\omega$ and ω increases from $1/4\omega_{now}$ to ω_{now} during the expansion. The moment of inertia I is of order of magnitude $I \sim MR^2$ and k is a numerical constant not too far from unity. The kinetic energy is actually negligible as compared to the gravitational potential energy. The reduction of the gravitational binding energy requires a compensating energy, which could come both from Earth interior or from the Earth's surface. Both effects would induce a cooling possibly inducing glaciations.

2. One expects that in the initial stages of the expansion there was just an expansion. This meant stretching requiring also energy. The formation of rifts leading to the formation of oceans as magma flowed out would have started already in the beginning of Proterozoic period. Eventually fractures were formed and in TGD framework one might expect that the distribution of fractures could have been fractal. A considerable fraction of fractures was probably volcanoes so that CO_2 begun to leak to the atmosphere and local 'oasis' were formed. Also hot springs liberating heat energy from Earth crust could have been formed as in Island. The pockets inside Earth increased in size and were filled with water. Life started to escaped to the walls of the fractures and to the water pockets. Also the recent oceans can be seen as widened cracks which transformed to the expanding sea floors whereas continents did not expand. As the continental crust ceased to expand no heat was needed for the expansion and this together with increased CO_2 content of atmosphere would explain why there was no further glaciations and heating of the Earth. At this period the flow of the magma from Earth core provided the energy needed to compensate the reduction of gravitational energy.

3. It must be emphasized that TGD variant of Expanding Earth theory is not in conflict with tectonic plate theory. It explains the formation of tectonic plates and the formation of magma flow from rifts giving also rise to subduction and is therefore a natural extension of the tectonic plate theory to times before the expansion ceased.

Estimate for the duration of the transition changing gravitational Planck constant

The reader without background in quantum physics and TGD can skip this section developing an estimate for the duration of the transition changing Planck constant and inducing the scaling of the radius of Earth by a factor two. The estimate is about 1.1 Gy. It must be emphasized that the estimate is not first principle calculation and relies strongly on quantum classical correspondence.

The duration of the quantum transition inducing the expansion of the gravitational space-time sheet of Earth and thus of Earth itself by a factor two can be estimated by using the same general formula as used to estimate the power of gravitational radiation emitted in a transition in which gravitational Planck constant assignable to star-planet system is reduced [51] .

1. The value of gravitational Planck constant characterizing the gravitational field body of Earth is GM^2/v_0, where the velocity parameter $v_0 < 1$ ($c = 1$) is expected to be larger than $v_0 \simeq 2^{-11}$ characterizing Sun-Earth system.

2. Assuming a constant mass density for Earth the gravitational potential energy of Earth is given by

$$V = \frac{M}{2}\omega^2 r^2 \ , \ \omega = \sqrt{\frac{6GM}{R^3}} \ . \tag{11.4.2}$$

   As far as radial oscillations are considered, the system is mathematically equivalent with a harmonic oscillator with mass M. The energies for the radial oscillations are quantized as $E = (n + 1/2)\hbar_{gr}\omega$.

3. The radii of Bohr quantized orbits for the harmonic oscillator scale like $\sqrt{\hbar}$ so that $\hbar \to 4\hbar$ is needed to obtain $R \to 2R$ rather than $\hbar \to 2\hbar$ as the naive Compton length argument would suggest. This requires the scaling $v_0 \to v_0/4$. The change of the ground state energy in this quantum transition is

$$\begin{aligned} \Delta E &= \frac{1}{2}(\hbar_{gr,f}\omega_f - \hbar_{gr,i}\omega_i) \ , \\ \hbar_{gr,f} &= 4\hbar_{gr,i} = \frac{4GMm}{v_{0,i}} \ , \\ \omega_i &= 2^{3/2}\omega_f = 2^{3/2}\sqrt{\frac{6GM}{R_f^3}} \ . \end{aligned} \tag{11.4.3}$$

   $R_f = R$ denotes the recent radius of Earth.

4. From the estimate for the power of gravitational radiation in similar transition the estimate for the duration τ of the quantum transition is

$$\begin{aligned} \tau &= a(v_{0,i}v_{0f})^{-k/2} \times \frac{(\hbar_{gr,i} + \hbar_{gr,f})}{2\Delta_E} \ , \\ &= a2^{-k}v_{0f}^{-k} \times \frac{1+r}{r\omega_f - \omega_i} \ , \ r = \frac{\hbar_f}{\hbar_i} = 4 \ . \end{aligned} \tag{11.4.4}$$

   The average of Planck constants associated with the initial and final states and geometric mean of the parameters v_{0i} and v_{0f} is dictated by time reversal invariance. The exponent k is chosen to be same as that obtained for from the condition that that the ratio of the power to the classical radiation power emitted in the transition between planetary Bohr orbits does not depend on v_0 (quantum classical correspondence). This gives $k = 5$. The condition that the power of gravitational radiation from Hulse-Taylor binary is same as the power predicted by the classical formula (quantum classical correspondence) gives $a = .75$.

5. The explicit expression for τ reads as

$$\begin{aligned} \tau &= K \times av_{0,f}^{-5} \times (\frac{R}{2GM})^{1/2} \times \frac{R}{c} \ , \\ K &= \frac{5 \times 2^{-7} \times (2 + 2^{1/2})}{3^{1/2}} \ . \end{aligned} \tag{11.4.5}$$

6. The basic data are $M_{Sun} = 332900M$ (mass of Sun using Earth's mass as unit) and the mnemonic $r_{S,Sun} = 2GM_{Sun} = 2.95 \times 10^3$ m: together with $R = 6371 \times 10^3$ m these data allow a convenient estimation of $R/2GM$. For $k = 10$ and $a = .75$ this gives $\tau = 1.17$ Gyr. This is twice the estimate obtained by requiring that the transition begins at about 750 Myr (the beginning of Sturtian glaciation) and ends around 100 My (the age of gigantic animals whose evolution would be favored by the reduction of surface gravity). The estimate would suggest that the quantum transition began already around 1.1 Gyr, which in the accuracy used corresponds to the beginning of Neoproterozoic at 1 Gyr [16] . The breaking of super-continent Rodinia indeed began already at this time.

7. Note that the value of v_{0f} for the gravitational field body of Earth as it is now would be $v_{0f} = 2^{-10}$ to be compared with $v_0 \simeq 2^{-11}$ for Sun-Earth gravitational field body.

Snowball Earth from TGD point of view

In TGD framework the main justification for Snowball Earth disappears since the samples believed to be from Equator would be from North pole and glaciation could be initiated from pole caps. Consider next in more detail the evidence for Snowball Earth from TGD point of view.

1. Low latitude glacial deposits, glacial sediments at tropical latitudes, tropical tillites, etc. providing support for snowball Earth [29] would be near North pole of at Northern latitudes. Ordinary glaciations proceeding from poles would explain the findings [10] . If total glaciations were present, a rough scaling suggests that the evidence from them should be found from southern latitudes around 45 degrees in the standard model framework.

   The testable prediction is that the evidence for glaciations in ice-ball Earth framework should be found only below Equator and near South Pole. This finding would be of course extremely weird and would strongly favor $R/2$ option. Interestingly, in Southern Brasil all indicators for glaciations are absent (see [39] and references therein). This region belonged to Godwana continent and there is evidence that its location was at middle latitudes at Southern Hemisphere.

2. Banded iron formations [29] are regarded as evidence for Snowball Earth and occur at tropical levels (near North Pole in $R/2$ model). Iron dissolved in anoxic ocean would have become in a contact with photosynthetically produced oxygen and implied the formation of iron-oxide. The iron formation would have been produced at the tipping points of anoxic and oxygenated ocean. One can consider also an explanation in terms of deep inland seas, which become stagnant and anoxic near the sea floor.

   In TGD framework sea floor near North Pole could contain banded iron formations. This would explain also why the banded iron formations are rather rare. The oxygen could have come also from underground after the formation of cracks and led to the oxygenation of inland seas from bottom. The assumption that oxygenation took place already during the first glaciation, could explain why banded iron formations are absent during the second glaciation.

3. Calcium carbonate deposits [29] have ^{13}C signature (per cent for the depletion of ^{13} isotope and large for organic material) is consistent with that for mantle meaning abiotic origin. The explanation of Calcium carbonate deposits in TGD framework could be the same as in Snowball Earth model. Atmospheric CO_2 could come from the volcanoes and react with the silicates during the ice-free periods to form calcium carbonate which then formed the deposits. CO_2 could have also biological origin and come from the underground life at the walls of the expanding fractures/volcanoes or in underground seas or lakes. In this case also methane is expected. This option would predict ^{13}C signature characteristic for organic matter. Also this kind of signatures have been observed and support ordinary glaciations. Also rapid fluctuations of the signature from positive to negative take place and might have signatures of temporary melting induced organic contribution to the calcium carbonate.

4. Iridium anomaly [29] is located at the base of Calcium Carbonate deposits. In Snowball Earth model Iridium deposits derive from the Iridium of cosmic rays arriving at the frozen ice surface. As the ice melts, Iridium deposits are formed. In $R/2$ model the condensation of Iridium would proceed through the same mechanism. The possible problem is whether the time is long enough

for the development of noticeable deposits. Near poles (Equator and South pole in standard model) this could be the case.

11.4.6 Paleo-magnetic data and Expanding Earth model

Paleomagnetic data from pre-Cambrian period might allow to test $R/2$ hypothesis. This data could in principle help to trace out the time development $R(t)$ from $R/2$ to R if the non-dipole contribution to magnetic field depends on $R(t)$.

About paleo-magnetism

Paleomagnetism [20] provides quantitative methods to determine the latitude at which the sample of sedimentary rock was originally. Magnetic longitude cannot be determined because of rotational symmetry so that other information sources must be used. There are several methods allowing to deduce the direction and also the magnitude of the local magnetic field and from this the position of the sample during the time the sample was formed.

1. Below the Curie point thermal remanent magnetization is preserved in basalts of the ocean crust and not affected by the later magnetic fields unless they are too strong. This allows to deduced detail maps from continental drifting and polar wander maps after 250 Myr (Pangea period). During pre-Cambrian period the ocean floors of hypothetical oceans would have disappeared by subduction. In $R/2$ model there are no oceans: only inland seas.

2. In the second process magnetic grains in sediments may align with the magnetic field during or soon after deposition; this is known as detrital remnant magnetization (DRM). If the magnetization is acquired as the grains are deposited, the result is a depositional detrital remnant magnetization (dDRM); if it is acquired soon after deposition, it is a post-depositional detrital remnant magnetization (pDRM).

3. In the third process magnetic grains may be deposited from a circulating solution, or be formed during chemical reactions, and may record the direction of the magnetic field at the time of mineral formation. The field is said to be recorded by chemical remnant magnetization (CRM). The mineral recording the field commonly is hematite, another iron oxide. Red-beds, clastic sedimentary rocks (such as sandstones) that are red primarily because of hematite formation during or after sedimentary diagenesis, may have useful CRM signatures, and magnetostratigraphy [13] can be based on such signatures. Snowball model predicts that nothing came to the bottoms of big oceans! How can we know that they existed at all!

During pre-Cambrian era the application of paleomagnetic methods [20] is much more difficult.

1. Reliable paleomagnetic data range up to 250 My, the period of Pangaea, and magnetization direction serves as a reliable information carrier allowing detailed polar wander maps. During pre-Cambrian era one cannot use polar wander maps and the polarity of the magnetic field is unknown. Therefore theoretical assumptions are needed including hypothetical super-continents, hypothetical oceans, and continental drift and plate tectonics. All this is on shaky grounds since no direct information about super-continents and ancient oceans exists. $R/2$ model suggests that continental drift and plate tectonics have not been significant factors before the expansion period when only inland seas and polar ice caps were present. Measurements have been however carried out about magnetization for pre-Cambrian sediments at continents recently and gives information about the strength of the magnetic field [12] : the overall magnitude of the magnetic field is same as nowadays.

2. At Precambrian period the orientation of iron rich materials can serve as a record. The original records can be destroyed by various mechanisms (diagenesis). Also the orientations of the sediments can change in geological time scales.

3. Tens of thousands of reversals of the magnetic polarity [7] have occurred during Earth's history. There have been long periods of stability and periods with a high frequency of reversals. The average duration of glaciation is around one Myr. The determination of the polarity of B possible by using samples from different points.

4. Mountain building orogeny [19] releases hot water as a byproduct. This water can circulate in rocks thousands of kilometers and can reset the magnetic signature. The formation of fractures during the expansion of Earth could have released hot water having the same effect.

Could paleomagnetic data kill or prove $R/2$ model?

The first question is how one might kill $R/2$ model using data from pre-Cambrian era. Paleomagnetic data could do the job.

1. Remanent magnetization is proportional to the value of magnetic field causing it in weak magnetic fields. Therefore the magnetization in principle gives information about the magnetic fields that prevailed in early times.

2. Suppose that the currents generating the magnetic field can be idealized to conserved surface currents K around cylindrical surfaces of radius r and height h scaled down to to $r/2$ and $h/2$ and that the value of K is not affected in the process. With this assumptions the magnetic moment behaves $\mu \sim Ir^2h \to \mu/8$. A continuous current vortices with $j = k/\rho$, which is irrotational outside the symmetry axis, produce a similar result if the radius of the vortices scales as $r \to r/2$. Since dipole magnetic field scales as $1/r^3$ and is scaled up by a factor 8 in $R \to R/2$, the scalings compensate and the dipole magnetic fields at surface do not allow to distinguish between the two options. Non-dipole contributions might allow to make the distinction.

3. The group led by Lauri J. Pesonen in Helsinki University [12] has studied paleomagnetic fields at pre-Cambrian era. The summary of results is a curve at the home page of the group and shows that the scale of the magnetic during pre-Cambrian era is same as nowadays. On the other hand, the recent thesis by Johanna Salminen- one of the group members- reports abnormally high values of magnetization in Pre-Cambrian intrusions and impact structures in both Fennoscandia and South Africa [51] . No explanation for these values has been found but it is probably not the large value of primary magnetization.

Another manner to do test the $R/2$ model is by comparing the signs of the magnetizations at magnetic equator and poles. They should be of opposite sign for dipole field. The polarity of magnetic field varies and there are no pre-Cambrian polar wander maps. One can deduce from the condition $B_r/rB_\theta = 2cot(\theta)$ holding true for dipole field the azimutal distance $\Delta\theta$ along the direction of the measured magnetic field to the pole along geodesic circle in the direction of the tangential component of B. One cannot however tell the sign of $\Delta\theta$, in other words whether a given pre-Cambrian sample belongs to Norther or Southern magnetic hemisphere. There are however statistical methods allowing to estimate the actual pole position using samples from several positions (for an excellent summary see [51]).

For instance, if the magnetic field is in North-South direction during Rodinian period [27] , standard model would predict that the sign at the Equator is opposite to that at South Pole. In $R/2$ model the sample would be actually near North Pole and polarizations would have same sign. The sign of magnetization at apparent southern latitude around 45 degrees would have been opposite to that at South pole which is in conflict with dipole field character. Maybe the global study of magnetization directions when magnetic field was approximately in North-South direction could allow to find which option is correct. Also the dependence of the strength of the magnetic field as function of θ could reveal whether $R/2$ model works or not. The testing requires precise dating and position determination of the samples and a detailed model for the TGD counterpart of Rodinia and its construction requires a specialist.

If the expansion continued after 250 Myr with an accelerating rate and Earth radius was still considerably below its recent value, the comparison of pole wandering charts deduced from ocean floor paleomagnetic data at faraway locations might allow to show that the hypothesis about dipole field is not globally consistent for R option. Even information about the time evolution of the radius could be deduced from the requirement of global consistency.

11.4.7 Did life go underground during pre-Cambrian glaciations?

The basic idea of Expanding Earth model is that the life developed in underground seas and emerged to the surface of Earth in Cambrian explosion. The series of pre-Cambrian glaciations explains why

the life escaped underground and how the underground seas were formed.

1. If one believes that the reduction of gravitational binding energy was responsible the cooling, then the expansion of Earth could have begun at the same time as Sturtian glaciation [4] . On the other hand, the TGD estimate for the duration of the expansion period giving 1.1 Gyr, suggests that the breakup of the Rodinia, which began in the beginning of Proterozoic period corresponds to the beginning of the expansion. The simplest assumption is that the radius of R at the beginning of Cambrian period was not yet much larger than $R/2$ and continued to increase during Cambrian period and ended up around 100 My, when dinosaurs and other big animals had emerged (possibly as a response to the reduction of gravity). This means that there were land bridges connecting the separate continents.

2. One must explain the scarcity of fossils during pre-Cambrian era. If the more primitive life forms at the surface of Earth did not have hard cells and left no fossils one can understand the absence of highly evolved fossils before Cambrian explosion [14] . If life-forms emerged cracks and underground seas there would be no fossils at the surface of Earth. In the case of volcanoes dead organisms would have ended to gone to the bottom of the water containing volcano and burned away.

3. The expansion had formed the underground pockets and fractures made possible for the water to flow from the surface to the pockets. Life would have evolved in fractures and pockets. The first multicellular fossils appeared during Ediacaran period (segmented worms, fronds, disks, or immobile bags) [5] and have little resemblance to recent life forms and their relationship with Cambrian life forms is also unclear. Ediacaran life forms could have migrated from the fractures and Cambrian fossils from from the underground seas and lakes. The highly evolved life-forms in Cambrian explosion could have emerged from underground seas through fractures.

One can make also questions about the underground life.

1. The obvious question concerns the sources of metabolic energy in underground seas. In absence of solar radiation photosynthesis was not possible plants were absent. The lowest levels in the metabolic hierarchy would have received their metabolic energy from the thermal or chemical energy of Earth crust or from volcanoes. The basic distinction between plants and animals might be that the primitive forms of plants developed at the surface of Earth and those of animals in underground seas.

2. At first it seems strange that the Cambrian life-forms had eyes although there was no solar radiation in the underground seas. This is actually not a problem. These life-forms had excellent reasons for possessing eyes and in absence of sun-light the life forms had to invent lamp. Indeed, many life forms in deep sea and sea trenches produce their own light [57] . It would be interesting to try to identify from Cambrian fossils the body parts which could have served as the light source.

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Chapter 12

A Model for Protein Folding and Bio-catalysis

12.1 Introduction

The model for the evolution of the genetic code leads [29] to the idea that the folding of proteins obeys a code inherited from the genetic code. One can imagine several variants of this code. One of them is that amino-acid behaves like the conjugate Y_c of the middle nucleotide of the codon XYZ coding for it. Conjugation for amino-acids would correspond to the hydrophilic-hydrophobic dichotomy. Also catalyst action could reduce to effective base pairing in this picture chemically and at the level of quarks associated with the flux tube to matter antimatter conjugation. The guess that amino-acid and its conjugate form pairs turned out to be wrong however and after various twists and turns I ended up with the hypothesis that the amino-acid in protein behaves like Y_cZ_c where Z corresponds to third nucleotide for some codon coding for the amino-acid.

There exists a wonderful book "Proteins: Structures and Molecular Properties" by Thomas E. Creighton published 1993 [124] and I am grateful for Timo Immonen for possibility to use the book. In the following I freely refer to the general facts discussed in this book rather than referring separately to every detail.

12.1.1 Flux tubes as correlates of directed attention at molecular level

After some trials one ends up with a general conceptualization of the situation with the identification of ("wormhole") magnetic flux tubes as correlates for attention at molecular level so that a direct connection with TGD inspired theory of consciousness emerges at quantitative level. Whether wormhole flux tubes or ordinary flux tubes are needed is not a completely settled question yet and the attribute "wormhole" will not be used in the sequel. This suggests a generalization of the DNA as topological quantum computer paradigm making it much more detailed.

There are too many uncertainties involved to allow anything except playing with the options that one is able to imagine. There are two kinds of flux tubes. Those between amino-acids and those between amino-acids and water molecules. The contractions of flux tubes in $\hbar$ changing phase transitions are expected to be important for protein folding and could also give rise to the interaction responsible for hydrophily and hydrophoby and be therefore highly relevant for protein folding. A basic question about which I became aware only about one year after working out the first draft of this chapter concerns the relative importance of these two kinds of flux tubes. The first model assumed that only amino-acid-aminoacid flux tubes are relevant and assumed strong selection rules inspired by DNA as tqc model. The second model which emerged year later represents an extreme in which only the flux tube connections between amino-acids and water molecules assumed to be responsible for hydrophily and hydrophoby induce the interactions between amino-acids as secondary interactions. This model works surprisingly well at qualitative level.

12.1.2 The model of folding code based on flux tube connections between amino-acids

The first model assumes that only the flux tubes between amino-acids are relevant for protein folding.

What kind of atoms can be connected by flux tubes?

1. Hydrogen bonds play a key role in bio-catalysis but are not understood completely satisfactorily in the standard chemistry. Hence the basic question is whether hydrogen bonds can be regarded as or are accompanied by short (wormhole) magnetic flux tubes: note that the subject-object asymmetry of directed attention would correspond to donor-acceptor asymmetry of they hydrogen bond. If this is the case, the identification of the magnetic flux tube connection as a prerequisite for a hydrogen bond or as hydrogen bond becomes natural. At least the atoms able to form hydrogen bonds could form flux tube contacts so that the model would be very predictive and would conform with the known important role of hydrogen bonds in bio-catalysis.

2. The fact that hydrogen bonds connect base pairs suggests a generalization of the notion of base pairing stating that under some conditions amino-acids coded by XYZ and UY_cV can behave like base pairs. These amino-acic pairs correspond to pairs of amino-acid residues which are hydrophilic *resp.* hydrophobic and hydrophobic residue do not form hydrogen bonds in general. These flux tubes would thus be more general and in general long. The model for DNA as topological quantum computer requires this kind of flux tubes and they would in general connect atoms or molecules which act as acceptors in hydrogen bonding: $O =$ atom in amino-acid and aromatic ring are basic examples.

3. If one assumes that both $N - H$ and $O =$ associated with the constant part of the amino-acid can act as flux tube terminals and represent Z and Y nucleotides of the codon XYZ coding for the amino-acid, one obtains $Y = Z$ pairing of $O = -O =$ flux tubes are allowed and $Y = Z_c$ pairing if only hydrogen bond like pairings are allowed.

Color inheritance by a reconnection of flux tubes

1. There should exist some mechanism allowing amino-acids to inherit the base pairing property from the tRNAs associated with them so that one can identify amino-acid with the middle nucleotide of the codon coding it. If tRNA middle nucleotide is connected to $O =$ of the amino-acid, this becomes possible since the reconnection of flux tubes preserves the "color" of the flux tubes coded by (A,T,G,C) that is by the quark or anti-quark coding for the nucleotide. The temporary formation of a hydrogen bond between $N - H$ and $O =$ of two amino-acids as in the case of alpha helix would allow $N - H$ to inherit the conjugate of the color associated with $O =$. Alternative interpretation is that this hydrogen bond is possible only if the predetermined color of $N - H$ is consistent with the inherited one. The inheritance of flux tube color would be a completely general mechanism and even the donor atoms in the residues of amino-acids could inherit the color of $O =$ in this manner.

2. A possible interpretation for the fixing of the flux tube color is in terms of quantum measurement selecting one color from quantum superposition in the reconnection process. This would mean that the unitary process can bring superposition back and reconnection process can change the inherited color. The hydrogen bonds between water molecules could correspond to quantum superpositions of different colors. This superposition property might relate to the wobble base pairing phenomenon for the third nucleotide in tRNA.

Folding code

The identification of $N - H$ as a representation for the conjugate of the third nucleotide Z means that amino-acids would remember which codon coded them. If only hydrogen bond like flux tubes are allowed, flux tubes can connect only amino-acids satisfying $Y = Z_c$. If $= O-O =$ flux tubes are allowed $Y = Z$ rule favored by the model of DNA as topological quantum computer follows. The isospin symmetry of the third nucleotide implies that both rules are quite flexible. If one identifies hydrogen bond with flux tube ($Y(n) = Z(n + k)$) the model works badly for both options. If one assumes

only that the presence of a flux tube connecting amino-acids in either direction ($Y(n) = Z(n+k)$ or $Z(n) = Y(n+k)$) is a prerequisite for the formation of hydrogen bond, the model works. $Y = Z$ rule is favored by the study of five enzymes: the possible average length of alpha helix is considerably longer than the average length of alpha helix if gene is the unique gene allowing to satisfy $Y = Z$ rule. The explicit study of alpha helices and beta sheets for these enzymes demonstrates that the failure to satisfy the condition for the existence of hydrogen bond fails rarely and at most for two amino-acids (for 2 amino-acids in single case only).

$Y = Z$ rule could mean a solution of the basic problem of proteonics: Do genes determine the folding of proteins and how this would take place? The interpretation would be that the information loss suggested by the many-to-one character of the genetic code is only apparent. The apparently lost information which corresponds to the $A - G$ and $T - C$ symmetries of the third nucleotide codes for the hydrogen bonding and hence for the folding of the protein. The model in its most stringent form is easy to kill since in the case of alpha helices and beta sheets the hydrogen bonding fixes completely the DNA sequence coding for the protein. A weaker variant of the model based on quantum variant of wobble base pairing: in this case there are no conditions on DNA sequence. It turns out that only this variant works. Hence hydrogen bonded amino-acid behave as if they were coded by the unique codon consistent with $Y = Z$ rule.

Quantitative model

The quantitative model relies on the assumption that the contribution of a flux tube connecting two amino-acids to the potential energy depends only on the distance between the molecules in question. The extremals of the total interaction energy are same for any choice of the potential and only the absolute minimum of the interaction energy depends on the choice of the potential. The simplest potential corresponds to harmonic oscillator potential and would explain formation of alpha helices and beta sheets and with the fact that hydrophilic and hydrophobic residues tend to have a large distance and only few flux tube contacts. For large Planck constant also long flux tubes could correspond to attractive harmonic oscillator potential. Also the contribution of other interactions between neighboring amino-acids are expected to be present but are neglected in the simplest model. The model predicts alpha helices and beta sheets, and more generally, periodic structures, as solutions to energy minimization equations.

12.1.3 A model for protein folding based on flux tubes between amino-acids and water molecules

This model represents a diametrical opposite of the first model in the sense in that it assumes flux tube connections only between amino-acids and water molecules. These flux tubes mediate an attractive (repulsive) interaction in the case of hydrophily (hydrophoby) due to the behavior of magnetic (presumably) interaction energy as a function of Planck constant (or integers characterizing the level of dark matter) assignable to the flux tube. For hydrophoby (hydrophily) the interaction energy is minimized for long (short) flux tubes. The interaction between amino-acids is induced by this interaction in a manner analogous to how the interaction between electrons and ions induces secondary interaction between the members of a Cooper pair. The model explains the basic qualitative aspects of protein folding and the quantitative model of folding based on amino-acid-amino-acid flux tubes allows a generalization which is however discussed at numerical level.

Several persons have helped me in writing this chapter. I want to express my gratitude to Ulla Mattfolk for informing about the idea of protein folding code and to Dale Trenary for interesting discussions, for suggesting proteins which could allow to test the model, and for providing concrete help in loading data help from protein data bank. Also I want to thank Timo Immonen for discussions and for loaning the excellent book "Proteins: Structures and Molecular Properties" of Creighton. I am also grateful for Pekka Rapinoja for writing the program transforming protein data file to a form readable by MATLAB.

12.2 A model for flux tubes

Biochemistry represents extremely complex and refined choreography. It is hard to believe that this reduces to a mere unconscious and actually apparent fight for chemical survival. In TGD Universe consciousness would be involved even at the molecular level and magnetic body would be the choreographer whose dance would induce the molecular activities. This picture combined with the idea of standard plugs and terminals at which flux tubes end, leads to a to a picture allowing to formulate a model for protein folding.

12.2.1 Flux tubes as a correlates for directed attention

Molecular survival is the standard candidate for the fundamental variational principle motivating the molecular intentional actions. There is entire hierarchy of selves and the survival at the higher level of hierarchy would force co-operation and altruistic behavior at the lower levels. One might hope that this hypothesis reduces to Negentropy Maximization Principle [44] , which states that the information contents of conscious experience is maximized. If this picture is accepted, the evolution of molecular system becomes analogous to the evolution of a society.

Directed attention is the basic aspect of consciousness and the natural guess would be that directed attention corresponds to the formation of magnetic flux tubes between subject and target. The directedness property requires some manner to order the subject and target.

1. The ordering by the values of Planck constant is what first comes in mind. The larger space-time sheet characterized by a larger value of Planck constant and thus at a higher level of evolutionary hierarchy would direct its attention to the smaller one.

2. Also the ordering by the value of p-adic prime characterizing the size scale of the space-time sheet could be considered but in this case directedness could be questioned.

3. Attention can be directed also to thoughts. Could this mean that attention is directed from real space-time sheets to p-adic space-time sheets for various values of primes but not vice versa? Or could the direction be just the opposite at least in the intentional action transforming p-adic space-time sheet to real space-time sheet? Perhaps directions are opposite for cognition and intention.

The generation of (wormhole) magnetic flux tubes could be the correlate for the directed attention, not only at molecular level, but quite generally. Metaphorically, the strands of braid would be the light rays from the eyes of the perceiver to the target and their braiding would code the motions of the target to a topological quantum computation like activity and form a memory representation at least. The additional aspect of directed attention would be the coloring of the braid strands, kind of coloring for the virtual light rays emerging from the eyes of the molecular observer. In the case of DNA this can induce a coloring of braid strands emerging from amino-acids and other molecules so that it would indeed become possible to assign to free amino-acid the conjugate of the codon XYZ coding for it.

Attention can be also redirected. For this process there is a very nice topological description as a reconnection of flux tubes. What happens is that flux tubes $A \to B$ and $C \to D$ fuse for a moment and become flux tubes $A \to D$ and $C \to B$. This process is possible only if the strands have the same color so that the values of the quark charges associated with A and B are the same.

1. Reconnection process can modify tqc programs. For instance, in the case of the flux tubes coming from nucleotides X and X_c and ending to the lipid layer this process means that X and X_c and corresponding lipids become connected and genome builds memory representation about this process via similar link.

2. Reconnection process makes also possible what might be called color inheritance allowing amino-acids to inherit the conjugate colors of the nucleotides of the codon coding it.

3. DNA would have memory representation about molecular processes via these changing braiding topologies, and one could say that these molecular processes reflect the bodily motions of the magnetic body. Entire molecular dynamics of the organism could represent an enormous tqc

induced by the motor activities of the magnetic body. At the level of sensory experience similar idea has been discussed earlier [74] : out of body experiences (OBEs) and illusions such as train illusion could be understood in terms of motor action of magnetic body inducing virtual sensory percepts.

Attention can be also switched on and off. Here the structure of the lipid ends containing two nearby situated $=O$:s suggest the mechanism: the short flux tube connecting $=O$:s disappears by reconnection mechanism with a pair of hydrogen bonded water molecules leading to a shortcut of the connecting flux tubes to $=O--H_2O$ hydrogen bonds. The minimization of Coulomb interaction energy at each end implies that re-appearance of the flux tubes creates a short flux tube with the original strand color.

12.2.2 Does directed attention generate memory representations and tqc like processes

Directed attention induces braiding if the target is moving and changing its shape. This gives rise to a memory representation of the behavior of the object of attention and also to a tqc like process. A considerable generalization of tqc paradigm suggests itself.

Tqc could be induced by the braiding between DNA and lipids, DNA and proteins via folding processes, DNA RNA braiding and braiding between DNA and its conjugate, DNA and protein braiding. The outcome of tqc would be represented as the temporal patterns of biochemical concentrations and rates and there would be hierarchy of p-adic time scales and those associated with the dark matter hierarchy.

For instance, the protein content of lipid membranes is about 50 per cent and varies between 25-75 per cent so that protein folding and lipid flow could define tqc programs as self-organization patterns. The folding of protein is dynamical process: alpha helices are created and disappear in time scale of 10^{-7} seconds and the side chains of protein can rotate.

The details of the tqc like process depend on what one assumes. The minimal scenario is deduced from the transcription and translation processes and from the condition that magnetic body keeps control or at least keeps book about what happens using genome as a tool. The picture would be essentially what one might obtain by applying a rough model for web in terms of nodes and links. The reader is encouraged to use paper and pencil to make the following description more illustrative.

1. Assume that mRNA and DNA remain connected by flux tubes after transcription and that only reconnection process can cut this connection so that mRNA inherits the conjugate colors of DNA. Assume same for mRNA and tRNA. Assume that amino-acid associated with tRNA has similar flux tube connections with the nucleotides of tRNA. Under these assumptions amino-acid inherits the conjugate colors of DNA nucleotides via the connection line DNA-mRNA-tRNA-amino-acid faith-fully if all links are correspond to quark pairs rather than their superpositions. Wobble pairing for Z nucleotide could actually correspond to this kind of superposition.

2. One can consider several options for the amino-acid-acid DNA correspondence but trial-and-error work showed that a realistic folding code is obtained only if X, Y, and Z correspond to $O-H$, $O=$, and NH_2 in the constant part of free amino-acid. During translation the formation of the peptide bond between amino-acids dehydration leads to a loss of $O-H$ and one H from NH_2. The flux tube from tRNA to $O-H$ becomes a flux tube to water molecule inheriting the color of X so that $O=-NH_2$ of the amino-acid inside protein represents the conjugate of YZ.

3. Hydrogen bonding between $O=$ and NH of n:th and $n+k$:th amino-acids inside alpha helices and n:th and $n+1$:th amino-acids inside beta strands reduces effectively to base pairing characterized by $Y=Z$ rule. Assuming that flux tube is only a prerequisite for the formation of hydrogen bond, $Y(n)=Z(n+k)$ or $Z(n)=Y(n+k)$ allows the existence of hydrogen bond. The identification of hydrogen bond with flux tube gives a more stringent condition $Y(n)=Z(n+k)$. The first option is favored. Either condition is extremely restrictive condition on the gene coding the amino-acid unless one assumes quantum counterpart of wobble base pairing for mRNA or tRNA-amino-acid pairing in the case of Z nucleotide (as one indeed must do). Note that the $O=$ atom of the amino-acid is in a special role in that it can have hydrogen bond flux tubes to donors and flux tube connections with $O=$:s of other amino-acids, the residues of amino-acids containing acceptors (say $O=$ or aromatic ring), and with the aromatic rings of say ATP.

4. The recombination process for two conjugate DNA-mRNA-tRNA-amino-acid links can transform the flux tubes in such manner that one obtains link between the $=O$:s of amino-acids A_1 and A_2 characterized by Y and Y_c. Besides hydrogen bonding this mechanism could be central in the enzyme substrate interaction. The process would pair tRNAs corresponding to Y and Y_c together to give DNA-mRNA-tRNA-tRNA-mRNA-DNA link providing a memory representation about amino-acid pairing $A_1 - A_2$. One could say that magnetic body creates with the mediation of the genome dynamical tqc programs to which much of the bio-molecular activity reduces. Not all however, since two amino-acid pairs $A_1 - A_2$ and $A_3 - A_4$ can recombine to $A_1 - A_4$ and $A_3 - A_2$ without DNA knowing anything about it. Magnetic body would however know.

5. The constant part of non-hydrogen bonded amino-acid inside protein would behave like Y_cZ_c if amino-acid is coded by XYZ. The $COOH$ end of protein would behave like $X_cY_cZ_c$. Also flux tubes connecting the residue groups become possible and protein does not behave like single nucleotide anymore. By color inheritance everything resulting in the reconnection process between $O=$ and NH_2 and residues reduces in a well-defined sense to the genetic code.

12.2.3 Realization of flux tubes

The basic questions about flux are following. Where do they begin, where do they end, and do they have intermediate plugs which allow temporary cutting of the flux tube.

Where do flux tubes begin from?

The view about magnetic body as a controller of biological body using genome as a control tool suggests that DNA is to a high degree responsible for directed attention and other molecules as targets so that flux tubes emanate from DNA nucleotides. The reason would be that the aromatic cycles of DNA correspond to larger value of Planck constant. Some chemical or geometric property of DNA nucleotides or of DNA nucleotides of DNA strand could raise them to the role of subject. Aromatic cycle property correlates with the symmetries associated with large value of Planck constant and is the best candidate for this property.

If this picture is accepted then also some amino-acid residues might act as subjects/objects depending on the option. Phe, His, Trp, Tyr contain aromatic cycle. The derivatives of Trp and Tyr act as neurotransmitters and His is extremely effective nucleophilic catalyst. This would make possible more specific catalytic mechanisms through the pairing of Phe, His, Trp, and Tyr with residues having flux tube terminals.

This raises the question about the physical interaction determining the color of the strand emerging from the aromatic cycle. The interaction energy of quark at the end of flux tube with the classical electromagnetic fields of nuclei and electrons of the ring should determine this. The wormhole contact containing quark/antiquark at the throat at space-time sheet containing nuclei and electrons could also delocalize inside the ring. One of the earliest hypothesis of TGD inspired model for living matter was that wormhole Bose-Einstein condensates could be crucial for understanding of the behavior of biomolecules [84] . Wormhole throats with quark and antiquark at their throats appear also in the model of high T_c superconductivity [12] . As far as couplings are considered, these wormhole contacts are in many respects analogous to the so called axions predicted by some theories of elementary particle physics. The wormhole contact like property is by no means exceptional: all gauge bosons correspond to wormhole contacts in TGD Universe.

The only manner for the electronic space-time sheet to feed its electromagnetic gauge flux to larger space-time sheets using exactly two wormhole contacts is to use wormhole contacts with $\overline{u}$ and d at their "upper" throat (T, G). For proton one would have $\overline{d}$ and u at their "upper" throat (A, C). The presence of electron or proton at nucleotide space-time sheet near the end of flux tube might allow to understand the correlation. The transfer of electrons and protons between space-time sheets with different p-adic length scale is basic element of TGD based model of metabolism so that there might be some relation.

Acceptors as plugs and donors as terminals of flux tubes?

Standardization constraint suggests that flux tubes are attached to standard plugs and terminals. The explicit study of various biological molecules and the role of water in biology gives some hints.

1. An attractive idea is that $=O$ serves as a plug to which flux arrives and from which it can also continue. For the minimal option suggested by hydrogen bonding $O=$ could be connected to two donors and $O=$ could not be connected to $O=$. The assumption that the flux tube can connect also two $O=$:s represents a hypothesis going outside the framework of standard physics. A stronger assumption is that all acceptors can act as plugs. For instance, the aromatic rings of DNA nucleotides could act as acceptors and be connected to a sequence of $O=$ plugs eventually terminating to a hydrogen bond.

2. Donors such as $O-H$ would in turn correspond to a terminal at which flux tube can end. One might be very naive and say that conscious bio-molecules have learned the fundamental role of oxygen and water in the metabolism and become very attentive to the presence of $=O$ and $O-H$. $=O$ appears in $COOH$ part of each amino-acid so that this part defines the standard plug. $=O$ appears also in the residues of Asp, Glu, Asn, Gln. $O-H$ groups appear inside the residues of Asp,Glu and Ser, Thr.

3. Hydrogen bonds $X-H--Y$ have the basic defining property associated with directed attention, namely the asymmetry between donor X and acceptor Y. Hence there is a great temptation consider the possibility that hydrogen bonds correspond to short flux tubes, that flux tubes could be seen as generalized hydrogen bonds. Quite generally, Y could be seen as the object of directed attention of X characterized by larger value of Planck constant. The assumption that two $O=$:s, or even two acceptors of a hydrogen bond, can be connected by a flux tube means more than a generalization of hydrogen bond the connection with a donor would correspond only to the final step in the sequence of flux tubes and plugs giving rise to a directed attention.

4. This hypothesis makes the model rather predictive. For instance, $N-H$, NH_2, $O-H$ and much less often $C-H$ and $S-H$ are the basic donors in the case of proteins whereas $O=$, $-O-$, $-N=S-S$, $-S^-$ and aromatic rings are the basic acceptors. Reconnection process should be involved with the dynamics of ordinary hydrogen bonding. Reconnection process implies inheritance of the flux tube color and means a realization of the symbol based dynamics. It turns out that this hypothesis leads to a model explaining basic qualitative facts about protein folding.

12.2.4 Flux tubes and DNA

The model of DNA as topological quantum computer gives useful guide lines in the attempt to form a vision about flux tubes. It was assumed that braid strands defined by "wormhole magnetic" flux tubes join nucleotides to lipids and can continue through the nuclear or cell membrane but are split during tqc. The hydrophilic ends of lipids attach to water molecules and self-organization patterns for the water flow in gel phase induce a 2-D flow in the lipid layer which is liquid crystal defining tqc programs at the classical level as braidings. The flow indeed induces braiding if one assumes that during topological computation the connection through the cell membrane is split and reconnected after the halting of tqc.

The challenge is to understand microscopically how the flux tube joins DNA nucleotide to the phospholipid [79] . Certainly the points at which the flux tubes attach should be completely standard plugs and the formation of polypeptide bonds is an excellent guide line here. Recall that phospholipid, the tqc dancer, has two hydrophobic legs and head. Each leg has at the hydrophilic end O=C-O-C part joining it to glyceride connected to monophosphate group in turn connected to a hydrophilic residue R. The most often appearing residues are serine, inositol, ethanolamine, and choline. Only three of these appear in large quantities and there is asymmetry between cell exterior and interior.

Let us denote by $=O_1$ and $=O_2$ the two oxygens (maybe analogs of right and left hemispheres!) in question. The proposal is that DNA nucleotide and $=O_1$ are connected by a flux tube: the asymmetry between right and left lipid legs should determine which of the legs is "left leg" and which $O=$ is the "left brain hemisphere". $=O_2$, the "holistic right brain hemisphere", connects in turn to the flux tube coming from the other symmetrically situated $=O_2$ at the outer surface of the second lipid layer. Besides this $=O_1$ and $=O_2$ are connected by a flux tube serving as switch on both sides of the membrane.

During tqc the short $O=-O=$ flux tube would experience reconnection with a flux tube acting as hydrogen bond between water molecules so that the connection is split and $O=$:s form hydrogen

bonds. The reversal of this reconnection creates the connection again and halts the computation. The lipid residue R couples with the flow of the liquid in gel phase. Since $=O$ is in question the quark or antiquark at the end can correspond to the DNA nucleotide in question. The necessary complete correlation between quark and antiquark charges at the ends of flux tubes associated with $=O_1$ and $=O_2$ can be understood as being due to the minimization of Coulomb interaction energy.

If one is ready to accept magnetic flux tubes between all acceptors then the aromatic rings of nucleotides known to be acceptors could be connected by a flux tube to the $O=$ atom of the lipid or to some intermediate $O=$ atom. The phosphate groups associated with nucleotides of DNA strand contain also $=O$, which could act as a plug to which the flux tube from the nucleotide is attached. The detailed charge structure of the aromatic ring(s) should determine the quark-nucleotide correspondence. The connection line to the lipid could involve several intermediate $O=$ plugs and the first plug in the series would be the $O=$ atom of the monophosphate of the nucleotide.

There is a strong temptation to assume that subset of XYP molecules, $X = A, G, T, C$, $Y = M, D, T$ act as standard plugs with X and phosphates connected by flux tubes to a string. This would make possible to engineer braid strands from standard pieces connected by standard plugs. DNA nucleotide XMP would have flux tube connection to the aromatic ring of X and the $O=$ of last P would be connected to next plug of the communication line. If so, a close connection with metabolism and topological quantum computation would emerge. Phosphorylation would be an absolutely essential for both metabolism and buildup of connection lines acting as braid strands. $O = -O =$ flux tubes could also act as switches inducing a shortcut of the flux tube connection by reconnecting with a hydrogen bond connecting two water molecules. This is an essential step in the model for how DNA acts as topological quantum computer.

This picture would fit with the fact that XYP molecules, in particular AMP, ADP, and ATP, appear in bio-molecules involved with varying functions such as signalling, control, and metabolism. $=O$ might act as a universal plug to which flux tubes from electronegative atoms of information molecules can attach their flux tubes. This would also provide a concrete realization of the idea that information molecules (neurotransmitters, hormones) are analogous to links in Internet [57] : they would not represent the information but establish a communication channel. The magnetic flux tube associated with the information molecule would connect it to another cell and by the join to $=O$ plug having flux tube to another cell, say to its nucleus, would create a communication or control channel.

12.2.5 Introns and DNA-protein attachment

An example is the situation in which protein acts as an enzyme attaching on DNA. Suppose that this process effectively reduces to a base pairing between amino-acid and DNA nucleotide. Protein can attach to any portion of DNA. The simplest interaction is the attachment to the gene coding for the amino-acid itself but much more general enzymatic interactions are possible. It must be however noticed that DNA sequence coding for given amino-acid sequences is considerably longer than amino-acid sequence: the sequence coding for 10 amino-acids is about 10 nm long whereas the corresponding straight amino-acid strand is about 4.7 nm long. It is known that DNA can change its conformation from strand during enzyme-DNA action [124] , and the contraction of DNA strand might make possible to have enzyme-DNA interaction involving fusion along several subsequent amino-acids. This kind of mechanism might work also in the case that attachment region corresponds to several exons. There is however no need to assume that subsequent amino-acids are form a contact with DNA.

One can of course ask whether genes containing introns tend to code for proteins which are used for topological quantum computations. Introns, perhaps the repeating sequences with no obvious function, would have at least this useful function but very probably much more useful ones too (they are now known to be transcribed to RNA and TGD suggest that language corresponds to intronic gene expression). The emergence of introns might be somewhat like the emergence of information society.

The folding of proteins tends to be conserved in the evolution whereas primary structure can change quite a lot apart from some amino-acids critical for enzymatic action. This confirms with the effective base pairing interaction between amino-acids and DNA to be discussed later and would mean that DNA-amino-acid tqc programs are rather robust against mutations.

12.3 Model for the folding code based on interactions mediated by flux tubes between aminoacids

The model for the protein folding to be discussed in this section relies on the hypothesis that dark flux tube connections between amino-acids and their contractions in $\hbar$ changing phase transitions determine the dynamics of the folding. A model in which flux tubes between amino-acids and water molecules alone induce the interactions between amino-acids will be discussed in separate section. A realistic model might involve both kind of flux tubes.

12.3.1 4-D spin glass energy landscape and code of catalytic action

There is a proposal that protein folding corresponds to a motion in a fractal spin glass energy landscape in presence of external perturbations due to the presence of water and leading to the bottom of some deep valley [114, 114] . In TGD framework 3-D spin glass landscape is replaced by 4-D one [62] . The vacuum degeneracy of Kähler action implies 4-D spin glass energy landscape in the sense that quantum jump sequences lead to space-time sheets representing asymptotic self organization patterns depending only weakly on the initial conditions (with respect to subjective time measured as quantum jumps). Proteins would be like skilled musicians possessing a repertoire of motor activities represented by deep valleys in 4-D spin glass landscape.

This picture generalizes to the functioning of living matter in various scales and the quantum dynamics of brain is a natural application giving also connection with p-adicity since ultametric topology is naturally associated with the space of valley bottoms. In the case of catalytic reactions a quantum jump changing Planck constant for some magnetic flux tubes connecting some living biomolecules (DNA, RNA, amino-acids, water(?),..) and changing the lengths of these flux tubes could be the basic mechanism leading from a given valley to a new one and the reduction of the genetic code to single nucleotide or di-nucleotide code would code this quantum jumps.

To me this proposal for the folding code - or rather, the code of entire biocatalysis - looks so beautiful that it deserves to be killedthis should be easy for a professional biochemist. If the hypothesis survives, it would provide a royal road to the understanding of the catalytic bio-chemistry.

12.3.2 Flux tubes and amino-acids

Matter antimatter asymmetry at the level of interactions of amino-acids

The first thing that I learned was that in the case of amino-acid belonging to protein interior second nucleotide Y in the codon XYZ coding for amino-acid is what matters. Only $Y = A, G$ amino-acid residue can form hydrogen bonds and is hydrophilic and thus interacts strongly with water and DNA and RNA. In T, C case the formation of hydrogen bonds is impossible or rare (ser,thr). In their interactions with water these amino-acids are passive, or rather-avoid water- and tend to interact with each other. This division is fundamental for the understanding of the interactions of amino-acids. The division of amino-acids to hydrophobic *resp.* non-hydrophobic ones corresponds to the assignment of quarks to A and G and antiquarks to T and C so that strong matter antimatter asymmetry is in question. Similar asymmetry appears in cosmology: in TGD Universe antimatter resides inside cosmic strings in the interior of big voids containing matter as galaxies at their boundaries so that one can understand why antimatter is not visible.

Flux tubes can connect with all electronegative atoms

The model for dinucleotide precursor code [29] involves precursors for which 3 precursors contain only oxygen ions or double bonded oxygens. The only possible conclusion is that oxygen can connect to any DNA letter (quark or antiquark) and that first letter-precursor correlation is a selection of the most probable alternative. Also in water oxygen atoms should form flux tube contacts with each other and amino-acids and DNA. Also nitrogen atoms might form similar flux tube connections and this was assumed in the model. Same would apply to sulphur appearing in met and tyr and to electronegative atoms in general.

What can one learn from the formation of alpha helices and beta sheets?

Assume that hydrogen bonds correspond to flux tubes. The formation of peptide bonds by the elimination of H_2O-molecules and generation of hydrogen bonds between $N-H$ and $O=$ is an essential step in the formation of alpha helices and beta sheets. Second observation is that free amino-acids decompose naturally into three parts corresponding to $O=COH$, R, and NH_2. One can also count $O=$ as a separate unit so that there would be four units in this case. This suggests that amino-acid could correspond to the entire DNA codon XYZ coding for it. In this case there would be 2 flux tubes per amino-acid and one can consider the following options.

1. Y could correspond to either R or $O=$. If hydrogen bonds correspond to flux tubes, $R-Y$ correspondence is not realistic. The reason is that R should be either donor or accept and hydrophobic amino-acids do not possess neither property. Hence only $O=$ can corresponds to Y.

2. $O-H$ could correspond to Z , $O=$ to Y, and NH_2 to X. For this option the amino-acid in protein would correspond to XY. If one identifies hydrogen bonds as special case of flux tubes, the hydrogen bonds of alpha helix would obey $X-Y_c$ rule which seems too restrictive.

3. $O-H$ could correspond to X , R or $O=$ to Y, and NH_2 to Z. For this option the amino-acid in protein would correspond to YZ. In this case the hydrogen bond of alpha helix would obey $Y=Z_c$ rule which by the isospin symmetry of the last nucleotide of the codon might be flexible enough.

Interactions of proteins with ions and electrons

Proteins interact also with electrons and ions. Typical process are the addition or removal of proton, electron, ion such Ca^{++}, or molecule such as O_2. These interactions are not well understood. For instance, the interactions involve the transfer of electrons between ligand protein and protein inducing oxidation (electron is given), reduction (electron is received) or redox reaction (both reduction and oxidation take place). In metabolism redox process is central. These reactions are reversible and it is difficult to understand how electrons are able make their long journey from the interior of the ligand so fast and avoiding dissipative effects. The formation of cyclotron Bose-Einstein condensates of bosonic ions and electronic Cooper pair condensates at the magnetic flux tubes connecting ligand and protein might provide the solution of the mystery. Note that the new nuclear physics predicted by TGD predicts nuclei which can have anomalous em charge associated with the color fluxtubes connecting nucleons to nuclear string so that fermionic ions Na^+, Cl^-, K^+ could have exotic bosonic counterparts.

12.3.3 Trying to identify the folding code

The basic question is what kind of generalized pairings are realistic for amino-acids. The identification of hydrogen bonds as flux tubes leads to rather unique identification of the pairing and excludes the naively expected $Y-Y_c$ pairing.

A trial for the folding code

Protein folding code is something which is expected to exist but is not understood [199] . This inspired a work which led to several trials for the folding code. Also a natural generalization to a code for catalysis emerged. In the most plausible candidate for the code flux tubes are identified as correlates of directed attention at molecular level. By their asymmetry hydrogen bonds are identified as a special case of flux tubes. Free amino-acid behaves like $X_cY_cZ_c$ and the amino-acid inside protein like Y_cZ_c. There are *two flux tubes* per amino-acid corresponding to $N-H$ and $O=$ representing Z_c and Y_c.

This leaves two options for pairing.

1. If $O=$ can act as a terminal for hydrogen bond and long flux tube then $N-H$ and Y can connect simultaneously to $O=$ and one has $Y=Z$ pairing.

2. If $O =$ can act as a terminal for only single flux tube representing Y then reconnection process for $N - H$ and $O =$ flux tubes creates the hydrogen bond and $Y = Z_c$ pairing for amino-acids results

Both pairings are highly flexible so that obvious inconsistencies with the data about alpha helices and beta sheets are avoided. A highly non-trivial and testable prediction of both pairings is that the two identical proteins coded by different DNA sequences can have different foldings since the allowed pairings are not identical. Thus amino-acids would remember at the level of the braidings which DNA sequence coded them. This prediction can be avoided only Z flux tube corresponds to a quantum superposition of the nucleotides coding for the amino-acid in question so that one has quantum superposition over quark pairs associated with the third nucleotide.

The two-point mutations possibly carried out intentionally by the magnetic body controlling the genome conserving amino-acid pairings by hydrogen bonds and thus perhaps also folding and the catalytic properties should transform $Y = Z_c$ ($Y = Z$) pair to an allowed pair of this kind so that quite wide repertoire of allowed 2-point mutations is available for this option.

$Y = Z_c$ or $Y = Z$ pairing might work

The isospin symmetry of the third nucleotide implies that $Y = Z_c$ pairing is quite flexible. Roughly, the rule would allow flux tube connections only between amino-acids for which Y and Z correspond to quark and antiquark. The amino-acid pairs can be classified to three types. The amino-acid pairs for which both amino-acids can act as acceptors and donors, the pairs for which amino-acids can act only as an acceptor or donor, and the pairs for which no flux tubes are possible.

There are two options to be considered.

Option 1: Flux tube in either direction between amino-acids is prerequisite for the existence of the hydrogen bond. In this case the condition is $Y(n) = Z(n + k)$ or $Z(n) = Y(n + k)$.

Option 2:Hydrogen bond is identified as a flux tube. The condition is $Y(n) = Z(n + k)$ and thus stronger than for the first option.

The following table summarizes the allowed and non-allowed pairings for $Y = Z_c$ and $Y = Z$ pairings. To understand the tables some notation conventions must be introduced.

1. Let X_{ij} denote the amino-acids in i:th and j:th column of the code table. $i, j = 1, 2$ corresponds to hydrophobic amino-acid residues and i, j=3,4 to hydrophilic amino-acid residues.

2. For $Y = Z_c$ option the sets t, T, U, V, W, X are defined as $t = \{phe\}$, $T = X_{12} - t$, $U = \{tyr, his, asn, asp, cys, arg, ser, gly\}$, $V = \{trp, gln, lys, glu, gly\}$, $W = \{gln, lys, glu, trp, arg, gly\}$, and $X = \{tyr, his, asn, asp, cys\}$.

3. For $Y = Z$ option the sets t, T, U, V, W, X are defined as t=$\{$met$\}$, $T = X_{12} - t$, $U = \{trp, gln, lys, glu, arg, gly\}$ $V = \{tyr, his, asn, asp, cys\}$, $W = \{tyr, his, asn, asp, cys, arg, ser, gly\}$, and $X = \{gln, lys, glu, trp\}$. ser has been excluded from V since it appears also in the second column of the code table.

	A and D	*A or D*	*no flux tubes*
$X_{12} \times X_{12}$	$T \times T$	$T \times t$	$t \times t$
$X_{34} \times X_{34}$	$U \times U$	$U \times V$	$V \times V$
$X_{12} \times X_{34}$	$X_{12} \times W$	$T \times X$	$t \times X$

Table 1. General structure of pairings for $Y = Z_c$ and $Y = Z$ options. *A and D* means that both amino-acids can act as acceptors and donors. *A or D* that only acceptor or donor property is possible.

Some clarifying comments about the table are in order.

1. Pro is an exception since Z nucleotide cannot be represented in this case and Pro can act as donor. This has not been taken into account in the tables.

2. The codons coding for the paired amino-acid give additional strong limitations on the pairing unless Z corresponds to quantum superposition of quark pairs associated with the third nucleotide for the codons coding for the amino-acid.

3. Depending on option either phe-phe or Met-Met hydrogen bonding is forbidden so that for hydrophobic amino-acids almost all pairings are possible. This might allow to select between the two options or kill both. The special role of met suggest that $Y = Z$ pairing might be the right option. Also the model for DNA as tqc assumes that $O =$ associated with lipids can act as a plug to which two flux tubes terminate. On the other hand, phe is also exceptional in the sense that it is the only amino-acid in X_{12} which has aromatic ring and can act as an acceptor.
4. The amino-acids which can act simultaneously as donors and acceptors are of special interest as far interactions between catalyst sites of protein and ligand are considered. Second flux tube could be involved with the structure of the catalyst site and second flux tube with the bonding of between catalyst sites. This kind of amino-acids correspond to $T \times T$, $U \times U$, $X_{12} \times W$. For both options hydrophobic amino-acid can be connected with any other hydrophobic amino-acid. In the case that the two amino-acids are connected by two flux tubes one has stronger conditions giving $(Y_1, Z_1) = (Z_2, Y_2)_c$ or $(Y_1, Z_1) = (Y_2, Z_2)$.
5. $T \times t$, $U \times V$, and $T \times X$ correspond to pairings for which amino-acids can act as donor or acceptor only. The triplets abc in which (a, b) belongs to one of these sets should not appear in alpha helices. For instance, for $Y = Z$ pairing hydrogen bonded $xmety$ triplets with x, y in X_{12} should not be possible.
6. The hydrogen bonds of alpha helices and beta sheets provide a test for the model. For instance, the appearance of gly in the hydrophobic portions of alpha helices is consistent with both $Y = Z_c$ and $Y = Z$ pairing. The alpha helix appearing as an example in [124] is consistent with both options.

2. Flux tube is identified as hydrogen bond

The following table summarizes the allowed and non-allowed pairings for $Y(n) = Z_c(n + k)$ and $Y(n) = Z(n + k)$ pairings in this case. The notational conventions are following.

1. Let X_{ij} denote the amino-acids in i:th and j:th column of the code table. $i, j = 1, 2$ corresponds to hydrophobic amino-acid residues and i, j=3,4 to hydrophilic amino-acid residues. Only the sets X_{12} and X_{23} are of interest.
2. For $Y = Z_c$ option the sets t_1, t_2, V, W are defined as $t_1 = \{phe, pro\}$, $t_2 = \{met, pro\}$, $V = \{trp, gln, lys, glu\}$, and $W = \{tyr, his, asn, asp, cys\}$.
3. For $Y = Z$ option the sets t_1, t_2, V, W are defined as $t_1 = \{met, pro\}$, $t_2 = \{phe, pro\}$, $V = \{tyr, his, asn, asp, cys\}$, and $W = \{trp, gln, lys, glu\}$. ser has been excluded from V since it appears also in the second column of the code table.

$A \times D$	*no flux tubes*
$X_{12} \times X_{12}$	$X_{12} \times t_1$
$X_{34} \times X_{34}$	$X_{34} \times V$
$X_{12} \times X_{34}$	$X_{12} \times W$
$X_{34} \times X_{12}$	$X_{34} \times t_2$

Table 2. General structure of pairings for $Y = Z_c$ and $Y = Z$ options. A and D refer to acceptor $(O =)$ and donor $N - H$ respectively. Only non-allowed hydrogen bonded pairs are listed.

Some clarifying comments about the table are in order.

1. The two options are related by the duality $t_1 \leftrightarrow t_2$, $V \leftrightarrow W$. Pro appears in the list because it contains no $N - H$ group and cannot therefore act as donor. The fact that Pro often appears as first amino-acid in alpha helix conforms with this.
2. The codons coding for the paired amino-acid give additional strong limitations on the pairing unless Z corresponds to quantum superposition of quark pairs associated with the third nucleotide for the codons coding for the amino-acid. This could be interpreted as counterpart of wobble base pairing.
3. Met (contains S), pro, and phe (only amino-acid with aromatic ring in X_{12}) are exceptional for both options. $X_{12} \times t_1$ and $X_{34} \times t_2 = O - -(H - N)$ hydrogen bonding is forbidden. This poses strong conditions at the boundaries of hydrophilic and hydrophobic regions.

One might hope that either of these models could give a solution to the basic problem of proteonics whether genes code for the protein folding and how: the apparently lost information in the mapping of codons to amino-acids codes for the folding determined hydrogen bonds and more general flux tubes. The hydrogen bonds of alpha helices and beta sheets provide a test for the model. In absence of quantum counterpart of wobble base pairing for Z both models allows to deduce from the mere aminoacid sequence and hydrogen

bonding the DNA sequence coding for the protein in the case of alpha helices and presumably also beta sheets. This is of course a testable prediction. For non-hydrogen bonded portions of protein this might not be possible and an interesting question is whether they tend to consist of aminoacids in sets t, V and $t \cup X$ so that hydrogen bonds are not allowed. In any case this would mean a solution to the basic problem of proteomics whether genes code for the protein folding and how: the apparently lost information in the mapping of codons to amino-acids codes for the folding determined hydrogen bonds and more general flux tubes.

Tests for $Y = Z$ and $Y = Z_c$ pairings

The test consists of deducing the number N of pairs which did not satisfy the condition $(a(ii), a(ii+4))$ not equal to (t,t), or does not belong to $(V \times V)$ or to $t \times V$). From this the average length L of portions satisfying alpha helix conditions $k = 4$ can be deduced as $L = N/N_{tot}$, where N_{tot} is the number of amino-acids in the sequence.

The test was carried out for one structural unit of asparagine synthetase [8] , xylose isomerase [104] , hydrolase [44] , glutathione s-transferase [39] , and restriction endonuclease BamHI [10] .

1. *Option 1: Flux tube from in direction is prerequisite for the formation of hydrogen bond*

The table below represents the results of the test when flux tube from $Y(n)$ to $Z(n+k)$ or from $Z(n)$ to $Y(n+k)$ is prerequisite for hydrogen bond.

protein	L(3)	L(4)	L(5)	L(6)
asparagin synthethase				
$Y = Z_c$	11.8	15.0	12.2	13.2
$Y = Z$	55.0	47.1	47.1	47.1
xylose isomerase				
$Y = Z_c$	10.2	9.7	12.4	11.3
$Y = Z$	24.8	24.8	16.5	26.4
hydrolase				
$Y = Z_c$	13.8	18.4	16.6	12.8
$Y = Z$	55.3	20.8	33.2	27.7
glutathione s-transferase				
$Y = Z_c$	12.4	12.4	13.1	15.0
$Y = Z$	35.0	35.0	26.3	30.0
BamHI				
$Y = Z_c$	9.7	8.5	10.7	10.7
$Y = Z$	30.4	23.7	30.4	35.5

Table 3. The average number $L(k)$ of aminoacids in the portion of amino-acid sequence satisfying the conditions making possible $(n, n+k)$ hydrogen bonding for $k = 3, 4, 5, 6$ for $Y = Z_c$ and $Y = Z$ option in the case that flux tube can connect $Y(n)$ to $Z(n+k)$ or $Z(n)$ to $Y(n+k)$.

From table 3 one finds that the test for values of k different from $k = 4$ for helix gave also surprisingly large values of $L(k)$ for $Y = Z$ option. The average length of alpha helix is 10 amino-acids so that both options could work. $Y = Z_c$ option gives results rather near to this value.

One can apply test also to individual alpha helices. For asparagin synthethase alpha helices correspond to the intervals [7,28], [76,84], [130,155], [170,177], [76,84], [170,177], [182,194], [256,268], [277,284], [297,305], [309,314], and [320,326] in the standard numbering of amino-acids. The test was done for $k = 3, 4, 5, 6$ assuming that the upper end of tested interval is 6 units higher. $N = (0, 0, 0, 0)$ results for both options for all intervals except for the interval $[7, 28]$ for $Y = Z_c$ for which one obtains $N = (4, 2, 3, 3)$. Hence $Y = Z$ option is favored.

In the case of remaining enzymes only long enough alpha helices were tested and the following table gives the results

alpha helix	$N(Y=Z)$	$N(Y=Z_c)$
xylose isomerase		
[74,93]	(2,1,0,1)(met-lys)	(1,5,1,0)
[111,129]	(0,1,0,1)(asn-asp)	(2,1,0,0)
[159,179]	(0,1,0,0)(asp-tyr)	(5,4,1,3)
[201,223]	(1,1,1,2)(met-tyr)	(4,3,4,3)
[245,255]	(2,0,0,0)	(0,1,1,0)
[278,287]	(0,1,0,0)(his-tyr)	(0,0,0,1)
[314,327]	(0,0,2,1)	(2,0,1,1)
[349,374]	(0,0,4,0)	(3,4,1,2)
[376,386]	(1,0,0,0)	(2,1,1,1)
[393,399]	(0,0,0,0)	(0,0,0,1)
[404,414]	(0,0,0,0)	(1,1,1,1)
[424,435]	(0,0,1,0)	(2,1,2,0)
hydrolase		
[39,50]	(0,0,0,1)	(2,1,2,1)
[60,79]	(0,1,0,0)(asn-asp)	(2,2,3,1)
[93,113]	(1,1,0,1)(val-gly)	(3,0,2,1)
[115,121]	(1,0,0,0)	(0,0,0,0)
[126,134]	(0,0,1,0)	(1,0,0,0)
[143,155]	(0,0,0,0)	(0,0,0,1)
glutathione s-transferase		
[12,24]	(0,0,1,0)	(0,0,0,0)
[65,76]	(0,0,1,0)	(0,1,0,0)
[83,108]	(3,2,3,1)(met-glu-asp)	(0,0,1,0)
[111,134]	(0,0,1,2)	(3,1,4,2)
[150,166]	(1,1,2,0)(asp-leu)	(1,1,1,0)
[174,184]	(0,0,0,0)	(0,0,0,1)
[187,194]	(0,0,0,0)	(0,0,0,0)
BamHI		
[10,18]	(0,0,0,0)	(0,0,0,0)
[20,34]	(0,0,0,0)	(0,1,1,1)
[58,72]	(1,0,1,1)	(0,0,0,0)
[79,84]	(0,0,0,0)	(0,0,0,0)
[117,132]	(0,0,0,0)	(0,0,0,0)
[146,150]	(1,1,0,0)	(0,0,0,0)
[159,169]	(0,0,0,0)	(0,0,0,0)
[200,205]	(0,0,0,0)	(0,0,0,0)

Table 4. The test for alpha helices of four enzymes. The first column gives the range of amino-acids defining the alpha helix in question. The vectors in second and third column give the numbers of failures for $k = 3, 4, 5, 6$ for $(n, n + k)$ helix ($k = 4$ is the most interesting value). The amino-acid-pairs for which the hydrogen bond does not exist for $Y = Z$ option are given.

The conclusions are following.

1. From table 4 it seems clear that $Y = Z_c$ option does not work satisfactorily whereas $Y = Z$ option has rather few failures.

2. In the case of xylose isomerase and $(Y = Z)$ option with $k = 4$ there are four helices for which failure occurs for single aminoacid. The prediction is that the corresponding hydrogen bonds are actually absent.

3. The worst failure occurs for glutathione s-transferase and involves two aminoacids which are at positions n and $n+4$. The hydrogen bonds are predicted to not exist between met-glu and glu-asp in met-glu-asp.

Beta sheets consist of beta strands which can be regarded as $(n, n + 1)$ helices so that stability conditions correspond to $k = 1$. As the table below shows, there are no failures for Y=Z option whereas $Y = Z_c$ option has several failures and very bad failure for glutathione s-transferase (3 failures for 4 units long strand).

beta sheet	$N(Y=Z)$	$N(Y=Z_c)$
asparagin synthethase		
[113,122]	0	2
[233,240]	0	0
[245,255]	0	0
[290,297]	0	3
xylose isomerase		
[43,47]	0	0
[96,100]	0	2
[134,140]	0	1
[262,267]	0	0
[291,295]	0	0
hydrolase		
[14,19]	0	0
[25,28]	0	0
glutathione s-transferase		
[3,7]	0	0
[28,32]	0	3
[54,58]	0	0
[60,63]	0	0
BamHI		
[2,8]	0	0
[46,48]	0	0
[70,72]	0	0
[95,100]	0	0
[105,112]	0	0
[138,144]	0	0
[174,180]	0	0
[183,185]	0	1

Table 5. The test for beta sheets of four enzymes. The first column gives the range of amino-acids defining the beta sheet in question. The vectors in second and third column give the numbers of failures for $k=1$ for $(n,n+1)$ helix.

One might think that loops could contain amino-acids for which the hydrogen bonds to neighbors are not possible. The test for BamHI showed that this is not the case. Only single loop failed for $Y=Z$ option for $k=1,2...,4$ and this occurred for $k=1$.

The remaining test is for whether the $Y=Z$ pairing indeed can fix the DNA sequence completely. BamHI begins as *met glu val glu lys glu phe ile.....* For beta sheet beginning from second amino-acid requires that the Y=Z rules holds true for subsequent codons in DNA sequence *aag ctt cct taa ttc cgg aag ...* [11] . By comparing the Z of a given codon in beta sheet to the Y of the next codon inside beta sheet one finds that the $Y(n)=Z(n+1)$ or $Z(n)=Y(n+1)$ fails. Similar conclusion follows from an analogous check for the first alpha helix. Situation is saved if the quantum counterpart of wobble base pairing is at work so that the flux tube from tRNA to $N-H$ would in superposition of colors (quark pairs) corresponding to superposition nucleotides Z in codons XYZ for given X and Y coding for the amino-acid in question. Hydrogen bonded amino-acid sequence would behave as if it were coded by the unique DNA sequence. Note that for a given amino-acid X is unique except for leu and arg and Y is unique except for ser. The $N-H$:s and O =:s for which hydrogen bonds are lacking could form hydrogen bonds with water molecules and O =:s could have long flux tubes with other O =:s in the protein.

2. Option 2: flux tube is identified as hydrogen bond

The following tables summarize the results of the test for $Y=Z$ and $Y=Z_c$ option when flux tube is identified as hydrogen bond. For the first option the average length of hydrogen bonded interval would be around 5 amino-acids for $k=4$ helix for $Y=Z$ and somewhat shorter for $Y=Z_c$. BamHI is exceptional since in this case the length is 16.8 (10.4) amino-acids. for $Y=Z$ ($Y=Z_c$). There is no clear difference between the two alternatives in the case of alpha helices and neither alternative looks promising in this case.

protein	L(3)	L(4)	L(5)	L(6)
asparagin synthethase				
$Y = Z$	4.5	4.9	4.6	4.9
$Y = Z_c$	4.2	4.7	5.3	4.6
xylose isomerase				
$Y = Z$	3.7	4.3	3.5	3.9
$Y = Z_c$	4.0	3.0	4.1	3.8
hydrolase				
$Y = Z$	5.7	5.1	4.2	4.3
$Y = Z_c$	4.6	5.0	6.1	5.1
glutathione s-transferase				
$Y = Z$	5.1	5.8	4.6	4.0
$Y = Z_c$	4.5	3.6	4.0	4.7
BamHI				
$Y = Z$	11.3	16.8	15.6	12.9
$Y = Z_c$	16.8	10.4	12.1	12.9

Table 6. The average number $L(k)$ of aminoacids in the portion of amino-acid sequence satisfying the conditions making possible $(n, n+k)$ hydrogen bonding for $k = 3, 4, 5, 6$ for $Y = Z_c$ and $Y = Z$ option in the case that flux tube can connect $Y(n)$ to $Z(n+k)$.

alpha helix	$N(Y = Z)$	$N(Y = Z_c)$
asparagin synthethase		
[7,28]	(4,4,4,2)	(6,4,3,5)
[76,84]	(1,0,1,1)	(2,2,1,1
[130,155]	(5,5,4,5)	(2,2,2,1)
[170,177]	(0,0,1,1)	(1,1,1,1)
[182,194]	(1,1,1,1)	(2,2,1,1)
[256,268]	(1,3,0,3)	(3,0,3,0)
[277,284]	(0,0,0,0)	(0,0,0,0)
[297,305]	(0,0,0,0)	(1,0,0,0)
[309,314]	(0,1,0,0)	(2,0,1,0)
[320,326]	(1,1,0,0)	(0,0,0,0)
xylose isomerase		
[74,93]	(6,1,6,4)	(2,5,4,3)
[111,129]	(3,3,4,2)	(4,4,4,3)
[159,179]	(3,4,6,3)	(4,3,1,3)
[201,223]	(3,6,5,4)	(5,7,4,4)
[245,255]	(1,1,1,1)	(0,1,0,0)
[278,287]	(2,1,1,0)(his-tyr)	(0,0,0,1)
[314,327]	(1,2,3,3)	(2,3,2,2)
[349,374]	(4,3,8,6)	(5,8,1,3)
[376,386]	(4,0,2,3)	(1,4,3,0)
[393,399]	(0,0,0,0)	(1,0,0,0)
[404,414]	(1,1,2,1)	(3,3,1,1)
[424,435]	(1,2,0,2)	(3,2,3,1)
hydrolase		
[39,50]	(2,3,0,2)	(2,1,3,1)
[60,79]	(4,2,2,4)(asn-asp)	(4,4,5,2)
[93,113]	(2,1,4,4)(val-gly)	(3,2,1,1)
[115,121]	(0,1,0,0)	(0,1,0,0)
[126,134]	(0,1,1,1)	(1,0,0,0)
[143,155]	(0,1,1,1)	(1,0,1,1)
glutathione s-transferase		
[12,24]	(1,4,2,4)	(5,2,3,1)
[65,76]	(3,1,1,0)	(2,1,1,1)
[83,108]	(5,3,5,5)	(5,3,3,2)
[111,134]	(4,5,5,4)	(4,5,3,3)
[150,166]	(2,2,3,0)(asp-leu)	(4,3,1,3)
[174,184]	(0,0,0,0)	(1,1,1,1)
[187,194]	(1,1,0,1)	(0,2,0,1)
BamHI		
[10,18]	(0,0,0,0)	(0,0,0,0)
[20,34]	(4,1,1,2)	(2,5,4,2)
[58,72]	(3,1,2,4)	(3,5,4,1)
[79,84]	(0,0,0,0)	(0,0,0,0)
[117,132]	(0,0,0,0)	(0,0,0,0)
[146,150]	(1,1,0,0)	(0,0,0,0)
[159,169]	(0,0,0,0)	(0,0,0,0)
[200,205]	(0,0,0,0)	(0,0,0,0)

Table 7. The test for alpha helices of four enzymes in the case of $Y(n) = Z(n+k)$ option. The first column gives the range of amino-acids defining the alpha helix in question. The vectors in second and third column give the numbers of failures for $k = 3, 4, 5, 6$ for $(n, n + k)$ helix ($k = 4$ is the most interesting value).

beta sheet	$N(Y=Z)$	$N(Y=Z_c)$
asparagin synthethase		
[113,122]	1	5
[233,240]	3	0
[245,255]	1	0
[290,297]	0	1
xylose isomerase		
[43,47]	0	1
[96,100]	2	4
[134,140]	2	0
[262,267]	2	1
[291,295]	0	1
hydrolase		
[14,19]	1	2
[25,28]	0	0
glutathione s-transferase		
[3,7]	0	1
[28,32]	1	3
[54,58]	4	1
[60,63]	0	0
BamHI		
[2,8]	0	0
[46,48]	0	0
[70,72]	2	0
[95,100]	0	0
[105,112]	4	0
[138,144]	0	0
[174,180]	0	0
[183,185]	1	2

Table 8. The test for beta strands of four enzymes for $Y(n) = Z(n+1)$ option. The first column gives the range of amino-acids defining the beta sheet in question. The vectors in second and third column give the numbers of failures for $k = 1$ for $(n, n+1)$ helix.

Are $= O - O =$ flux tubes present?

$Y = Z$ option for the folding code assumes that flux tubes can connect acceptor atoms by flux tubes. The pairing would be $Y - Y_c$ pairing considered in the original model as the only possible pairing. In amino-acids only $O =$:s not acting as acceptors for ordinary hydrogen bonds could have flux tube connections of this kind with each other or other molecules.

1. In the case of amino-acids $Y - Y_c$ pairing would be between amino-acid in X_{12} and amino-acid in X_{34} part of the code table. These connections would be typically associated with the portions of the protein between alpha helices and beta sheets. The $k:th$ amino-acid ($k = 3, 4$ or 5) following Pro would be an exception to this rule and this kind of flux tubes could be involved with the long scale stabilization of proteins.
2. The $O =$ atom would effectively behave like Y_c. Depending on whether it corresponds to quark or anti-quark, the corresponding amino-acid would be typically hydrophilic or hydrophobic- or rather - able to form hydrogen bonds or not. Since hydrophilic and hydrophobic residues tend to avoid each other the flux tubes in question should be rather long. The phase transitions increasing Planck constant might make this possible. This would bring in a strong long range correlation between the dynamics of the amino-acid residues belonging to the first and third (second and fourth) column of the code table.
3. $= O - O =$ flux tubes could be also between different proteins. In the case of protein-ligand complex the Planck constant changing phase transition reducing the length of this kind of flux tube could bring proteins together after which a recombination process the hydrogen bond connecting two water molecules would transform the bond to hydrogen bonds of $O =$:s with water molecules.
4. The phase transition increasing $\hbar$ would allow hydrophobic amino-acids to increase their distance from water molecules in a controlled manner. This could be essential for folding and make possible the

formation of pockets connected by flux tubes of large $\hbar$ to water. In quantum models for evolution of consciousness these pockets are believed to play a prominent role. Molecular sex in this sense would mean a correlation tending to keep partners at large distance except when $\hbar$ reducing phase transition occurs.

Evolution and amino-acid pairings

The evolution at the molecular level corresponds to the emergence of increasingly complex molecules using as basic building blocks amino-acid chains and non-translated residues attached to them in the post-translational processing of the amino-acid chains. Also increasingly complex reaction paths emerge. Molecular survival and the competition for the metabolic resources at molecular level could be seen as the basic driving force of this evolution.

Typically, in the original situation the enzymes would have received the substrate molecules from the environment but sooner or later this would have become difficult. The solution would have been a synthesis of the substrate from simpler ingredients by starting from some precursor.

If molecules (with magnetic bodies included) are conscious entities able to direct attention, one can imagine that magnetic body controlling them with the mediation of genome and able to actively modify it, could help through modifications of the genome to create to the catalyst a binding site able to bind the precursor. Immune system is doing this very intensively. If the enzyme binding the precursor already exists, a combination of genes coding for the enzyme and the enzyme having the metabolites as ligands could allow to achieve this. All this would reduce to the motor activities of magnetic body, in particular reconnection of flux tubes, a kind of dance of Shiva. Genome would not be anymore a sequence of DNA developing through random mutations under selection pressures.

In this framework amino-acids would have appeared before their precursors and possessed some function in RNA world, say the catalysis of join of RNA_2 dinucleotides to the increasing chain as proposed in [29] . Competition might have led to a situation in which RNA_2 learned to catalyze selectively the generation of amino-acids from much simpler precursors (three of the proposed precursors contain only C, $=O$, and O^-) giving rise to positive feedback implying an exponential amplification of RNA and amino-acid populations. The reduced genetic code would have been present at two levels. The reader can decide whether this is a shortcoming of the model or a fundamental biochemical duality.

Can one make any clear cut predictions about preferred mutations?

1. In TGD framework mutations are not expected to be always random point mutations but could be even a result of a purposeful action of the magnetic body. Chemical similarity is expected to be conserved in good mutations. This is known to be the case. For $Y = Z$ or $Y = Z_c$ pairing the simplest mutations should leave both Y and Z invariant so that only the first nucleotide X can suffer a mutation.

2. Also bi-local mutations of the second and third nucleotides of codons forming $Y = Z$ ($Y = Z_c$) pair and conserving this property might occur and could be crucial for the coherence of the organisms. As found, the formation of flux tube between amino-acids A_1 and A_2 induces a flux tube between nucleotides Y and Z at the corresponding genes. This flux tube could force the possibly intentional mutations to occur as simultaneous mutations of the two genes so that $Y = Z$ ($Y = Z_c$) condition remains true for amino-acids connected by flux tube.

3. A new element is that isospin rotation of Z nucleotide ($A \leftarrow G$, $T \leftarrow C$) which does not affect amino-acid, affects its folding so that same protein might have different folding patterns and different catalytic properties corresponding to different codons coding for it. This would mean a breaking of the central dogma a the level of magnetic body. Some examples are in order. The mutations Ala/Ser, Ser/Thr, Ile/Val/Leu, Asp/Glu do not change Y. Lys/Arg (A/G)), Tyr/Phe (A/U), gly/Ala (G/C),... are also prevalent and one might hope that they correspond to binary mutations in some important cases.

4. Folding is known to be more conserved than amino-acid sequence [124] . Since folding is a collective property of gene, local chemistry might not be enough and the proposed non-local conservation laws might be needed. Two-point mutations would also correlate the mutations of the binding sites of protein and ligand. For the model assuming two flux tubes per amino-acid, the prediction would be conserved $Y = Z$ ($Y = Z_c$) pairs in genes coding for protein and ligand and these pairs might allow to deduce the paired points. This is consistent with the fact that hydrophobic (-philic) regions tend to be paired in the protein-ligand complex. The paired nucleotides need not belong to the same strand since genes are evenly distributed between strand and its conjugate and characterized by A,G surplus.

5. If the flux tubes can connect also side chains, the situation becomes more complex. There is a temptation to think that these flux tubes would connect only the nearby amino-acids of the same peptide and do not therefore affect the large scale dynamics of folding. This would be the case if the value of Planck constant associated with these flux tubes is smaller than for the flux tubes connecting amino-acids as basic units. If flux tubes can begin from the aromatic side chains, the replacement of an aromatic side

chain with an aromatic side chain is favored (also chemical similarity explains this). The most basic facts about folding do not provide obvious support for the idea about flux tubes between residues.

i) Hydrophobic residues tend to cluster in dense packing in protein interior (antimatter at quark level) and Val (T), Leu (T), Ile (T), Phe (T), Ala (C), and gly (G) make 63 percent of the interior of protein: the special role of gly (matter rather than antimatter at quark level) is due to the reduction of the side chain to hydrogen atom.

ii) Asp (A), Glu (A), Lys (A) and Arg (G) with ionized residues are mostly at the surface of protein and make 23 per cent of protein surface and 4 per cent of interior. As noticed earlier, matter and antimatter at quark level tend to be far from each other. This is consistent with $Y = Z$ pairing between nearby amino-acids and absence of flux tubes between matter and antimatter if there are two flux tubes per amino-acid.

iii) Polar groups tend to be paired by hydrogen bonds and oppositely charged groups tend to be near each other. Acidic Cys residues tend to be in positions where they can form $S - S$ bonds. This can be explained as being induced by $Y - Y$ pairing in the proposed scenario. Aromatic residues tend to have favorable electrostatic interactions with each other and with S, O and amino groups.

12.4 A simple quantitative model for protein folding and catalyst action assuming flux tubes between amino-acids

Levinthal paradox states that if protein folding is a process in which protein checks for all possible conformations, folding would take astrophysical time. Small single domain proteins with lengths below 100 residues however fold in single step in millisecond time scale and longest folding times are measured in days. This suggests that protein folding is in some sense guided dynamical process and flux tubes would be the natural guides.

It is possible to construct a simple quantitative model for protein folding and catalyst action assuming a long range interaction mediated by flux tubes between amino-acids obeying base pairing rule in some sense. A further assumption is that hydrogen bonds correspond to flux tubes. There are two options to consider.

1. If there is only single flux tube per amino-acid the rule implies that conjugate amino-acids are connected by a flux tube: this is conflict with the empirical facts.
2. If there are two flux tubes per amino-acid base pairing predicts that amino-adic pairing obeys $Y = Z$ or $Y = Z_c$ rule depending on whether $O =$:s can act as intermediate plugs for flux tubes or not.

The model is consistent with quantum criticality, and the general vision about 4-D spin glass landscape. The extremals are not completely deterministic just as vacuum extremals of Kähler action and only absolute minimization of energy selects minima. The cautious interpretation is that absolute minimization of energy stabilizes various unstable patterns generated spontaneously by ordinary chemical interactions such as alpha helices and beta sheets. The interpretation of hydrogen bond in terms of flux tube suggests more bold interpretation.

The principle is flexible enough to carry out this purpose but also poses strong constraints on how these patterns integrate to higher level structures. The disappearance of a subset of flux tubes does not spoil the extremal property although it increases its non-determinism and makes folding less predictable and in the case of binding sites it reduces the selectivity of catalyst action. The interpretation would be in terms of molecular ageing. The density of flux tubes can be seen as an analog for the resolution of quantum measurement which is in a fundamental role in quantum TGD, as well as a direct correlate for cognitive and sensory resolutions. The model extends to a model of catalyst dynamics if one the relative motion of reactant molecules is slow in the time scale of folding dynamics so that adiabaticity assumption makes sense. In the following I often use the basic data which can be found from [124] without explicit reference.

12.4.1 The model

Let us assign potential energy to the flux tube connecting i:th and $k(i)$:th amino-acid and depending only on the distance $r_{i,k(i)}$. What comes in mind first is the potential energy of harmonic oscillator:

$$V(r) = \frac{kr^2}{2} . \tag{12.4.1}$$

$k > 0$ corresponds to harmonic oscillator. Also $k < 0$ is possible in which case the distance between amino-acid and its conjugate tends to be maximized in equilibrium: this option turns out to be the more plausible one and conforms also with the notion of quantum criticality. Besides this there is the constraint that the distances

between amino-acid and its follower are constant: $r_{i+1,i} = R$. Using Lagrange multipliers this gives rise to the action

$$L \quad = \quad -E = -\frac{k}{2}\sum_i r^2_{i,k(i)} + \sum_i \lambda_i r^2_{i+1,i} \quad . \tag{12.4.2}$$

Energy is the negative of this action for static solutions. One could consider also adding kinetic term to this action to describe the dynamics of folding. This action is hoped to give only a qualitative view about folding and the ordinary chemical interactions should fix the details of the folding and select between different folding patterns. Several amino-acid chains could be present and have mutual long range interactions.

If $N-H$ and $O=$ both can be connected by flux tubes, each amino-acid gives two terms to the energy corresponding to the flux tube beginning from $N-H$ and flux tube ending at $O=$.

The extremals of this action satisfy

$$\frac{\partial L}{\partial r^k_i} \quad = \quad 0 \quad , \quad i = 1, ..., N \quad . \tag{12.4.3}$$

1. If there is only *single flux tube per amino-acid*, this gives the conditions

$$\begin{aligned} \lambda_{i+1}\overline{r}_{i+1,i} - \lambda_{i-1}\overline{r}_{i,i-1} &= -k\overline{r}_{i,k(i)} \quad , \\ r_{j+1,j} &= R \quad . \end{aligned} \tag{12.4.4}$$

   The geometric content of these conditions is that the vectors $\overline{r}_{i,k(i)}$, $\overline{r}_{i+1,i}$, and $\overline{r}_{i,i-1}$ are in the same plane.

2. If there are *two flux tubes per amino-acid* ($= O_i - -(N-H)_{k_1(i)}$ and $(N-H)_i - -(O=)_{k_2(i)}$)

$$\begin{aligned} \lambda_{i+1}\overline{r}_{i+1,i} - \lambda_{i-1}\overline{r}_{i,i-1} &= -k[\overline{r}_{i,k_1(i)} + \overline{r}_{i,k_2(i)}] \quad , \\ r_{j+1,j} &= R \quad . \end{aligned} \tag{12.4.5}$$

   In this the resultant of the vectors $\overline{r}_{i,k_1(i)} + \overline{r}_{i,k_2(i)}$ would be in the plane determined by $\overline{r}_{i+1,i}$ and $\overline{r}_{i,i-1}$. Note that due to the lack of $N-H$ in Pro it can happen that there is only single flux tube per amino-acid.

Long range interactions of amino-acids with their conjugates would dictate the local folding of the amino-acid chain but extremum property alone does not say much about the lengths of the flux tubes.

Suppose that $\overline{r}_i$, $\overline{r}_{i,k(i)}$, $\overline{r}_{i,i-1}$, λ_{i-1} are known. Can one solve λ_{i+1} and $\overline{r}_{i+1,i}$? Since the vectors are in the same plane, the linear dependence does not fix the direction of $\overline{r}_{i+1}$ in this plane but only the value of λ_i in this plane once $\overline{r}_{i+1}$ is fixed or vice versa. Therefore the direction in the plane remains un-determined and equations of motion are not fully deterministic as far as extremals are considered. Absolute minimization however eliminates this non-determinism by maximizing the distances $r_{i,i(k)}$ for $k > 0$ option. The expressions for λ_i result from elementary linear algebra by introducing dual basis of non-orthogonal basis defined by $\overline{r}_{i,k(i)}$ and $\overline{r}_{i,i-1}$.

1. In the case that there is *single flux tube per amino-acid*, one has

$$\begin{aligned} &\lambda_{i+1} = -k\overline{e}_{i+1}\cdot\overline{r}_{i,k(i)} \quad , \quad \lambda_{i-1} = -k\overline{e}_{i-1}\cdot\overline{r}_{i,k(i)} \quad , \\ &\overline{e}_{i+1}\cdot\overline{r}_{i+1,i)} = 1 \quad , \qquad \overline{e}_{i+1}\cdot\overline{r}_{i,i-1)} = 0 \quad , \\ &\overline{e}_{i-1}\cdot\overline{r}_{i+1,i)} = 0 \quad , \qquad \overline{e}_{i-1}\cdot\overline{r}_{i,i-1)} = 1 \quad . \end{aligned} \tag{12.4.6}$$

   The non-determinism does not make it easy to find absolute minimum since non-determinism corresponds to circle $(S^1)^{2N}$ for amino-acid sequence with N flux tube pairings. These conditions do not make sense when $\overline{r}_{i+1,i)}$ and $\overline{r}_{i,i-1)}$ are parallel: in this case the force must be parallel to $\overline{r}_{i+1,i)}$.

2. For *two flux tubes per amino-acid* one has a slightly more complex expression for these conditions:

$$\begin{aligned} &\lambda_{i+1} = -k\overline{e}_{i+1}\cdot[\overline{r}_{i,k_1(i)} + \overline{r}_{i,k_2(i)}] \quad , \quad \lambda_{i-1} = -k\overline{e}_{i-1}\cdot[\overline{r}_{i,k_1(i)} + \overline{r}_{i,k_2(i)}] \quad , \\ &\overline{e}_{i+1}\cdot\overline{r}_{i+1,i)} = 1 \quad , \qquad \overline{e}_{i+1}\cdot\overline{r}_{i,i-1)} = 0 \quad , \\ &\overline{e}_{i-1}\cdot\overline{r}_{i+1,i)} = 0 \quad , \qquad \overline{e}_{i-1}\cdot\overline{r}_{i,i-1)} = 1 \quad . \end{aligned} \tag{12.4.7}$$

The strong resemblance with the dynamics defined by Kähler action predicting spin glass degeneracy associated with vacuum extremals of Kähler action and removed by small deformations to non-vacuum extremals raises the hope that the model indeed catches something essential about the notions of 4-D spin glass degeneracy and quantum criticality.

12.4.2 Basic mathematical consequences

Consider first the basic consequences of the variational equations.

1. Absolute minimization of energy is very powerful selection principle and expected to choose highly symmetric configurations such as α helices, β sheets, and more complex structures. If combined with adiabaticity assumption it could also allow to understand the dynamics of binding between two proteins and protein and DNA/RNA.

2. The extremals of $k > 0$ action are mirror images of $k < 0$ action so that the energy minimum for $k > 0$ is energy maximum for $k < 0$. If energy minimization is applied also the choice of $Y - Y$ flux tubes, the connected amino-acids should be as near as possible which favors alpha helices and beta sheets. In light of this $k > 0$ option looks the realistic one. It could however be that for large distances the sign of the potential energy changes. For $k > 0$ option long flux tubes are not favored by energy minimization. The simplest cure would be large value of Planck constant changing the scale of the potential. If the potential energy changes sign at large distances the situation changes also and $r_{i,k(i)}$ would be as large as possible subject to the condition from fixed chain length.

3. If the amino-acid is not paired, it does not experience the long range force and one has

$$\lambda_{i+1}\overline{r}_{i+1,i} - \lambda_{i-1}\overline{r}_{i,i-1} \quad = \quad 0 \ . \tag{12.4.8}$$

   Situation becomes non-deterministic and the portions of the amino-acid chain for which the amino-acids do not have a pair behave like random coils. This is encouraging since this kind of portions are present in folded amino-acids. The absence of $N - H$ from Pro allows to understand the very special role of Pro as being associated with turns of alpha helices and beta sheets.

4. The disappearance of some flux tubes does not destroy a given solution of the conditions but makes it increasingly non-deterministic. The interpretation as a degradation or ageing at molecular level conforms with the interpretation of braiding as a basic characteristic of life. An attractive interpretation of the density of flux tubes is as correlate for resolution for cognition and sensory perception and motor action as counterpart of measurement resolution which is fundamental notion of quantum TGD.

12.4.3 Model for the helical structures

α helix [124, 6] , which is only one member of a rich family of helical structures possible for amino-acid chains, serves as the first test for the model. As a matter fact, the specific properties of α helix are not relevant for the model discussed.

1. α helix has nearly vertical $NH - - - O =$ hydrogen bond between i:th and $i - 4$:th amino-acid. Also $(i, i-3)$ and $(i, i-5)$ bondings are possible. There are 3.6 residues per turn so that the basic structural unit has 5 turns and consists of 18 amino-acids. One residue corresponds to a vertical translation of 1.5 Angstrom. The chain contains single amino-acid per length of about 3.8 Angstrom and the angular separation of subsequent amino-acids is 100 degrees in the planar projection.

2. Isolated α helices are not stable but can be stabilized by secondary coiling: their lifetime is of order $10^{-5} - 10^{-7}$ seconds. If the flux tubes are associated with hydrogen bonds, the instability would be naturally due to a reconnection process involving water molecules.

Consider now the model.

1. Assume that hydrogen bond is accompanied by a special case of a flux tube resulting in the reduction of the value of Planck constant. Short flux tubes (hydrogen bonds) would connect $i - k$:th, i:th and $i + k$:th amino-acids, $k = 3, 4$ or 5. The forces between $i - k$:th and i:th and i:th and $i + k$:th amino-acid compensate each other exactly for an ideal helix so that the conditions are satisfied identically. This kind of mechanism work also for more general helices. $Y = Z$ ($Y = Z_c$) pairing poses special conditions on the helical structures themselves and also on the genes coding for these structures.

2. gly helices are consistent with both $Y = Z$ and $Y = Z_c$ pairings. The spontaneous generation of unstable helices in sequences consisting of mere gly could be understood as the instability of gly-gly flux tubes against reconnection with hydrogen bonds connecting surrounding water molecules. Also the sequences

consisting of mere Pro can give rise to unstable helices. Pro does not possess $N-H$ and the residue cannot act as a donor in hydrogen bond. This suggests that the residue of Pro can have flux tubes connecting it to $O=$ but not identifiable as ordinary hydrogen bond.

There are also more complex structures formed form helices [124] . For coiled coils of two or more alpha helices consisting of repeating heptad unit of 7 amino-acids first and fifth amino-acids tend to be conjugates so that horizontal flux tubes connecting first and fifth amino-acids of neighboring could be responsible for the stability and make also possible the hydrophobic bonding between first and fourth residues. Collagen [25] is a triplet helix and appears as a basic constituent of bones, tendons, skin, ligaments, blood vessels, and supporting membraneous tissues. The units of collagen triple helix consists of very long repetitive sequences of type $(gly-XY)_n$, with a preponderance of Pro for X (also Lys residues are possible). gly-Pro-Y and gly-X-Hyp appear often: here X and Y are arbitrary amino-acids (Hyp denotes hydroxyprolin with $O=$ replaced with OH: this transforms Pro from acceptor to donor). Heating of collagen triple helix unfolds it and converts it to gelatin, in which polypeptide chains are dissociated, unraveled and disordered. Cooling regenerates these conformations for short stretches.

Consider as a example collagen triplet helix [25] having $gly-Pro-Y$ as a repeating unit. Assume $Y=Z$ or $Y=Z_c$ pairing. $Y-Y$ hydrogen bonds are possible if Y belongs to the group T or U. Only phe ($Y=Z_c$) or met ($Y=Z$) is excluded from T. $Y=Z_c$ corresponds to $U=\{tyr, his, asn, asp, cys, arg, ser, gly\}$ and $Y=Z$ to $U=\{trp, gln, lys, glu, arg, gly\}$. This prediction might kill the model. glys can be connected for both options.

1. The first model goes like follows. Alpha helix structure is guaranteed by hydrogen bonds between the Y:s inside each collagen unit ($k=3$). The amino-acids gly_i, $i=1,2,3$, are connected by almost horizontal flux tubes cyclically as gly_1-gly_2, gly_2-gly_3, gly_3-gly_1. This cyclic bonding would induce the coiling of alpha helices. The free $O=$:s of Pros could act as acceptors in the hydrogen bonds with the surrounding water molecules (for instance). For gly-X-Hyp one would have similar structure but Hyp would act as donor in the hydrogen bonds with water molecules. The objection is that if long hydrogen bonds are possible they would have been observed.

2. Second model is based on the philosophy that coiling is a long range effect and must be due to $=O-O=$ flux tubes. gly ($Y=G$) and Pro ($Y=C$) can be connected for both options but only by single flux tube by the special properties of Pro: this bonding would give $n, n+4$ hydrogen bond of alpha helix. The simultaneous presence of $n, n+3$ $Y-Y$ bonds and $n, n+4$ pro-gly bonds might be made possible by coiling. Hence the free $O=$ in gly could be connected with a similar $O=$ in the neighboring strand. gly_1-gly_2, gly_2-gly_3, gly_3-gly_1 cannot form a closed cycle but the repeating helical pattern gly_1-gly_2, gly_3-gly_1, gly_2-gly_3 is possible and could produce the coiling.

12.4.4 Model for β sheets

Beta strands are typically 4-5 amino-acids long structures. Hydrogen bonds are of type $(n, n+1)$ and β strands have 2 amino-acids per turn so that $\overline{r}_{i-1,i}$ and $\overline{r}_{i,i+1}$ span a vertical plane and the equations of the model are trivially satisfied. Beta strands as such are not stable. Beta sheets [13] consisting of β strands which can be either parallel or antiparallel and are glued together by the interactions between residues. Beta sheets are also slightly twisted which relates to the chirality of amino-acids. In the antiparallel case strand returns back and forms at the ends of sheet a loop so that so called β hairpin is formed. In parallel case the strand returns as alpha helix to the lower end of the sheet. At the time of writing of [124] the mechanism of formation of β sheets was not understood.

If horizontal flux tubes between neighboring strands assignable to hydrogen bonds or =O-O= flux tubes between the residues are responsible for the stabilization of the beta sheet structure, then given residue must have two hydrogen bonds with same length to the amino-acids at right and left so that the contributions from right and left side to the force compensate each other and the force is automatically vertical as implied by the twisting angle of π per amino-acid in beta sheet. For self connecting flux tubes inside loops the force would be in the plane of loop and if the force is repulsive loop like structure is expected.

The slight twisting of beta sheet represents a challenge for the model. TGD predicts large parity breaking and thus the twisting and preferred helicity at the level of principle but it is not clear whether the simplest model can explain the twisting.

12.4.5 Secondary protein structures

Protein structures are divided into four classes on basis of their secondary structures [124, 90] . All these structures are consistent with the general model.

1. (α) containing only α helices, which must stabilize each other by horizontal flux tubes.

2. (β) containing only β sheets both usually antiparallel, which appear always in pairs packing against each other. Horizontal flux tubes connecting the β sheets must act as stabilizers.
3. ($\alpha + \beta$) proteins can contain only single β sheet, usually antiparallel, with α helices clustering together at one or both ends of the β sheet. Antiparallel β sheet stabilizes itself.
4. (α/β) in which sheets and helices interact and often alternate along the polypeptide chain. Single parallel β sheet and so called β barrel, kind of sandwich like structure, are basic examples here. The most spectacular barrel consists of 4+4 parallel β strands with α helices outside the barrel.

Concerning the organization of alpha helices and beta sheets to higher level structures the simplest guess is that the large Planck constant flux tubes connecting random coil portions of the amino-acid sequence with each other or with free $O =$ accompanying Pros. The mere assumption that a given portion of coil has only long flux tubes to distant parts of the protein could explain random coil character. The failure of $Y = Z$ condition implies this too. The notion of long hydrogen bond is somewhat questionable and long flux tubes connecting $= O$:s look more favorable. Also free $O =$:s inside alpha helices and beta strands could be connected in this manner.

12.4.6 Model for protein-protein binding sites

Binding sites obey geometric complementarity and are known to resemble protein interior being closely packed. This is also taken to mean that amino-acid chains run parallel to the surface although this statement is not made explicitly in [124] : one could see binding sites as part of interior which is in a direct contact with exterior, somewhat like a sensory organ like eye. The interface between similar sized proteins is large and tends to be flat (not expected if proteins make sharp turns at the interface rather than running parallel to the surface). Various bonds eliminate electromagnetic interactions at the interface.

The basic mechanism of binding would be based on the reduction of Planck constant for the flux tubes connecting amino-acids. The high flexibility of $Y = Z$ and $Y - Z_c$ pairings -especially in the hydrophobic regions in the center of the binding site where it allows all but met-met and phe-phe flux tubes- makes it an excellent candidate for a folding code.

The question is whether complementary of bonded amino-acids should induce the geometric complementary of the binding sites in the proposed model.

1. The binding sites could be connected by only very few flux tubes or flux tubes could connect all amino-acids in a pairwise manner: the first extreme is highly flexible whereas second extreme would produce maximal selectivity. Complementary can thus be partial and its degree is predicted to correlate with the selectivity. The interpretation of disappearance of flux tubes as molecular ageing conforms with the gradual loss of selectivity implying reduced performance of immune system.
2. From the example of [124] about the interface of identical proteins in the quaternary structure of dimer one learns that the geometrically and physically conjugate interfaces of identical monomers pair to form sandwich like structures via so called isologous and heterologous pairings such that valleys and hills fit. The interfaces are reported to resemble closely packed protein interiors and contain hydrophobic residues in the center and hydrophilic residues at periphery. In the case of identical monomers $Y - Z$ and $Y - Z_c$ pairing is possible for a very wide class of amino-acids. The prediction in the case of identical monomers would be that catalyst sites contain only very few amino-acids in the sets V and t defined previously.
3. Also the flux tubes between $= O$ atoms could be in key role in the protein-ligand interaction. The interfaces can be thought of as cutting protein along its interior: in center there are hydrophobic amino-acids and in periphery hydrophilic ones. The $= O - O =$ flux tubes would connect periphery of A (B) to the center of B (A). The reduction of Planck constant for would reduce the length of these flux tubes and bring protein and ligand close to each other so that hydrogen bond formation between residues could being. In this process the flux tube connecting $O =: s$ could by reconnection transform to two hydrogen bonds connecting $O =$:s to water molecules. After the catalysis the reverse of this process would occur.
4. For single flux tube between $O =$:s of amino-acid and ligand the force would be along the line $r_{i,k(i)}$ connecting them, In the improbable case that the amino-acids of protein and ligand are connected by *two* hydrogen bond like flux tubes the force is in the direction of $\overline{r}_{i,k_1(i)} + \overline{r}_{i,k_2(i)}$. The force is predicted to be in the plane spanned by $\overline{r}_{i+1,i}$ and $\overline{r}_{i,i-1}$ for protein and in the corresponding plane for ligand. This is true if the amino-acid sequence at the surface is slightly curved in the direction of the conjugate amino-acid or in opposite direction. This condition is guaranteed by the geometric complementarity.
5. The mechanism for the formation of ligand-protein pairs would be very simple: the binding sites of protein and ligand could be coded by same gene or its mutation respecting the Y so that the formation of copies of gene in DNA would be the simplest mechanism to guarantee the prerequisites for geometric

conjugation. Geometric conjugation would result automatically if the flux tubes between interior and periphery of binding site determine its shape.

6. Slow enough relative motion of molecules induces an adiabatic variation of the shapes of the binding sites so that lock and key mechanism becomes dynamical. The simplest possibility is that binding site and its conjugate behave like two eyeballs gazing each other as proteins move with respect to each other. This is possible if binding sites are separated from the rest of the protein by random pieces of chain. The analogy with eye might be actually deeper: I have proposed long time ago that directed attention in vision has as a space-time correlate flux tubes of topological light rays or both of these. Wormhole magnetic flux tubes might indeed connect perceiver and the object perceived and serve as correlates of attention in macroscopic length scales.
7. Also the hydrogen bonds between residues are important for the protein folding. The donor atoms of the residues can inherit the conjugate of the color of $O =$ and acceptor atoms can inherit the color of $N - H$ by temporary reconnection. Therefore also the hydrogen bonds between residues of hydrophilic residues containing both donor and acceptor atoms would be restricted by the colors of atoms and would reflect genetic code.
8. Geometric and physical conjugation (acids and basics combine in the interface) means that a virtual protein A+B is cut to pieces along the surface in the interior defining the interfaces. Could this chopping of bigger proteins to smaller ones able to bind allow a realization at the level of genome in the sense that glued portions of protein would originate from same gene or its reversed version and thus satisfy $Y = Z_c$ or $Y = Z$ rule approximately? Could also protein interior involve pairings analogous to catalyst and ligand pairings? This would partially explain why protein folding is more sensitive to the mutations in the interior of protein.

12.5 A model for protein folding based on flux tubes connections between water molecules and amino-acids

The overall feelings about the model just discussed are somewhat mixed.

1. The ideas about flux tube as a correlates for a directed attention and about the connection between hydrogen bond formation and flux tube contraction involving change of Planck constant are attractive. It would be nice if flux tubes between amino-acids could force the portions of amino-acid sequences to form representation about each other in their own geometry. What would be also nice that the notions of finite measurement resolution and cognitive resolution which are fundamental notions of quantum TGD would have direct correlates at the level of flux tube dynamics.
2. The model for protein folding involving only flux tube connections between amino-acids satisfying the proposed selection rules has however failures. This could be due to simple fact that the proposed selection rules are quite too restrictive. Also the flux tube connections between amino-acids and water are important and might even determine the folding patters to a high degree via the induced secondary interactions between amino-acids.

Second model for protein folding to be discussed represents an extreme in which the flux tube connections between amino-acids and water molecules determined the dynamics of the folding. It seems that this model leads to a realistic qualitative picture about folding. Also quantitative model can be constructed as a straightforward generalization of the model involving only the flux tube connections between selected amino-acids.

12.5.1 Could there be new physics behind hydrophily and hydrophoby?

One could accept just as a fact that magnetic flux tubes to the magnetic body of water mediate an interaction which is attractive or repulsive between water molecules and amino-acids and attractive between DNA molecules and water. Accepting that this induces interaction between amino-acids one could proceed to model building without any mention about TGD.

One could also try to dig deeper and ask what might be the origin of this interaction.

1. **Option I**: Could one understand the interaction in terms of phase transitions changing the Planck constant of the magnetic flux tube. The interaction would be repulsive (attractive) would result if the interaction energy increases (decreases) when Planck constant is reduced. Magnetic interaction energy is certainly the best candidate and could also imply the equivalence of the divisor code and dark baryon code.
2. **Option II**: Could hydrophily and hydrophoby be described in terms of em interactions of quarks representing nucleotides in the model of DNA as tqc. For instance, could amino-acids and water molecules

be characterized by charges which are of opposite sign for water molecules and hydrophilic molecules and of same sign for water molecules and hydrophobic molecules.

For **Option I**, which represents completely new physics (using the standards of TGD!), the situation looks promising. The magnetic interaction energy assignable to the flux tube is a function of the integers (n_a, n_b) characterizing the corresponding page of the book like structure associated with generalized imbedding space - in particular of the Planck constant of the flux tube - and the minimization is performed by keeping the charges of the quarks possibly at its ends fixed. This new physics fits also nicely with the idea that magnetic body controls the living matter by utilizing phase transitions changing Planck constant.

What comes in mind in the case of **Option II** is that the ends of the flux tube carry opposite charges correlating with the codon coding for the amino-acid and giving rise to ordinary gauge interactions. Unfortunately this scenario does not seem to work.

1. It was already found that (denoting codons by XYZ) only $Y = A, G$ type amino-acid residue can form hydrogen bonds and is hydrophilic and thus interacts strongly with water and DNA and RNA. If water end of flux tube corresponds to anti-quarks the attractive interaction between quark and anti-quark at the ends of flux tube could relate to hydrophily. For hydrophobic amino-acids one would have interaction between identical quarks and already Fermi statistics would cause repulsion. In DNA as tqc model based on the coding of A,G and T,C in terms of quarks u,d and their anti-quarks hydrophily-hydrophoby dichotomy corresponds to matter-antimatter dichotomy for quark assigned to the ends of the flux tube. Quarks and anti-quark have opposite charges. Hence the flux tube ends of hydrophilic amino-acids could correspond to quarks and water and hydrophobic ends of flux tubes to anti-quarks. Therefore the DNA as tqc model would predict the needed behavior of the forces. In the case of Gly containing only hydrogen as residue the flux tube might be simply absent.
2. DNA codons A,T,C,G are bases and thus polar and hydrophilic. In the case of DNA charge conjugation for quarks corresponds to the puridine-pyrimidine complementarity corresponding to conjugation of nucleotides. The rule applying in the case of amino-acids would predict T,C to be hydrophobic nucleotides which does not make sense. Therefore it seems that hydrophily and hydrophoby cannot reduce to the interactions of dark quarks and that they only represent conjugation of nucleotides symbolically.

12.5.2 An improve model for protein folding

To begin with let us summarize some basic facts about protein folding.

1. Hydrophily and hydrophoby play a key role in protein folding and dictate to a high degree the resulting folding patterns. This suggests that one cannot neglect the role of water in the process.
2. Protein folding proceeds from short to long length scales starting with the formation of secondary structures such as alpha helices, beta sheets, and random coil portions and is followed by the formation of tertiary and higher structures.
3. The formation of hydrogen bonds is in a decisive role in the formation of secondary structures. The mechanism leading to their formation might be contraction of magnetic flux tube by a phase transition changing Planck constant.
4. The folding patterns do not depend strongly on the precise primary structure, that is precise amino-acid decomposition which suggests that instead of the detailed chemistry the forces between quarks and anti-quarks mediated by flux tubes is what matter so that hydrophily and hydrophoby would become the basic characterizers of the interaction. The phase transitions changing Planck constant would indeed represent this kind of universal interactions independent of the chemistry.
5. In the first approximation amino-acids could be labeled by a variable telling whether it is hydrophobic, hydrophilic, or neither or these (Gly). This approximation would be broken by special amino-acids which appear in edges if beta sheets (Pro) and Cys which often appear as S-S boded pair in junctions. By bringing in forces depending on the angles between tangent vectors of successive amino-acids and on amino-adics themseles this tendency could be modeled.

12.5.3 A model for which the magnetic body of water is involved

The alternative approach to protein folding starts from the general vision about magnetic body containing dark matter as a controller of visible matter in living system. The protein and its magnetic body would be regarded as a living system in itself.

1. Magnetic body must have large number of flux tube contacts to the visible matter. An excellent candidate for the magnetic body is that assignable with water and having flux tube connections to DNA and both hydrophilic and hydrophobic amino-acids. The magnetic body could control and at least fasten

the self-organization process leading to the folding pattern which - by applying standard argument - would otherwise take astronomical time otherwise. The two-step attractive connections between all hydrophilic amino-acids would be possible via the magnetic body of water. The non-hydrophilic amino-acids not in direct contact with water are known to be more like passive structural stuff responsible for a fixed structure but not so relevant for the functioning of the bio-molecule. Hydrophily and hydrophoby would reflect the dependence of interaction energy on the value of Planck constant associated with the flux tube mediating the interaction.

2. This picture implies a straightforward modification of the earlier model. The simplest model would minimize a potential function V expressible as a sum $V = V_1 + V_2 + V_3$ of three terms. V_1 would be sum of the values of a universal two-particle potential function $V_{phi,phi}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophilic amino-acid pairs and giving rise to an attractive force. V_2 would be a sum of a universal two-particle potential function $V_{pho,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophobic amino-acid pairs. V_3 would be would be sum of the values of a universal potential function $V_{phi,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all pairs of hydrophilic and hydrophobic amino-acids. This potential function would induce a repulsive force. Besides this a constraint force due to the fact that amino-acids form a sequence would be present.

3. The resultant of the forces along lines connecting amino-acids would be parallel to the amino-acid sequence in the mechanical equilibrium. Hydrogen bonds and other bonds are indeed formed between neighboring hydrophilic amino-acids and the contraction of the flux tubes connecting the amino-acids in question to the magnetic body of water could be the mechanism. The model seems to be consistent with the basic qualitative facts about folding. The quantitative testing of the model would require determination of the conformations minimizing the potential function subject to the constraint provided by amino-acid sequence. Here of course the freedom to choose the three functions provides a considerable flexibility and symmetry arguments might allow to pose conditions on the form of these functions.

4. One could also include to the potential function describing a direct interaction with water molecules depending on parameters like pH affecting the folding pattern. The resultant for a given amino-acid would be sum of forces directed from a hydrophilic amino-acids to neighboring water molecules. It is not clear whether the normal component of this force could be compensated by the induced forces between amino-acids in a typical equilibrium configuration and the formation of hydrogen bonds involving the contraction of the flux tube could be the manner to achieve this.

The alternative model is more complicated numerically than the model discussed and it would require a considerable amount of work to test it. In particular, the three universal potential functions involve free parameters even if one makes simplifying assumptions about their functional form (say simple behavior under scaling).

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Chapter 13

Three new physics realizations of the genetic code and the role of dark matter in bio-systems

13.1 Introduction

This chapter represents an attempt to integrate three different models of genetic code [26, 77, 82] with each other and with DNA as topological quantum computer (tqc) hypothesis [26] as well as the general ideas behind the model of protein folding and bio-catalysis [3] . The considerations lead to a modification of the earlier model of protein folding.

13.1.1 The notions of dark matter and magnetic body

The generalization of the imbedding space to a book like structure (see Appendix) with pages labeled by two non-negative integers (n_a, n_b) characterizing the singular coverings of M^4 (or actually of causal diamond of M^4 defined as intersection of future and past directed light-cones) and of CP_2 together with pages representing singular coverings and represented similarly by a pair of integers (or equivalently inverses of non-negative integers) provides a possible mathematical realization of dark matter hierarchy. Dark matter is interpreted as phases of ordinary matter at various pages of the book like structure. The pages of the book are partially characterized by a hierarchy of Planck constants. The notion of darkness is only a relative concept in this picture. The phase having $(n_a, n_b) = (1, 1)$ can be identified as ordinary visible matter.

Magnetic body is second key concept in TGD based model of quantum biology. Magnetic body has onion like structure with layers characterized by a spectrum of values of (n_a, n_b) identifiable as orders of the cyclic groups Z_{n_a} *resp.* Z_{n_b} acting in the fiber of singular covering space or factor space assignable M^4 *resp.* CP_2 degrees of freedom. Also the extensions of these groups obtained by adding reflection can be considered. Phase transitions changing the values of (n_a, n_b) and thus also the length of magnetic tubes correspond to a tunneling between two pages of the book and in general change the value of Planck constant. The basic selection rule is familiar from the sub-group rule for phase transitions and means that either n_{a_1} (n_{b_1}) divides n_{a_2} (n_{b_2}) or vice versa. These phase transitions are in a key role in TGD inspired model of bio-catalysis.

The reconnections of flux tubes represents second basic mechanism of bio-catalysis. Together these two mechanisms could be at least partially responsible for the amazing aspects of bio-catalysis such as extreme selectivity and the ability of distant bio-molecules to find each other in the dense soup of bio-molecules.

13.1.2 Realizations of genetic code

I have proposed several realization of the genetic code during past 15 years. There are three realizations which are especially interesting physically.

1. The first realization is based on the map of G,C *resp.* A,T codons to quarks u,d *resp.* their anti-quarks. This code was proposed to realize DNA as tqc with braid strands represented as flux tubes connecting nucleotides with the lipids of cell membrane [26] . The quantum states at the ends of braid strands -would be represented by many particle states of quarks and anti-quarks in this model and entanglement of quarks and anti-quarks would be essential for tqc and affected by the braiding induced by the 2-D liquid flow of the lipids.

2. Second realization is based on the observation that the neutral states of dark baryons consisting of u and d quarks in nuclear string model can be regarded as counterparts of DNA, RNA, amino-acids and perhaps even tRNA [34, 77] . Nuclear strings would represent DNA and other polymers at the level of dark matter.
3. Third realization is based on the interpretation of divisor code discovered by Khrennikov and Nilsson [24] in terms of the sub-group rule for phase transitions [77] . Second realization and this one are in 1-1 correspondence under certain prerequisites. The magnetic- interaction energy of the dark baryon depends on the projections of the total quark spin and total color flux tube spin to the direction of the magnetic field labeling both DNA codons and amino-acids. This interaction energy is a function of (n_a, n_b) and minimized for some pair (n_a, n_b). This gives 1-1 correspondence the states of dark baryon and page of the book and since the page numbering allows to interpret physically the divisor code, one might hope that this correspondence is consistent with both codes.
4. I have also proposed number theory based thermodynamical models for the genetic code [19, 82] discussed also by others [11, 22] , and a suitable modification of this kind of model could allow to model the thermodynamics based on magnetic interaction energy.

I have also suggested realizations of the genetic code in terms of electromagnetic field patterns and computer metaphor encourages to think that standard genetic code is just one possible realization among many.

13.1.3 Questions

These ideas raise a bundle of questions.

1. There are three candidates for the realization of the genetic code. Are all these realizations needed? Are the realizations based on dark baryons and divisor code equivalent?
2. The realization based on correspondence with DNA nucleotides and quarks and anti-quarks works nicely for DNA as tqc hypothesis. Can one consider also a realization of DNA as tqc in terms of dark baryons?
3. How dark baryon realization relates with ordinary chemical realizations and to evolution of pre-biotic life forms? Could it be that the life based on nuclear string genetic code gradually moved from the dark pages of the book to the page containing visible matter as chemical realizations of the analogs of DNA, RNA, amino-acids and even tRNA gradually developed? Note that the process bears formal similarity to the transition of life from sea to land. Is it possible to transcribe the counterparts of DNA,RNA, and amino-acids to their real counterparts? Is pre-biotic era continuing still inside dark magnetic flux tubes and could it make possible genetic engineering?

13.2 A vision about evolution and codes

The fact is that the only thing we really know about dark matter is that 95 percent of matter is dark (matter or dark matter and energy depending on theoretical framework used). Therefore the ideas about dark baryon code are necessarily speculative. One can however base the speculations to some vision in order achieve internal consistency if nothing else.

13.2.1 Basic insights

The idea that biological life was preceded by dark life with subset for the counterparts of DNA, RNA, amino-acids and tRNA dominating the scene looks like a plausible starting point. Second attractive assumption is that this era still continues at magnetic bodies and makes possible genetic engineering based on experimentation and transcription of at least dark baryon analog of DNA to ordinary DNA.

The transformations for RNA and amino-acids to dark matter and vice versa seems necessary if the experimentation with new variants of genes is to be carried out unless one is satisfied with the testing of the modified genes in a small scale. Reconnection and $\hbar$ changing phase transitions of flux tubes would serve as the basic mechanism of bio-catalysis in TGD Universe. One can imagine two basic mechanisms involving reconnection of flux tube and transforming dark nuclear strings to polymers.

1. Given bio-molecule could be accompanied by a closed flux tube of the magnetic field containing dark matter and extending to some page of the book characterized by two numbers x_a *resp.* x_b, which are integers for singular coverings of M^4 *resp.* CP_2 and inverse integers for singular factor spaces of M^4 *resp.* CP_2. For bio-molecules for which x_a and x_b are identical these closed loops could reconnect to form a pair of flux tubes connecting bio-molecules (see Fig. 13.2.1). A phase transition reducing Planck constant would bring the molecules close to each other. This would provide a general recognition mechanism central in the reactions of bio-molecules.

2. These flux tube connections between two molecules could also involve only single *permanently* existing flux tube (this is a rather strong prediction which might be used to kill this option). In this case the reconnection for the flux tubes connecting molecules X and Y *resp.* U and V would give rise to connections $X - U$ and $Y - V$ for instance. The general recipe for achieving these transformations is based on the assumption that molecule and its dark conjugate connected by flux tubes can be present and that reconnection process given exchange of particles describable in terms of diagrams analogous to stringy diagrams is possible. This means that pairings $X - dY$ and $U - dV$ can be transformed to pairings $X - U$ and $dY - dV$ and $X - dV$ and $U - dY$ (see Fig. 13.2.1). This process would extend the variety of possible transcription like processes to allow also transcription of dark variants of DNA, RNA and amino-acids to visible ones and vice versa.

Figure 13.1: Illustration of the reconnection by magnetic flux loops.

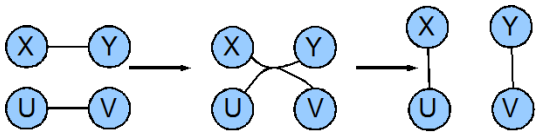

Figure 13.2: Illustration of the reconnection by flux tubes connecting pairs of molecules.

Genetic engineering would be possible by the fact that the dark nuclear string variants of genes could be easily transferred around the biological body unlike modified DNAs. In particular, modified dark genes could be transferred to the nuclei of germ cells. Essentially the TGD inspired mechanism of homeopathy would be in question [34] .

There is analogy with the evolution of language. Both DNA codons and representation of nucleotides in terms of quarks and anti quarks (perhaps accompanying the intronic portions of DNA) mean a representation of codons as three-letter sequences. Since dark baryons represent genetic codons as indecomposable structures in terms of quantum entanglement, the emergence of both representations would be analogous to the emergence of written language when spoken words forming indecomposable units decomposed into letters having no meaning as such. The findings that there are major differences between the genomes of blood and tissue cells [133] and that the genetic variation due to jumping genes is highest in brain and germ cells [169] is consistent with the view about dark evolution modifying at least intron portion of the genome.

RNA world [168, 158, 164] represents a dominating vision about pre-biotic evolution. The idea is RNA era was first and that somehow DNA and amino-acids emerged in some later stage. It has not been possible yet to reproduce replicating RNA sequences in laboratory so that there is still room for alternatives. Dark baryon realization of the genetic code predicts that the analogs of DNA, RNA, amino-acids and even tRNA anticodons might have been there all the time. This might apply also to the primitive chemical representations of DNA, RNA, tRNA, and amino-acids. It is of course possible that the chemical representation of RNA evolved first. This era could still continue inside cell nuclei and make possible genetic engineering as experimentation with dark baryon genes producing amino-acids and RNA and then possibly transforming the resulting RNAs to DNA by reverse transcription. Also a direct transcription to DNA could take place.

13.2.2 The simplest scenario

The evolution could might have proceed as a gradual transition of life from dark pages to the visible page allowing chemical realization of the genetic code.

1. Dark matter era would replace RNA and already this era involved at least the dark counterparts of DNA, RNA, amino-acids and perhaps even $64 - 40 \to 40 - 20$ two-step realization of the genetic code with tRNA anticodons representing a particular example of 40-D realization intermediate between DNA and amino-acids. Maximum number of different tRNA codons is indeed around 40 [99] . Without further assumptions the pairing of all dark DNA and RNA codons coding for the same amino-acid was

possible. The situation changes if one assumes 1-1 correspondence between dark baryon realization and the realization of the divisor code in terms of dark magnetic flux tubes to be discussed later. This era could still continue at magnetic bodies and make genetic experimentation and genetic engineering possible.

2. Dark nuclear strings became gradually associated with the magnetic bodies of DNA, RNA and amino-acids and a machinery transforming DNA to mRNA to tRNA to amino-acids developed. Flux tube connections could have formed between nuclear strings and the magnetic bodies of the bio-molecules. A stronger condition is that dark nuclear strings became part of the magnetic bodies of DNA, RNA and amino-acids forming helical structures running parallel to the corresponding molecular structures. For this option base pairing could have made the dark counterparts of DNA-DNA and DNA-mRNA pairings unique (also the equivalence of dark baryon and divisor codes could have guaranteed this). mRNA-tRNA base is pairing is not unique but wobble base pairing made possible for all mRNA codons except stopping codons to pair to tRNA anticodons. Whether RNA appeared first or whether the counterparts of the basic bio-molecules were present from the beginning remains an open question.
3. Topological quantum computation based on the map of A,G *resp.* T,C to quarks *resp.* anti-quarks emerged later as something analogous to written language and would naturally correspond to the intron portions of genome for which the decomposition into triplets is not essential and the nucleotide composition is not too essential since it is braiding which defines topological quantum computation (the 4 different colors of the braid strands are not necessary).

13.2.3 How dark baryon code could be involved with transcription and translation mechanisms?

In the following it is assumed that one can talk about magnetic flux tubes containing dark nucleon strings as independent objects and therefore not identified as a helical string parallel to DNA, RNA or amino-acid sequence as one might also imagine. Therefore it is not necessary to assume that dark baryons have the same size scale as corresponding molecular units. One can also assume that one can connect flux tubes associated with nuclear strings by magnetic flux tubes.

Genetic engineering makes sense if the transcription of nuclear string counterparts of DNA, RNA, tRNA, and amino-acids to their chemical counterparts is possible.

1. One can classify flux tube connections by introducing the notion of order of flux tube connection expected to characterize the probability of flux tube connection. First order means a flux tube entirely in given page of the book like structure defined by the generalized imbedding space, second order to a flux tube between two different pages, third order a flux tube traversing through an intermediate page between two pages, and so on. Reconnection of the magnetic flux tubes provides a general mechanism for this transformations and as already explained there are two general recipes for the formation of reconnection.
2. **Option I** - the simpler one - involves a reconnection of the closed flux tubes associated with the molecules to be paired. This mechanism would make it possible for a bio-molecule X to catch a partner Y if the corresponding closed flux tubes reside at same page of the book s(see Fig. 13.2.1). This mechanism provides a straightforward description of replication, transcription and translation as well as their generalizations allowing to transform dark nuclear strings to their molecular counterparts and vice.
3. **Option II** is more complex (see Fig. 13.2.1) and can be formulated in terms of two stringy diagrams with two strings connecting objects X and Y *resp.* U and V at their ends touch and transform to strings with X and V *resp.* U and V or X and U *resp.* Y and V at their ends. The process can be visualized as exchange of half strings and stringy diagrams represent various processes. Denote by dX the dark matter counterpart of X which can be DNA,RNA, or amino-acid and assume that all combinations obtained by the reconnection process are possible so that one would has pairings $X-Y, X-dY, dX-Y$, and $dX-dY$ defined by flux tube connections. All these variants present and $X-Y$ and $dX-dY$ can be first order connections whereas $X-dY$ and $dX-Y$ are second or higher order connections. This option requires permanent flux tube connections.
4. These are the simplest options. One can wonder whether the hydrogen bonds associated with base pairs correspond to a pair $(A-T)$ or triplet $(G-C)$ of contracted flux tubes. It is of course possible to have more than two flux tubes. If the third hydrogen bond for $G-C$ corresponds to a flux tube a permanent flux tube connection between G and C nucleotides would exist.

One could think that only few bio-molecules can have flux tubes at the page at which the particular dark nuclear string typically resides (minimization of the magnetic interaction energy could fix the most probable candidate for this page and imply connection between dark baryon code and divisor code) and that bio-molecules are gradually selected from these particular molecules. The process would be still in progress.

Vertebrate nuclear code would be however identical with the dark baryon code. For tRNA anti-codons the situation would be far from ideal.

Replication

In the following $'\circ'$ means one or two bonds depending on whether Option I or II is in question.

Option I: Let $(X \circ Y)$ denote DNA double helix with two flux tubes connecting them and U a V DNA nucleotides. The opening of DNA double strand means reconnection of these flux tubes so that two closed loops are obtained. These flux tubes transform to dark flux tubes and reconnect with dark flux tubes associated with U and V respectively and a phase transition reducing $\hbar$ brings U and V near sequences X and Y where they combine with already existing new sequence.

Option II: Let $(X \circ Y)$ denote DNA double helix and $(U \circ V)$ to a pair of codon and anticodon assumed to be connected by a long flux tube (this should be a testable prediction). Replication of DNA would correspond to $(X \circ Y) + (U \circ V) \to X \circ U \to Y \circ V$ with reconnection taking place for the flux tubes.

With the same conventions the transcription of dark DNA to ordinary DNA and vice versa would correspond to a process $dX \circ dY + U + V \to dX \circ U \to V \circ dY$ giving rise to ordinary-dark DNA double strand. This process would be followed by $(dX \circ U) + (dV \circ Y) \to dX \circ dV \to U \circ Y$ proceeding like DNA replication.

$DNA \to mRNA$ transcription

Let $X \circ Y$ denote DNA double helix in the sequel. For Option I the transcription process would occur in straightforward manner by the transformation of double connection between X and Y to loops and the reconnection of loop associated with Y with that assignable to $mRNA$ codon followed by $\hbar$ reducing phase transition leading to a generation of DNA and mRNA sequences with nucleotides connected by flux tube pairs. The third step would be reconnection transforming double flux tube bonds between DNA and mRNA nucleotides to loops.

Consider next Option II:

1. Let $U \circ V$ denote mRNA-cmRNA that is pair of mRNA codon and its conjugate assumed to be connected by a long flux tube. Ordinary transcription $DNA \to mRNA$ could correspond to the $(X \circ Y) + (U \circ V) \to X \circ U \to Y \circ V$ followed by its reversal but mRNAs arranged to a sequence. Note that every mRNA would have long flux tube connection with the conjugate mRNA.
2. Let $U \circ V$ could denote mRNA-dcmRNA. The same process would give mRNA sequence with each codon connected by a long flux tube to dcmRNA codon.
3. For a third realization $U - V$ would denote the pair $mRNA - dtRNA$. The same process as above would give mRNA sequence with each mRNA codon connected by a long flux tube to $dtRNA$ anticodon.

This process has also variants allowing to assign mRNA to dDNA and to DNA dmRNA.

Translation as a sequence of reconnections

For Option I the description of translation should be obvious on basis of previous examples. For Option II translation could be realized as a sequence of reconnections in several manners. The basic idea is that the reconnections and their reversals transform the tRNA_1-AA pairs with $tRNA_1$ denotes $tRNA$ without amino-acid AA to a sequence of them but $tRNA_1$ connected to amino-acid by a long flux tube. In the decay of the amino-acid this long tRNA would reduce to ordinary tRNA: this serves as a killer prediction.

For instance, let $X - Y = mRNA - dmRNA$ mRNA sequence with dark mRNA codons connected to mRNA codons and let $U - V = tRNA_1 - AA$ denote tRNA. Reconnection would allow to arrange tRNAs to sequence of "long" tRNAs while keeping $X - Y$ as such. One could also replace Y by $dtRNA$. Obviously the process has several variants. When amino-acid sequence decays ordinary "short" tRNAs are formed again. Also the translation of dark mRNA to ordinary amino-acid sequence with long flux tubes to either dark tRNA or ordinary tRNA.

13.3 DNA as topological quantum computer: realization of the genetic code in terms of quarks and anti-quarks

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Large values of Planck constant makes possible all kinds of quantum computations [3, 11, 8, 26] . What makes topological quantum computation (tqc) [21, 16, 20, 17] , [8] so attractive is that the computational operations are very robust and there are hopes that external perturbations do not spoil the quantum coherence in this case. The basic problem is how to create, detect, and control the dark matter with large $\hbar$. The natural

looking strategy would be to assume that living matter, say a system consisting of DNA and cell membranes, performs tqc and to look for consequences.

There are many questions. How the tqc could be performed? Does tqc hypothesis might allow to understand the structure of living cell at a deeper level? What does this hypothesis predict about DNA itself? One of the challenges is to fuse the vision about living system as a conscious hologram with the DNA as tqc vision. The experimental findings of Peter Gariaev [147, 192] might provide a breakthrough in this respect. In particular, the very simple experiment in which one irradiates DNA sample using ordinary light in UV-IR range and photographs the scattered light seems to allow an interpretation as providing a photograph of magnetic flux tubes containing dark matter. If this is really the case, then the bottle neck problem of how to make dark matter visible and how to manipulate it would have been resolved in principle. The experiment of Gariaev and collaborators [192] also show that the photographs are obtained only in the presence of DNA sample. This leaves open the question whether the magnetic flux tubes associated with instruments are there in absence of DNA and only made visible by DNA or generated by the presence of DNA.

13.3.1 Basic ideas of tqc

The basic idea of topological quantum computation (tqc) is to code tqc programs to braiding patterns (analogous to linking and knotting). A nice metaphor for tqc is as dance. Dancing pattern in time direction defines the tqc program. This kind of patterns are defined by any objects moving around so that the Universe might be performing topological quantum computation like activities in all scales.

One assigns to the strands of the braid elementary particles. The S-matrix coding for tqc is determined by purely topological consideration as a representation for braiding operation. It is essential that the particles are in anyonic phase: this means in TGD framework that the value of Planck constant differs from its standard value. Tqc as any quantum computation halts in state function reduction which corresponds to the measurement of say spins of the particles involved.

As in the case of ordinary computers one can reduce the hardware to basic gates. The basic 2-gate is represented by a purely topological operation in which two neighboring braid strands are twisted by π. 1-particle gate corresponds to a phase multiplication of the quantum state associated with braid strand. This operation is not purely topological and requires large Planck constant to overcome the effects of thermal noise.

In TGD framework tqc differs somewhat from the ordinary one.

1. Zero energy ontology means that physical states decompose into pairs of positive and negative energy states at boundaries of causal diamond formed by future and past directed lightcones containing the particles at their light-like boundaries. The interpretation is as an event, say particle scattering, in positive energy ontology. The time like entanglement coefficients define S-matrix, or rather M-matrix, and this matrix can be interpreted as coding for physical laws in the structure of physical state as quantum superposition of statements "A implies B" with A and B represented as positive and negative energy parts of quantum state. The halting of topological quantum computation would select this kind of statement.

2. The new view about quantum state as essentially 4-D notion implies that the outcome of tqc is expressed as a four-dimensional pattern at space-time sheet rather than as time=constant final state. All kinds of patterns would provide a representation of this kind. In particular, holograms formed by large $\hbar$ photons emitted by Josephson currents, including EEG as a special case, would define particular kind of representation of outcome.

13.3.2 Identification of hardware of tqc and tqc programs

One challenge is to identify the hardware of tqc and realization of tqc programs.

1. Living cell is an excellent candidate in this respect. The lipid layers of the cell membrane is 2-D liquid crystal and the 2-D motion of lipids would define naturally the braiding if the lipids are connected to DNA nucleotides. This motion might be induced by the self organization patterns of metabolically driven liquid flow in the vicinity of lipid layer both in interior and exterior of cell membrane and thus self-organization patters of the water flow would define the tqc programs.

2. This identification of braiding implies that tqc as dancing pattern is coded automatically to memory in the sense that lipids connected to nucleotides are like dancers whose feet are connected to the wall of the dancing hall define automatically space-like braiding as the threads connected to their feet get braided. This braiding would define universal memory realized not only as tissue memory but related also to water memory [29] .

3. It is natural to require that the genetic code is somehow represented as property of braids strands. This is achieved if strands are "colored" so that A,T,C,G correspond to four different "colors". This leads to the hypothesis that flux tubes assignable to nucleotides are wormhole magnetic flux tubes such that the

ends of the two sheets carry quark and anti-quark (*resp.* anti-quark and quark) quantum numbers. This gives mapping A,T,C,G to u, u_c, d, d_c. These quarks are not ordinary quarks but their scaled variants predicted by the fractal hierarchy of color and electro-weak physics. Chiral selection in living matter could be explained by the hierarchy of weak physics. The findings of topologist Barbara Shipman about mathematical structure of honeybee dance led her to proposed that the color symmetries of quarks are in some mysterious manner involved with honeybee cognition and this model would justify her intuition [30] .

4. One should identify the representation of qubit. Ordinary spin is not optimal since the representation of 1-gates would require a modification of direction of magnetic field in turn requiring modification of direction of flux tubes. A more elegant representation is based on quark color which means effectively 3-valued logic: true, false, and undefined, also used in ordinary computers and is natural in a situation in which information is only partial. In this case 1-gates would correspond to color rotations for space-time sheets requiring no rotation of the magnetic field.

In this framework genes define the hardware of tqc rather than genetic programs. This means that the evolution takes place also at the level of tqc programs meaning that strict genetic determinism fails. There are also good reasons to believe that these tqc programs can be inherited to some degree. This could explain the huge differences between us and our cousins in spite of almost the identical genetic codes and explains also cultural evolution and the observation that our children seem to learn more easily those things that we have already learned [202] . It must be added that DNA as tqc paradigm seems to generalizedDNA, lipids, proteins, water molecules,... can have flux tubes connecting them together and this is enough to generate braidings and tqc programs. Even water could be performing simple tqc or at least building memory representations based on braiding of flux tubes connecting water molecules.

13.3.3 How much tqc resembles ordinary computation?

If God made us to his own image one can ask whether we made computers images of ourselves in some respects. Taking this seriously one ends up asking whether facts familiar to us from ordinary computers and world wide web might have counterparts in DNA as tqc paradigm.

1. Can one identify program files as space-like braiding patterns. Can one differentiate between program files and data files?
2. In ordinary computers electromagnetic signalling is in key role. The vision about living matter as conscious holograms suggests that this is the case also now. In particular, the idea that entire biosphere forms a tqc web communicating electromagnetically information and control signals looks natural. Topological light rays (MEs) make possible precisely targeted communications with light velocity without any change in pulse shape. Gariaev's findings [147] that the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind of picture. Also the model of EEG in which the magnetic body controls the biological body also from astrophysical distances conforms with this picture.
3. The calling of computer programs by simply clicking the icon or typing the name of program followed by return is an extremely economic manner to initiate complex computer programs. This also means that one can construct arbitrarily complex combinations from given basic modules and call this complex by a single name if the modules are able to call each other. This kind of program call mechanism could be realized at the level of tqc by DNA. Since the intronic portion of genome increases with the evolutionary level and is about 98 per cent for humans, one can ask whether introns would contain representations for names of program modules. If so, introns would express themselves electromagnetically by transcribing the nucleotide to a temporal pattern of electromagnetic radiation activating desired subprogram call, presumably the conjugate of intronic portion as DNA sequence. A hierarchical sequence of subprogram calls proceeding downwards at intronic level and eventually activating the tqc program leading to gene expression is suggestive.

   Gariaev [147] has found that laser radiation scattering from given DNA activates only genomes which contain an address coded as temporal pattern for the direction of polarization plane. If flux tubes are super-conducting and there is strong parity breaking (chiral selection) then Faraday rotation for photons traveling through the wormhole flux tube code nucleotide to an angle characterizing the rotation of polarization plane. User id and password would be kind of immune system against externally induced gene expression.
4. Could nerve pulses establish only the connection between receiver and sender neurons as long magnetic flux tubes? Real communication would take place by electromagnetic signals along the flux tube, using topological light ray (ME) attached to flux tube, and by entanglement. Could neural transmitters specify which parts of genomes are in contact and thus serve as a kind of directory address inside the receiving genome?

13.3.4 Basic predictions of DNA as tqc hypothesis

DNA as tqc hypothesis leads to several testable predictions about DNA itself.

Anomalous em charge

The model for DNA as tqc assigns to flux tubes starting from DNA an anomalous em charge. This means that the total charge of DNA nucleotide using e as unit is $Q = -2 + Q(q)$, where -2 is the charge of phosphate group and $Q(q) = -/ + 2/3, +/ - 1/3$ is the electromagnetic charge of quark associated with "upper" sheet of wormhole magnetic flux tube. If the phosphate group is not present one has $Q = Q(q)$. In the presence of phosphate bonds the anomalous charge makes possible the coding of nucleotides to the rotation of angle of polarization plane resulting as photon travels along magnetic flux tube. The anomalous em charge should be visible as an anomalous voltage created by DNA. It would be relatively easy to test this prediction by using various kinds of DNA:s.

Does breaking of matter antimatter and isospin symmetries happen at the level of DNA and mRNA?

The nice feature of the model is that it allows to interpret the slightly broken A-G and T-C symmetries of genetic code with respect to the third nucleotide Z of codon XYZ in terms of the analog of strong isospin symmetry at quark level at wormhole magnetic flux tubes. Also matter-antimatter dichotomy has a chemical analog in the sense that if the letter Y of codon corresponds to quark u, d (anti-quark u_c, d_c), the codon codes for hydrophobic (hydrophilic) amino-acid. It is also known that the first letter X of the codon codes for the reaction path leading from a precursor to an amino-acid. These facts play a key role in the model for code of protein folding and catalysis. The basic assumption generalizing base pairing for DNA nucleotides is that wormhole flux tubes can connect an amino-acid inside protein only to molecules (amino-acids, DNA, mRNA, or tRNA) for which Y letter is conjugate to that associated with the amino-acid. This means that the reduction of Planck constant leading to the shortening of the flux tube can bring only these amino-acids together so that only these molecules can find each other in biocatalysis: this would mean kind of code of bio-catalysis.

The fact that matter-antimatter and isospin symmetries are broken in Nature suggests that the same occurs at the level of DNA for quarks and anti-quarks coding for nucleotides. One would expect that genes and other parts of genome differ in the sense that the anomalous em charge, isospin, and net quark number (vanishes for matter antimatter symmetric situation) differ for them. From Wikipedia [209] one learns that there are rules about distribution of nucleotides which cannot be understood on basis of chemistry. The rules could be understood in terms of new physics. Chargaff's rules state that these symmetries hold true in one per cent approximation at the level of entire chromosomes. Szybalski's rules [209] state that they fail for genes. There is also a rule stating that in good approximation both strands contain the same portion of DNA transcribed to mRNA. This implies that at mRNA level the sign of matter antimatter asymmetry is always the same: this is analogous to the breaking of matter antimatter asymmetry in cosmology (only matter is observed).

It would be interesting to study systematically the breaking of these symmetries for a sufficiently large sample of genes and also other in parts of genome where a compensating symmetry breaking must occur. that the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind of picture. Also the model of EEG in which magnetic body controls biological body from astrophysical distances conforms with this picture.

13.4 Realization of genetic code in terms of dark baryons

Either dark baryon code or code based on u,d and their anti-quarks could be involved with various pairings. For dark baryon code DNA would not decompose into codons. For latter code this would be the case. One could also consider the possibility that the regions genes realized the dark baryon code and the regions between them are realized in terms of udubardbar code. The latter code could be also involved with tqc.

13.4.1 Dark nuclear strings as analogs of DNA-, RNA- and amino-acid sequences and baryonic realization of genetic code?

Water memory is one of the ugly words in the vocabulary of a main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [1, 34, 77] , [1] , [178] . The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of

sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

The question is whether dark nuclear strings might provide a representation of the genetic code. In fact, I posed this question year before the results of the experiment came with motivation coming from attempts to understand water memory. The outcome was a totally unexpected finding: the states of dark nucleons formed from three quarks can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, and 20 amino-acids and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

The basic idea is simple. Since baryons consist of 3 quarks just as DNA codons consist of three nucleotides, one might ask whether codons could correspond to baryons obtained as open strings with quarks connected by two color flux tubes. This representation would be based on entanglement rather than letter sequences. The question is therefore whether the dark baryons constructed as string of 3 quarks using color flux tubes could realize 64 codons and whether 20 amino-acids could be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner.

The following model indeed reproduces the genetic code directly from a model of dark neutral baryons as strings of 3 quarks connected by color flux tubes.

1. Dark nuclear baryons are considered as a fundamental realization of DNA codons and constructed as open strings of 3 dark quarks connected by two colored flux tubes, which can be also charged. The baryonic strings cannot combine to form a strictly linear structure since strict rotational invariance would not allow the quark strings to have angular momentum with respect to the quantization axis defined by the nuclear string. The independent rotation of quark strings and breaking of rotational symmetry from SO(3) to SO(2) induced by the direction of the nuclear string is essential for the model.

   Baryonic strings could form a helical nuclear string (stability might require this) locally parallel to DNA, RNA, or amino-acid) helix with rotations acting either along the axis of the DNA or along the local axis of DNA along helix. The rotation of a flux tube portion around an axis parallel to the local axis along DNA helix requires that magnetic flux tube has a kink in this portion. An interesting question is whether this kink has correlate at the level of DNA too. Notice that color bonds appear in two scales corresponding to these two strings. The model of DNA as topological quantum computer [26] allows a modification in which dark nuclear string of this kind is parallel to DNA and each codon has a flux tube connection to the lipid of cell membrane or possibly to some other bio-molecule.

2. The new element as compared to the standard quark model is that between both dark quarks and dark baryons can be charged carrying charge $0, \pm 1$. This is assumed also in nuclear string model and there is empirical support for the existence of exotic nuclei containing charged color bonds between nuclei.

3. The net charge of the dark baryons in question is assumed to vanish to minimize Coulomb repulsion:

$$\sum_q Q_{em}(q) = -\sum_{flux\ tubes} Q_{em}(flux\ tube) \quad . \tag{13.4.1}$$

   This kind of selection is natural taking into account the breaking of isospin symmetry. In the recent case the breaking cannot however be as large as for ordinary baryons (implying large mass difference between Δ and nucleon states).

4. One can classify the states of the open 3-quark string by the total charges and spins associated with 3 quarks and to the two color bonds. Total em charges of quarks vary in the range $Z_B \in \{2, 1, 0, -1\}$ and total color bond charges in the range $Z_b \in \{2, 1, 0, -1, -2\}$. Only neutral states are allowed. Total quark spin projection varies in the range $J_B = 3/2, 1/2, -1/2, -3/2$ and the total flux tube spin projection in the range $J_b = 2, 1, -1, -2$. If one takes for a given total charge assumed to be vanishing one representative from each class (J_B, J_b), one obtains $4 \times 5 = 20$ states which is the number of amino-acids. Thus genetic code might be realized at the level of baryons by mapping the neutral states with a given spin projection to single representative state with the same spin projection. The problem is to find whether one can identify the analogs of DNA, RNA and amino-acids as baryon like states.

States in the quark degrees of freedom

One must construct many-particle states both in quark and flux tube degrees of freedom. These states can be constructed as representations of rotation group SU(2) and strong isospin group SU(2) by using the standard tensor product rule $j_1 \times j_2 = j_1 + j_2 \oplus j_1 + j_2 - 1 \oplus ... \oplus |j_1 - j_2|$ for the representation of SU(2) and Fermi statistics and Bose-Einstein statistics are used to deduce correlations between total spin and total isospin (for

instance, $J = I$ rule holds true in quark degrees of freedom). Charge neutrality is assumed and the breaking of rotational symmetry in the direction of nuclear string is assumed.

Consider first the states of dark baryons in quark degrees of freedom.

1. The tensor product $2 \otimes 2 \otimes 2$ is involved in both cases. Without any additional constraints this tensor product decomposes as $(3 \oplus 1) \otimes 2 = 4 \oplus 2 \oplus 2$: 8 states altogether. This is what one should have for DNA and RNA candidates. If one has only identical quarks *uuu* or *ddd*, Pauli exclusion rule allows only the 4-D spin 3/2 representation corresponding to completely symmetric representation -just as in standard quark model. These 4 states correspond to a candidate for amino-acids. Thus RNA and DNA should correspond to states of type uud and ddu and amino-acids to states of type *uuu* or ddd. What this means physically will be considered later.
2. Due to spin-statistics constraint only the representations with $(J, I) = (3/2, 3/2)$ (Δ resonance) and the second $(J, I) = (1/2, 1/2)$ (proton and neutron) are realized as free baryons. Now of course a dark -possibly p-adically scaled up - variant of QCD is considered so that more general baryonic states are possible. By the way, the spin statistics problem which forced to introduce quark color strongly suggests that the construction of the codons as sequences of 3 nucleons - which one might also consider - is not a good idea.
3. Second nucleon like spin doublet - call it 2_{odd} - has wrong parity in the sense that it would require $L = 1$ ground state for two identical quarks (*uu* or *dd* pair). Dropping 2_{odd} and using only $4 \oplus 2$ for the rotation group would give degeneracies $(1, 2, 2, 1)$ and 6 states only. All the representations in $4 \oplus 2 \oplus 2_{odd}$ are needed to get 8 states with a given quark charge and one should transform the wrong parity doublet to positive parity doublet somehow. Since open string geometry breaks rotational symmetry to a subgroup SO(2) of rotations acting along the direction of the string and since the boundary conditions on baryonic strings force their ends to rotate with light velocity, the attractive possibility is to add a baryonic stringy excitation with angular momentum projection $L_z = -1$ to the wrong parity doublet so that the parity comes out correctly. $L_z = -1$ orbital angular momentum for the relative motion of *uu* or *dd* quark pair in the open 3-quark string would be in question. The degeneracies for spin projection value $J_z = 3/2, ..., -3/2$ are $(1, 2, 3, 2)$. Genetic code means spin projection mapping the states in $4 \oplus 2 \oplus 2_{odd}$ to 4.

States in the flux tube degrees of freedom

Consider next the states in flux tube degrees of freedom.

1. The situation is analogous to a construction of mesons from quarks and anti-quarks and one obtains the analogs of π meson (pion) with spin 0 and ρ meson with spin 1 since spin statistics forces $J = I$ condition also now. States of a given charge for a flux tube correspond to the tensor product $2 \otimes 2 = 3 \oplus 1$ for the rotation group.
2. Without any further constraints the tensor product $3 \otimes 3 = 5 \oplus 3 \oplus 1$ for the flux tubes states gives 8+1 states. By dropping the scalar state this gives 8 states required by DNA and RNA analogs. The degeneracies of the states for DNA/RNA type realization with a given spin projection for $5 \oplus 3$ are $(1, 2, 2, 2, 1)$. $8\times$ 8 states result altogether for both *uud* and *udd* for which color bonds have different charges. Also for *ddd* state with quark charge -1 one obtains $5 \oplus 3$ states giving 40 states altogether.
3. If the charges of the color bonds are identical as the are for *uuu* type states serving as candidates for the counterparts of amino-acids bosonic statistics allows only 5 states ($J = 2$ state). Hence 20 counterparts of amino-acids are obtained for *uuu*. Genetic code means the projection of the states of $5 \oplus 3$ to those of 5 with the same spin projection and same total charge.

Analogs of DNA,RNA, amino-acids, and of translation and transcription mechanisms

Consider next the identification of analogs of DNA, RNA and amino-acids and the baryonic realization of the genetic code, translation and transcription.

1. The analogs of DNA and RNA can be identified dark baryons with quark content *uud*, *ddu* with color bonds having different charges. There are 3 color bond pairs corresponding to charge pairs $(q_1, q_2) = (-1, 0), (-1, 1), (0, 1)$ (the order of charges does not matter). The condition that the total charge of dark baryon vanishes allows for *uud* only the bond pair $(-1, 0)$ and for *udd* only the pair $(-1, 1)$. These thus only single neutral dark baryon of type *uud resp. udd*: these would be the analogous of DNA and RNA codons. Amino-acids would correspond to *uuu* states with identical color bonds with charges $(-1, -1)$, $(0, 0)$, or $(1, 1)$. *uuu* with color bond charges (-1,-1) is the only neutral state. Hence only the analogs of DNA, RNA, and amino-acids are obtained, which is rather remarkable result.

2. The basic transcription and translation machinery could be realized as processes in which the analog of DNA can replicate, and can be transcribed to the analog of mRNA in turn translated to the analogs of amino-acids. In terms of flux tube connections the realization of genetic code, transcription, and translation, would mean that only dark baryons with same total quark spin and same total color bond spin can be connected by flux tubes. Charges are of course identical since they vanish.
3. Genetic code maps of $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ to the states of 4×5. The most natural map takes the states with a given spin to a state with the same spin so that the code is unique. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1, 2, 3, 2\}$ and $D_b \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of amino-acids coded by D codons would be

$$[N(1), N(2), N(3), N(4), N(6)] = [2, 7, 2, 6, 3] \quad .$$

   The correct numbers for vertebrate nuclear code are $(N(1), N(2), N(3), N(4), N(6)) = (2, 9, 1, 5, 3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2, 9, 1, 5, 3)$!
4. Stopping codons would most naturally correspond to the codons, which involve the $L_z = -1$ relative rotational excitation of uu or dd type quark pair. For the 3-plet the two candidates for the stopping codon state are $|1/2, -1/2\rangle \otimes \{|2, k\rangle\}$, $k = 2, -2$. The total spins are $J_z = 3/2$ and $J_z = -7/2$. The three candidates for the 4-plet from which two states are thrown out are $|1/2, -3/2\rangle \otimes \{|2, k\rangle, |1, k\rangle\}$, $k = 1, 0, -1$. The total spins are now $J_z = -1/2, -3/2, -5/2$. One guess is that the states with smallest value of J_z are dropped which would mean that $J_z = -7/2$ states in 3-plet and $J_z = -5/2$ states 4-plet become stopping codons.
5. One can ask why just vertebrate code? Why not vertebrate mitochondrial code, which has unbroken $A - G$ and $T - C$ symmetries with respect to the third nucleotide. And is it possible to understand the rarely occurring variants of the genetic code in this framework? One explanation is that the baryonic realization is the fundamental one and biochemical realization has gradually evolved from non-faithful realization to a faithful one as kind of emulation of dark nuclear physics. Also the role of tRNA in the realization of the code is crucial and could explain the fact that the code can be context sensitive for some codons.

If the pairing is based on the assumption that total quark spins and total flux tube spins are identical, the pairing of dark variants of DNA and its conjugate and DNA and mRNA are are not unique at the level of dark matter but respect the genetic code. Divisor code to be discussed later and equivalent with dark baryon code in realization based on magnetic flux tubes predicts similar non-uniqueness.

Is the genetic code a composite of $64 \to 40$ and $40 \to 20$ codes?

As found, dark baryon counterpart of tRNA could correspond to the multiplet of states containing 40 states. According to [103] most organisms have fewer the 45 species of tRNA. Typical value of anticodons is around 30 and in some organisms the number is as low as 22. This means that the number of different anticodons in tRNA is not larger than 45 and could be at most 40. Unfortunately I do not know what the real situation is. The realization of mRNA-tRNA pairing is known to be based on wobble base pairing [103] . This means that the pairing is not unique for the third nucleotide of the anticodon so that all mRNA codons can pair with tRNA in a manner consistent with the genetic code.

This finding suggests that tRNA could correspond to a 40-plet of anticodons at the level of dark matter then for tRNA-amino-acid genetic code the numbers of codons $N(k)$ with given degeneracy k would be $(N(1), N(2), N(3)) = \{5, 10, 5\}$. The interpretation would be as $DNA \to tRNA$ dark baryon genetic code projection of states of $4 \oplus 2 \oplus 2$ to states of 4 with the same spin in color bond degrees of freedom to a state with same spin in $J = 2$ multiplet with 5 states. Numbers of dark aminocids with given degeneracy k would $(N(1), N(2)) = \{16, 24\}$. Ordinary genetic code would result as a composite of the projections associated with these codes. If the identification in terms of 40-plet makes sense one might consider the possibility that the evolution for tRNA-dtRNA correspondence has not yet achieved the ideal situation in which tRNA anti-codons would be in 1-1 correspondence with their dark counterparts.

Objections

Consider next some particle physicist's objections against this picture.

1. The realization of the code requires the dark scaled variants of spin 3/2 baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one has a scaled up variant of hadron physics:

possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states can be scaled up.

2. Both the absolute and relative mass differences between Δ and N *resp.* ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant 1/137 - so that the mass splittings could be so small as to make decays impossible.

3. Dark hadrons could have lower mass scale than the ordinary ones if scaled up variants of quarks in p-adic sense are in question. Note that the model for cold fusion that inspired the idea about genetic code requires that dark nuclear strings have the same mass scale as ordinary baryons. In any case, the most general option inspired by the vision about hierarchy of conscious entities extended to a hierarchy of life forms is that several dark and p-adic scaled up variants of baryons realizing genetic code are possible.

4. A heavy objection relates to the addition of $L_z = -1$ excitation to $S_z = |1/2, \pm 1/2\rangle_{odd}$ states which transforms the degeneracies of the quark spin states from $(1, 3, 3, 1)$ to $(1, 2, 3, 2)$. The most plausible answer is that the breaking of the full rotation symmetry induced by nuclear string reduces $SO(3)$ to $SO(2)$. Also the fact that the states of massless particles are labeled by the representation of $SO(2)$ might be of some relevance.

The conclusion is that genetic code can be understand as a map of stringy baryonic states induced by the projection of all states with same spin projection to a representative state with the same spin projection. Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin. Charge neutrality is essential for having only the analogs of DNA, RNA and amino-acids and would guarantee the em stability of the states.

13.4.2 DNA as tqc hypothesis and dark baryon code

The coding of DNA codons by assigning to A,G *resp.* T,C of u and d quarks *resp.* their anti-quarks works nicely in the model of DNA as topological quantum computer. One can however consider also the option for which dark baryons code for entire DNA codons.

1. DNA as tqc using dark baryons to represent DNA codons would require that DNA strand is accompanied by a nuclear string parallel to it. If the pairing of baryons at the ends of string requires only opposite total quark spins and total flux tube spins the map would obey genetic code rather than being 1-1. The situation changes if dark baryon states are in 1-1 correspondence with the integers (n_a, n_b) labeling the page of book at which magnetic body of the codon resides.

2. The condition that the other end of flux tube beginning from the DNA codon contains nuclear string made from anti-baryons is natural but matter antimatter asymmetry if present also for dark matter does not favor this while mesonic strings with quarks at their ends are natural.

3. Rotating kinks assignable to 16 codons might be problematic from the point of tqc unless they represent codons with some special significance and play some special role - perhaps representing control commands in tqc program.

4. The flux tubes assignable to codons -instead of nucleotides as for earlier realization - would be basic units connected to lipids. The entanglement between dark baryon states of dark nuclear string would replaced the entanglement between quarks and anti-quarks at the ends of the flux tubes.

5. Only the portions of DNA having interpretation as gene have a natural decomposition to codons. Hence the dark baryon representation of codons is not attractive idea in intronic portions of the genome forming the most plausible candidates for quantum computing part of DNA since the portion of introns has been increasing during evolution and highest variation of this portion is encountered in human brain [169] . Hence one might think that tqc as relatively late outcome of the evolution and that only this part of genome is responsible for tqc so that the mpa of nucleotides to quarks would realize genetic code. Furthermore, braiding matters in tqc much more than the colors of braid strands determined by nucleotides so that intronic portions could quite well be repeating sequences without any obvious as information carriers in standard sense and therefore interpreted as junk DNA. There would be also an analogy between emergence of written language meaning that words as holistic entities were replaced with sequences of letters having as such no meaning.

13.5 Flux tube realization of the divisor code

Divisor code discovered by Khrennikov and Nilsson [82] allows a flux tube realization and a close connection with dark baryon code seems to be possible.

13.5.1 Divisor code

The idea of divisor code discussed in [24] is inspired by the following observations.

1. Consider the number $N(n)$ of integer divisors for integers n in the range $[1, 21]$ corresponding to amino-acids with stopping sign counted as amino-acid.
2. Denote the number of integers $n \leq 21$ for which the number of divisors is k by $B(k)$. Also stopping sign is counted as an amino-acid and $n = 0$ corresponds to amino-acid also. This number $N(k)$ varies in the range $[1, 6]$. $B(k)$ has the values $(1, 8, 2, 5, 1, 3)$ where k runs from 1 to 6.
3. Denote by $A(k)$ the number of amino-acids coded by k DNA codons. $A(k)$ has the values $2, 9, 2, 5, 0, 3$.

The spectrum of $A(k)$ is very similar to that of $B(k)$ and this raises the question whether one could understand genetic code as a divisor code in the sense that the degeneracy of amino-acid would be dictated by the number of the integers $1 \leq n \leq 21$ coding it. One might also ask whether the amino-acids which are abundant and thus important are coded by integers with a large number of divisors. Also one can ask whether the divisor structure possibly correlates with the structure of the amino-acid.

Divisor code in this form would be only approximate and one can wonder could try to imagine some simple symmetry breaking mechanism. In this respect the crucial observations might be following.

1. The number of DNAs needed to realize divisor code would be 70 instead of 64. One must drop 6 codons and by choosing them suitably one might hope of getting correct degeneracies.
2. The most natural manner to break the symmetry is to drop the 4 codons from the codons coding for 5-plet which would thus become 1-plet. 5-plet corresponds to integer $n = 16$ and its product compositions $(16, 1), (1, 16), (2, 8), (8, 2), (4, 4)$ correspond to the DNAs coding for it. $(4, 4)$ would naturally correspond to singlet.
3. By dropping 2 codons from some 4-plet one obtains 2-plet and correct degeneracies. One candidate for 4-plet corresponds to $n = 8$ and its product decompositions $(1, 8), (8, 1), (2, 4), (4, 2)$. By dropping two of these one obtains correct degeneracies. It might that power of 2 property of $n = 8$ and $n = 16$ somehow relates to 2-adicity and to the special role of these amino-acids.
4. A possible interpretation is in terms of symmetry based on cyclic group $Z(n)$ serving as a symmetry of DNA codons coding for amino-acid labeled n. Z_n allows decompositions $Z_n = Z_{n_1} \times Z_{n_2}$, $n = n_1 \times n_2$ and if the representations are invariant under Z_{n_2} and thus reduce to those of Z_{n_1} codons coding for a given amino-acid correspond to the product decompositions. Symmetry breaking would be due to the lacking 6 codons and would mean that only Z_4 invariant states would be realized for Z_{16} and Z_1 and Z_8 of Z_2 and Z_4 invariant states are realized for $n = 8$. $n = 4$ could correspond to triplet of stopping codons so that powers of 2 would be in special role for vertebrate code suggesting 4-adicity. 4-adicity is also suggests by the almost exact A-G and T-C symmetries of the last nucleotide.

13.5.2 Topological interpretation of the divisor code in TGD framework

The most concrete physical interpretation of the divisor code found in TGD framework is topological and based on TGD inspired vision about the role of dark matter in biology [82] .

1. The generalized 8-D imbedding space has a book like structure with pages glued together along back which is 4-D surface of $H = M^4 \times CP_2$ [27, 54] . Particles at different pages are dark relative to each other since they cannot have local interactions (appear in the same vertex of Feynman diagram). The pages are partially characterized by the value of Planck constant which can be arbitrary large. This explains the macroscopic quantum coherence of living matter. Matter can leak between different pages meaning a phase transition changing Planck constant.
2. The notion of magnetic body with flux tubes carrying dark matter and connecting different bio-molecules central for the TGD inspired model of living matter [26] . Magnetic bodies of bio-molecules can be also connected by magnetic flux tubes, even those in different pages of the book. For instance, the phase transition reducing $\hbar$ reduces the distance between two bio-molecules connected in this manner and forces them near to each other. This explains the extreme selectivity of bio-catalysis and the miraculous ability of two bio-molecules to find each other in the dense soup of bio-molecules. In particular, DNA and its conjugate codons, mRNA codons, and tRNA would be connected by this kind of flux tubes. Also amino-acids would be connected to tRNA codons in this manner since tRNA molecules catch the

amino-acids and bring them to the mRNA-amino-acid translation site. Genetic code could reduce to the selection rules for the flux tube connections connecting in general situation magnetic bodies belonging to different pages of the book.

3. The pages of book are almost copies of $M^4 \times CP_2$. This means that M^4 is replaced with n_a-fold singular covering and CP_2 with n_b-fold singular covering. The coverings have cyclic groups Z_{n_a} and Z_{n_b} act as discrete symmetries for the wave functions of particles in the covering. A given page is thus labeled by two pager numbers (n_a, n_b). Two pages contain common points and thus a direct tunneling of 3-surfaces between these pages is possible only if the number n_{a_1} of the sheets of covering divides n_{a_2} or vice versa. Same holds true for n_{b_1} and n_{b_2}. This rule is just the basic rule about how symmetries of system can change in phase transition. This number theoretic rule could be behind genetic code and the extreme selectivity of bio-catalysis.

4. Suppose that both bio-molecules correspond to ordinary matter with $n_a = n_b = 1$ but that the magnetic body of a given amino-acid corresponds to $(n_a(A), n_b(A))$ and DNA, RNA, and tRNA codon to $(r_a(DNA), r_b(DNA))$. Since the flux tube from tRNA codon to the amino-acid page is essential for the process in which amino-acid is attached to tRNA, only tRNA for with $r_a(tRNA)$ divides $n_a(A)$ can catch an amino-acid labeled by n_a. Same applies to r_b and n_b.

5. Without the presence of the integer n_b the code would fail since DNA codon labeled by r_a would code for all amino-acids for which n_a has r_a as a factor. n_b can indeed save the situation. Suppose that one has $r_b(tRNA) = n_b(A)$ if DNA codes for an amino-acid. Assume also that $n_b(a)$ is prime: $n_b(A) = p_b(A)$, and different for each amino-acid. This prime does not correspond to p-adic prime, which is expected to be very large in the length scales of atomic physics (electron corresponds to $M_{127} = 2^{127} - 1$). Note that the assumption that amino-acids are labeled by small primes was made in both TGD inspired number theoretical models of the genetic code.

6. The assumptions mean that tRNA and amino-acid can be connected by a magnetic flux tube only if one has

$$p_b(tRNA) = p_b(A)$$

and $r_a(tRNA)$ divides $n_a(A)$. If the pages numbers n_a vary in the range $[1, 21]$ the divisor code follows from the argument of the previous section. Taking the previous argument seriously, one should also understand why there is no amino-acid labeled by $n_a = 4$ and why corresponding DNAs correspond to prime characterizing $n_a = 4$, why the number of DNA codons labeled by the factors of $n_a = 8$ is two, and why the number of codons associated with $n_a = 16$ only one.

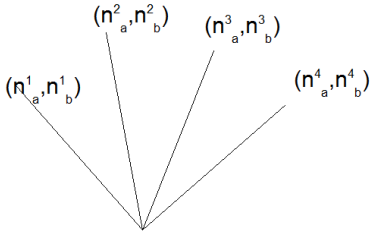

Figure 13.3: Illustration of the book-like structure of the generalized imbedding space.

Some further comments are in order.

1. The realization of the genetic code is not unique since the integers r_a and n_a could be replaced with Nn_a, where N is a product of primes larger than $p = 19$. It is also enough that the integers characterizing amino-acids are relative primes (have not common factors). The simplest assumption would be that the primes $p(A)$ satisfy $p(A) > 19$ so that $p(A)$ does not divide $n(A)$ for any A. If $p(A)$ is as small as possible the value spectrum of $p(A)$ is

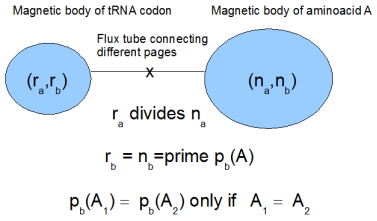

Figure 13.4: Illustration of the selection rules for magnetic flux tubes connecting magnetic bodies of tRNA and amino-acid.

$$\{23, 29, 31, 37, 41, 43, 47, 53, 59, 61, 67, 71, 73, 79, 83, 89, 97, 101, 103, 107, 109\} \quad .$$

If one assumes that the two additional aminoacids coded in some cases by non-vertebrate genetic code correspond to primes also the primes $113, 127$ are included.

What is interesting is that Mersenne prime $M_7 = 2^7 - 1 = 127$ appears in the model of genetic code based on the notion of Combinatorial Hierarchy [33]. This model assumes that DNA codons correspond to 64 integers in the range $1, ..., 127$. This realization of the genetic code cannot however be consistent with the divisor code realized in the proposed manner since it would require that the integers $n(A)p(A)$ belong to the range $1, .., 127$. The prime factors of these integers can however belong to this range.

2. The quantum states of dark baryons realize vertebrate genetic code with very general assumptions group theoretically [1, 34, 77] , [1] . Since dark matter is involved in both cases, one might wonder whether these codes could be related somehow. A one-one correspondence between the quantum states of dark nucleons representing codon and the integers r_a, p_b is required in order to have this connection. The simplest possibility is that that energy minimization implies that given dark nucleon resides with high probability at aflux tube labeled by unique value of r_a. Same applies to amino-acids.

3. The model in principle allows an infinite number of analogous codes and an interesting question is whether the bio-catalysis involves this kind of codes. The quantum antenna model for remote replication discussed in [34] allows a dynamical interpretation for the flux tube realization of the genetic code as a divisor code in terms of quantum antenna hypothesis [50], and predicts that sequences of DNA codons serve as names for polar molecules quite generally so that genetic code would define a universal language in living matter. This leads to an identification of the basic mechanism responsible for the functioning and evolution of the immune system.

13.5.3 About detailed correspondence between DNA codons, dark baryon codons, and their divisor code counterparts

One can make some conclusions also about the detailed correspondence between DNA codons and dark baryon codons as well as their divisor code counterparts. $L_z = -1$ requires that there is a rotating kink in flux tube representing nuclear string. One can ask whether also the corresponding DNA codons could be somehow special.

1. Maximal spin projections for both quarks ($J_z^q = 3/2$) and flux tube $J_z^f = \pm 2$ correspond to amino-acids met and trp coded by single codon. For the proposed interpretation of the divisor code these codons would correspond to $n = 1$ and $n = 16$.

2. Amino-acids coded by two codons correspond to $(J_z^q = 3/2, J_z^f \in \{1, 0, -1\})$ and $(J_z^q \in \{1/2, -1/2\}, J_z^f \in \{2, -2\})$. For the divisor code these amino-acids correspond to 8 primes plus lacking 9:th doublet results when one drops two codons from one 4-plet ($n = 8$ 4-plet is a good candidate).

3. For the baryonic realization 2 3-plets $J_z^q = -3/2, J_z^f \in \{2, -2\}$) contain one member corresponding to rotating kink. The first corresponds to ile and the DNA codon coding for met if T-C symmetry of the

third nucleotide were exact. Second corresponds to stop codon coding for trp if T-C symmetry were exact. In divisor code triplets corresponds to $n = 4$ (stop codon?) and $n = 9$.

4. Three 6-plets correspond to ($J_z^q = -3/2, J_z \in \{1, 0, -1\}$ contain one anomalous member each and the corresponding codon would naturally belong to the doublet part of 6-plet in the code table. In divisor code 6-plets correspond to $n \in \{12, 18, 20\}$.

5. Three of the six 4-plets ($J_z^q = 1/2, -3/2, J_z \in \{1, 0, -1\}$ contain 2 anomalous members. From one 4-plet 2 codes for nothing or formally stop codon so that it becomes 2-plet: naturally these codons correspond to $L_z = -1$ and a rotating kink in the helix model of the nuclear string. From second 3-plet one $L_1 = -1$ codon would codes for nothing becoming formally stop codon and one obtains second 2-plet.

6. The only regularity which comes in mind is that the 3 anomalous 4-plets and 2 anomalous doublets could populate the lowest row of the code table. The 16 oddballs would reside at the boundaries of the code table. In divisor code these would correspond to $n \in \{6, 8, 10, 14, 15, 21\}$. Dropping from $n = 8$ 4-plet 2 codons one would obtain 5 4-plets and 9 2-plets as required. Besides this one must drop 4 codons from $n = 16$ 5-plet to get singlet. As already noticed, 2-adicity suggests that $n = 2^k$ represents something special.

13.6 A model for protein folding and catalytic action

It would be fascinating if the vision about the role of flux tube connections would generalize to interactions of all molecules in living matter. The mere selection rules would mean hidden simplicity behind extremely complex looking interactions in living matter. The model for protein folding and catalytic action discussed in [3] is the first attempt in this direction. In the following this model is briefly summarized and the improvement of the model inspired by recent considerations is suggested.

13.6.1 Earlier model for the folding code

The model for the evolution of the genetic code led [29] to the idea that the folding of proteins obeys a code inherited from the genetic code. One can imagine several variants of this code. One of the is that amino-acid behaves like the conjugate Y_c of the middle nucleotide of the codon XYZ coding for it. Conjugation for amino-acids would correspond to the hydrophilic-hydrophobic dichotomy. Also catalyst action could reduce to effective base pairing in this picture chemically and at the level of quarks associated with the flux tube to matter antimatter conjugation. The guess that amino-acid and its conjugate form pairs turned out to be wrong however and after various twists and turns I ended up with the hypothesis that the amino-acid in protein behaves like $Y_c Z_c$ where Z corresponds to third nucleotide for some codon coding for the amino-acid.

It however turned that the model as such is probably too restrictive and not fully consistent in the particular cases studied. In the following this model is discussed briefly and later an improved model for protein folding is proposed.

Flux tubes as correlates of directed attention at molecular level

After some trials one ends up with a general conceptualization of the situation with the identification of ("wormhole") magnetic flux tubes as correlates for attention at molecular level so that a direct connection with TGD inspired theory of consciousness emerges at quantitative level. Whether wormhole flux tubes or ordinary flux tubes are needed is not a completely settled question yet and the attribute "wormhole" will not be used in the sequel. This allows a far reaching generalization of the DNA as topological quantum computer paradigm and makes it much more detailed. The final outcome is very simple quantitative model for both protein folding and catalyst action based on minimization of energy, which seems to be consistent with basic experimental facts as well as general ideas.

What kind of atoms can be connected by flux tubes?

1. Hydrogen bonds play a key role in bio-catalysis but are not understood completely satisfactorily in the standard chemistry. Hence the basic question is whether hydrogen bonds can be regarded as or are accompanied by short (wormhole) magnetic flux tubes: note that the subject-object asymmetry of directed attention would correspond to donor-acceptor asymmetry of they hydrogen bond. If this is the case, the identification of the magnetic flux tube connection as a prerequisite for a hydrogen bond or as hydrogen bond becomes natural. At least the atoms able to form hydrogen bonds could form flux tube contacts so that the model would be very predictive and would conform with the known important role of hydrogen bonds in bio-catalysis.

2. The fact that hydrogen bonds connect base pairs suggests a generalization of the notion of base pairing stating that under some conditions amino-acids coded by XYZ and UY_cV can behave like base pairs. These amino-acic pairs correspond to pairs of amino-acid residues which are hydrophilic *resp*. hydrophobic and hydrophobic residue do not form hydrogen bonds in general. These flux tubes would thus be more general and in general long. The model for DNA as topological quantum computer requires this kind of flux tubes and they would in general connect atoms or molecules which act as acceptors in hydrogen bonding: $O=$ atom in amino-acid and aromatic ring are basic examples.
3. If one assumes that both $N-H$ and $O=$ associated with the constant part of the amino-acid can act as flux tube terminals and represent Z and Y nucleotides of the codon XYZ coding for the amino-acid, one obtains $Y=Z$ pairing of $O=-O=$ flux tubes are allowed and $Y=Z_c$ pairing if only hydrogen bond like pairings are allowed.

Color inheritance by a reconnection of flux tubes

1. There should exist some mechanism allowing amino-acids to inherit the base pairing property from the tRNAs associated with them so that one can identify amino-acid with the middle nucleotide of the codon coding it. If tRNA middle nucleotide is connected to $O=$ of the amino-acid, this becomes possible since the reconnection of flux tubes preserves the "color" of the flux tubes coded by (A,T,G,C) that is by the quark or anti-quark coding for the nucleotide. The temporary formation of a hydrogen bond between $N-H$ and $O=$ of two amino-acids as in the case of alpha helix would allow $N-H$ to inherit the conjugate of the color associated with $O=$. Alternative interpretation is that this hydrogen bond is possible only if the predetermined color of $N-H$ is consistent with the inherited one. The inheritance of flux tube color would be a completely general mechanism and even the donor atoms in the residues of amino-acids could inherit the color of $O=$ in this manner.
2. A possible interpretation for the fixing of the flux tube color is in terms of quantum measurement selecting one color from quantum superposition in the reconnection process. This would mean that the unitary process can bring superposition back and reconnection process can change the inherited color. The hydrogen bonds between water molecules could correspond to quantum superpositions of different colors. This superposition property might relate to the wobble base pairing phenomenon for the third nucleotide in tRNA.

Folding code

The identification of $N-H$ as a representation for the conjugate of the third nucleotide Z means that amino-acids would remember which codon coded them. If only hydrogen bond like flux tubes are allowed, flux tubes can connect only amino-acids satisfying $Y=Z_c$. If $=O-O=$ flux tubes are allowed $Y=Z$ rule favored by the model of DNA as topological quantum computer follows. The isospin symmetry of the third nucleotide implies that both rules are quite flexible. If one identifies hydrogen bond with flux tube ($Y(n)=Z(n+k)$) the model works badly for both options. If one assumes only that the presence of a flux tube connecting amino-acids in either direction ($Y(n)=Z(n+k)$ or $Z(n)=Y(n+k)$) is a prerequisite for the formation of hydrogen bond, the model works. $Y=Z$ rule is favored by the study of five enzymes: the possible average length of alpha helix is considerably longer than the average length of alpha helix if gene is the unique gene allowing to satisfy $Y=Z$ rule. The explicit study of alpha helices and beta sheets for these enzymes demonstrates that the failure to satisfy the condition for the existence of hydrogen bond fails rarely and at most for two amino-acids (for 2 amino-acids in single case only).

$Y=Z$ rule could mean a solution of the basic problem of proteonics: Do genes determine the folding of proteins and how this would take place? The interpretation would be that the information loss suggested by the many-to-one character of the genetic code is only apparent. The apparently lost information which corresponds to the $A-G$ and $T-C$ symmetries of the third nucleotide codes for the hydrogen bonding and hence for the folding of the protein. The model in its most stringent form is easy to kill since in the case of alpha helices and beta sheets the hydrogen bonding fixes completely the DNA sequence coding for the protein. A weaker variant of the model based on quantum variant of wobble base pairing: in this case there are no conditions on DNA sequence. It turns out that only this variant works. Hence hydrogen bonded amino-acid behave as if they were coded by the unique codon consistent with $Y=Z$ rule.

Quantitative model

The quantitative model relies on the assumption that the contribution of a flux tube connecting two amino-acids to the potential energy depends only on the distance between the molecules in question. The extremals of the total interaction energy are same for any choice of the potential and only the absolute minimum of the interaction energy depends on the choice of the potential. The simplest potential corresponds to harmonic oscillator potential and would explain formation of alpha helices and beta sheets and with the fact that

hydrophilic and hydrophobic residues tend to have a large distance and only few flux tube contacts. For large Planck constant also long flux tubes could correspond to attractive harmonic oscillator potential. Also the contribution of other interactions between neighboring amino-acids are expected to be present but are neglected in the simplest model. The model predicts alpha helices and beta sheets, and more generally, periodic structures, as solutions to energy minimization equations.

The model fails to catch completely the basic rules of protein folding, and the predictions are not fully consistent with empirical facts in the cases studied. A model in which the hydrophilic and hydrophobic interactions are mediated by flux tubes between magnetic bodies of the molecule and water molecule and in this manner induce long range interactions between amino-acids - somewhat like the attractive interactions of electrons with ions induce attractive interaction between the members of a Cooper pair - looks more attractive. This model is however computationally much heavier and is not discussed in [3] . In the sequel a formulation of this model is discussed.

13.6.2 Hydrophily and hydrophoby number theoretically

Amino-acids can be classified to hydrophilic and hydrophobic ones whereas all DNA codons are hydrophilic. Hydrophily and hydrophoby are believed to relate to the standard chemistry alone and this might be the case. One can however just for fun ask whether hydrophily and hydrophoby could have a connection with divisor code, formation of flux tubes connecting the molecule to water molecules, and phase transitions changing the value of Planck constant and changing the length of flux tube. I have discussed this idea already in the model of protein folding [3] .

To simplify the model assume that only single dark page is associated with water molecule and labeled by (n_a^W, n_b^W). Of course, several levels characterized by different integers are also possible and this would bring in additional flexibility. Both hydrophoby and hydrophily would mean interaction mediated by the flux tubes to the magnetic body of water with the sign of the force differing for hydrophilic and hydrophobic amino-acids. There is no need to assume that quarks and anti-quarks generate the interaction. Gly for which the residue is just hydrogen atom does not allow classification as a hydrophilic or hydrophobic which would suggest that it does not have any flux tube connections with the magnetic body of the water. The interaction mediated by flux tubes between amino-acids and water molecules would be analogous to the interaction induced by the interaction between electrons and ions inducing attractive interaction between the members of Cooper pair. It would induce attractive interaction between hydrophilic amino-acids and repulsive interaction between hydrophilic and hydrophobic amino-acids favoring the formation of hydrophilic outer surfaces and hydrophobic inner surfaces.

One could understand hydrophily/hydrophoby dichotomy number theoretically for both options. The discussion of the first option makes clear that also second option is possible to realize.

1. Assume that n_a^W is divisible by all integers n_a^{DNA} associated with DNA codons and thus involves suitable powers of primes $p \leq 19$. It could contain also an integer factor which is product of primes larger than $p = 19$. This is necessary for achieving hydrophily of DNA codons.
2. Hydrophily of DNA codons also requires n_b^W must be proportional to the product of coprime integers n_b^W (primes for the simplest option) assignable to DNA codons. n_b^W could involve also a factor proportional to second integer expressible as product of primes $p > 19$. The simplest option is that this integer equals to 1.
3. For hydrophobic amino-acids integers n_b^A must be of form $mn_b^A = n_b^{DNA} m_b$ such that m_a does not divide n_b^W and n_b^W. This is enough to guarantee that magnetic flux tubes in either direction are impossible so that hydrophoby is guaranteed in the proposed sense. This definition extends also to other molecules and can be expressed in terms of the integers (n_a, n_b) labeling the magnetic body of the molecule.
4. Second option is obtained by assigning the integer m_b only to *Gly* which is neither hydrophilic nor hydrophobic.

13.6.3 Could there be new physics behind hydrophily and hydrophoby

One could accept just as a fact that magnetic flux tubes to the magnetic body of water mediate an interaction which is attractive or repulsive between water molecules and amino-acids and attractive between DNA molecules and water. Accepting that this induces interaction between amino-acids one could proceed to model building without any mention about TGD.

One could also try to dig deeper and ask what might be the origin of this interaction.

1. **Option I**: Could one understand the interaction in terms of phase transitions changing the Planck constant of the magnetic flux tube. The interaction would be repulsive (attractive) would result if the interaction energy increases (decreases) when Planck constant is reduced. Magnetic interaction energy is certainly the best candidate and could also imply the equivalence of the divisor code and dark baryon code.

2. **Option II**: Could hydrophily and hydrophoby be described in terms of em interactions of quarks representing nucleotides in the model of DNA as tqc. For instance, could amino-acids and water molecules be characterized by charges which are of opposite sign for water molecules and hydrophilic molecules and of same sign for water molecules and hydrophobic molecules.

For **Option I**, which represents completely new physics (using the standards of TGD!), the situation looks promising. The magnetic interaction energy assignable to the flux tube is a function of the integers (n_a, n_b) -in particular of the Planck constant of the flux tube- and the minimization is performed by keeping the charges of the quarks possibly at its ends fixed. This new physics fits also nicely with the idea that magnetic body controls the living matter by utilizing phase transitions changing Planck constant.

What comes in mind in the case of **Option II** is that the ends of the flux tube carry opposite charges correlating with the codon coding for the amino-acid and giving rise to ordinary gauge interactions. Unfortunately this scenario does not seem to work.

1. In [3] it was found that (denoting codons by XYZ) only $Y = A, G$ type amino-acid residue can form hydrogen bonds and is hydrophilic and thus interacts strongly with water and DNA and RNA. If water end of flux tube corresponds to anti-quarks the attractive interaction between quark and anti-quark at the ends of flux tube could relate to hydrophily. For hydrophobic amino-acids one would have interaction between identical quarks and already Fermi statistics would cause repulsion. In DNA as tqc model based on the coding of A,G and T,C in terms of quarks u,d and their anti-quarks hydrophily-hydrophoby dichotomy corresponds to matter-antimatter dichotomy for quark assigned to the ends of the flux tube. Quarks and anti-quark have opposite charges. Hence the flux tube ends of hydrophilic amino-acids could correspond to quarks and water and hydrophobic ends of flux tubes to anti-quarks. Therefore the DNA as tqc model would predict the needed behavior of the forces. In the case of Gly containing only hydrogen as residue the flux tube might be simply absent.

2. DNA codons A,T,C,G are bases and thus polar and hydrophilic. In the case of DNA charge conjugation for quarks corresponds to the puridine-pyrimidine complementarity corresponding to conjugation of nucleotides. The rule applying in the case of amino-acids would predict T,C to be hydrophobic nucleotides which does not make sense. Therefore it seems that hydrophily and hydrophoby cannot reduce to the interactions of dark quarks and that they only represent conjugation of nucleotides symbolically.

13.6.4 An improved model for protein folding

To begin with let us summarize some basic facts about protein folding.

1. Hydrophily and hydrophoby play a key role in protein folding and dictate to a high degree the resulting folding patterns. This suggests that one cannot neglect the role of water in the process.

2. Protein folding proceeds from short to long length scales starting with the formation of secondary structures such as alpha helices, beta sheets, and random coil portions and is followed by the formation of tertiary and higher structures.

3. The formation of hydrogen bonds is in a decisive role in the formation of secondary structures. The mechanism leading to their formation might be contraction of magnetic flux tube by a phase transition changing Planck constant.

4. The folding patterns do not depend strongly on the precise primary structure, that is precise amino-acid decomposition which suggests that instead of the detailed chemistry the forces between quarks and anti-quarks mediated by flux tubes is what matter so that hydrophily and hydrophoby would become the basic characterizers of the interaction. The phase transitions changing Planck constant would indeed represent this kind of universal interactions independent of the chemistry.

5. In the first approximation amino-acids could be labeled by a variable telling whether it is hydrophobic, hydrophilic, or neither or these (Gly). This approximation would be broken by special amino-acids which appear in edges if beta sheets (Pro) and Cys which often appear as S-S boded pair in junctions. By bringing in forces depending on the angles between tangent vectors of successive amino-acids and on amino-adics themselves this tendency could be modeled.

The earlier approach to protein folding inspired by DNA as tqc idea did not start from this picture but assumed that direct flux tube connections between amino-acids rather than the interactions induced by flux tube connections with the magnetic bodies of water molecules were responsible for the folding. The model did not lead to any spectacular results and the proposed rules were not fully consistent in the cases studied.

13.6.5 The model for which the magnetic body of water is involved

The improved approach to protein folding starts from the general vision about magnetic body containing dark matter as a controller of visible matter in living system. The protein and its magnetic body would be regarded as a living system in itself.

1. Magnetic body must have large number of flux tube contacts to the visible matter. An excellent candidate for the magnetic body is that assignable with water and having flux tube connections to DNA and both hydrophilic and hydrophobic amino-acids. The magnetic body could control and at least fasten the self-organization process leading to the folding pattern which - by applying standard argument - would otherwise take astronomical time otherwise. The two-step attractive connections between all hydrophilic amino-acids would be possible via the magnetic body of water. The non-hydrophilic amino-acids not in direct contact with water are known to be more like passive structural stuff responsible for a fixed structure but not so relevant for the functioning of the bio-molecule. Hydrophily and hydrophoby would reflect the dependence of interaction energy on the value of Planck constant associated with the flux tube mediating the interaction.

2. This picture implies a straightforward modification of the earlier model. The simplest model would minimize a potential function V expressible as a sum $V = V_1 + V_2 + V_3$ of three terms. V_1 would be sum of the values of a universal two-particle potential function $V_{phi,phi}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophilic amino-acid pairs and giving rise to an attractive force. V_2 would be a sum of a universal two-particle potential function $V_{pho,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophobic amino-acid pairs. V_3 would be would be sum of the values of a universal potential function $V_{phi,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all pairs of hydrophilic and hydrophobic amino-acids. This potential function would induce a repulsive force. Besides this a constraint force due to the fact that amino-acids form a sequence would be present.

3. The resultant of the forces along lines connecting amino-acids would be parallel to the amino-acid sequence in the mechanical equilibrium. Hydrogen bonds and other bonds are indeed formed between neighboring hydrophilic amino-acids and the contraction of the flux tubes connecting the amino-acids in question to the magnetic body of water could be the mechanism. The model seems to be consistent with the basic qualitative facts about folding. The quantitative testing of the model would require determination of the conformations minimizing the potential function subject to the constraint provided by amino-acid sequence. Here of course the freedom to choose the three functions provides a considerable flexibility and symmetry arguments might allow to pose conditions on the form of these functions.

4. One could also include to the potential function describing a direct interaction with water molecules depending on parameters like pH affecting the folding pattern. The resultant for a given amino-acid would be sum of forces directed from a hydrophilic amino-acids to neighboring water molecules. It is not clear whether the normal component of this force could be compensated by the induced forces between amino-acids in a typical equilibrium configuration and the formation of hydrogen bonds involving the contraction of the flux tube could be the manner to achieve this.

Could one regard amino-acids and DNAs of given type as analog of species?

An interesting idea raised by the work with the model for protein folding is that the magnetic bodies amino-acids or DNA codon of a given type could behave like single phase on their respective page of the book so that the mutual interactions of their magnetic bodies could affect considerably the behavior of this phase to first order although amino-acids themselves are at different positions and one might expect only small correlations between their motions. Whether the dynamics of amino-acids of given type in protein folding are strongly correlated could be tested.

In certain sense one could speak of single species formed by amino-acids of given type and folding as long range interaction could be seen as an outcome of self-organizing interaction between members of various species and between species themselves plus short range constraints due to the fact that amino-acids form a sequence. The question applies to DNA and RNA codons and also to larger units such as genes formed to which one could assign their own page of the book. Water would represent the page to which all DNAs can send flux tubes. Even the notion of biological species could involve common dark space-time sheet(s) where the magnetic bodies of the members of species are and interact making the members of species to behave like single coherent unit.

13.7 Appendix: Generalization of the notion of imbedding space

This section summarizes the the attempt to understand how the hierarchy of Planck constants is realized at the level of imbedding space and what quantum criticality for phase transitions changing Planck constant means.

13.7.1 Hierarchy of Planck constants and the generalization of the notion of imbedding space

In the following the recent view about structure of imbedding space forced by the quantization of Planck constant is summarized. The question is whether it might be possible in some sense to replace H or its Cartesian factors by their necessarily singular multiple coverings and factor spaces. One can consider two options: either M^4 or the causal diamond CD. The latter one is the more plausible option from the point of view of WCW geometry.

The evolution of physical ideas about hierarchy of Planck constants

The evolution of the physical ideas related to the hierarchy of Planck constants and dark matter as a hierarchy of phases of matter with non-standard value of Planck constants was much faster than the evolution of mathematical ideas and quite a number of applications have been developed during last five years.

1. The starting point was the proposal of Nottale [10] that the orbits of inner planets correspond to Bohr orbits with Planck constant $\hbar_{gr} = GMm/v_0$ and outer planets with Planck constant $\hbar_{gr} = 5GMm/v_0$, $v_0/c \simeq 2^{-11}$. The basic proposal [65] was that ordinary matter condenses around dark matter which is a phase of matter characterized by a non-standard value of Planck constant whose value is gigantic for the space-time sheets mediating gravitational interaction. The interpretation of these space-time sheets could be as magnetic flux quanta or as massless extremals assignable to gravitons.
2. Ordinary particles possibly residing at these space-time sheet have enormous value of Compton length meaning that the density of matter at these space-time sheets must be very slowly varying. The string tension of string like objects implies effective negative pressure characterizing dark energy so that the interpretation in terms of dark energy might make sense [66] . TGD predicted a one-parameter family of Robertson-Walker cosmologies with critical or over-critical mass density and the "pressure" associated with these cosmologies is negative.
3. The quantization of Planck constant does not make sense unless one modifies the view about standard space-time is. Particles with different Planck constant must belong to different worlds in the sense local interactions of particles with different values of $\hbar$ are not possible. This inspires the idea about the book like structure of the imbedding space obtained by gluing almost copies of H together along common "back" and partially labeled by different values of Planck constant.
4. Darkness is a relative notion in this framework and due to the fact that particles at different pages of the book like structure cannot appear in the same vertex of the generalized Feynman diagram. The phase transitions in which partonic 2-surface X^2 during its travel along X^3_l leaks to another page of book are however possible and change Planck constant. Particle (say photon -) exchanges of this kind allow particles at different pages to interact. The interactions are strongly constrained by charge fractionization and are essentially phase transitions involving many particles. Classical interactions are also possible. It might be that we are actually observing dark matter via classical fields all the time and perhaps have even photographed it [77] .
5. The realization that non-standard values of Planck constant give rise to charge and spin fractionization and anyonization led to the precise identification of the prerequisites of anyonic phase [54] . If the partonic 2-surface, which can have even astrophysical size, surrounds the tip of CD, the matter at the surface is anyonic and particles are confined at this surface. Dark matter could be confined inside this kind of light-like 3-surfaces around which ordinary matter condenses. If the radii of the basic pieces of these nearly spherical anyonic surfaces - glued to a connected structure by flux tubes mediating gravitational interaction - are given by Bohr rules, the findings of Nottale [10] can be understood. Dark matter would resemble to a high degree matter in black holes replaced in TGD framework by light-like partonic 2-surfaces with a minimum size of order Schwartschild radius r_S of order scaled up Planck length $l_{Pl} = \sqrt{\hbar_{gr} G} = GM$. Black hole entropy is inversely proportional to $\hbar$ and predicted to be of order unity so that dramatic modification of the picture about black holes is implied.
6. Perhaps the most fascinating applications are in biology. The anomalous behavior ionic currents through cell membrane (low dissipation, quantal character, no change when the membrane is replaced with

artificial one) has a natural explanation in terms of dark supra currents. This leads to a vision about how dark matter and phase transitions changing the value of Planck constant could relate to the basic functions of cell, functioning of DNA and aminoacids, and to the mysteries of bio-catalysis. This leads also a model for EEG interpreted as a communication and control tool of magnetic body containing dark matter and using biological body as motor instrument and sensory receptor. One especially amazing outcome is the emergence of genetic code of vertebrates from the model of dark nuclei as nuclear strings [1, 77] , [1] .

The most general option for the generalized imbedding space

Simple physical arguments pose constraints on the choice of the most general form of the imbedding space.

1. The fundamental group of the space for which one constructs a non-singular covering space or factor space should be non-trivial. This is certainly not possible for M^4, CD, CP_2, or H. One can however construct singular covering spaces. The fixing of the quantization axes implies a selection of the sub-space $H_4 = M^2 \times S^2 \subset M^4 \times CP_2$, where S^2 is geodesic sphere of CP_2. $\hat{M}^4 = M^4 \backslash M^2$ and $\hat{CP}_2 = CP_2 \backslash S^2$ have fundamental group Z since the codimension of the excluded sub-manifold is equal to two and homotopically the situation is like that for a punctured plane. The exclusion of these sub-manifolds defined by the choice of quantization axes could naturally give rise to the desired situation.

2. CP_2 allows two geodesic spheres which left invariant by $U(2$ *resp.* $SO(3)$. The first one is homologically non-trivial. For homologically non-trivial geodesic sphere $H_4 = M^2 \times S^2$ represents a straight cosmic string which is non-vacuum extremal of Kähler action (not necessarily preferred extremal). One can argue that the many-valuedness of $\hbar$ is un-acceptable for non-vacuum extremals so that only homologically trivial geodesic sphere S^2 would be acceptable. One could go even further. If the extremals in $M^2 \times CP_2$ can be preferred non-vacuum extremals, the singular coverings of M^4 are not possible. Therefore only the singular coverings and factor spaces of CP_2 over the homologically trivial geodesic sphere S^2 would be possible. This however looks a non-physical outcome.

   (a) The situation changes if the extremals of type $M^2 \times Y^2$, Y^2 a holomorphic surface of CP_3, fail to be hyperquaternionic. The tangent space M^2 represents hypercomplex sub-space and the product of the modified gamma matrices associated with the tangent spaces of Y^2 should belong to M^2 algebra. This need not be the case in general.

   (b) The situation changes also if one reinterprets the gluing procedure by introducing scaled up coordinates for M^4 so that metric is continuous at $M^2 \times CP_2$ but CDs with different size have different sizes differing by the ratio of Planck constants and would thus have only piece of lower or upper boundary in common.

3. For the more general option one would have four different options corresponding to the Cartesian products of singular coverings and factor spaces. These options can be denoted by $C-C$, $C-F$, $F-C$, and $F-F$, where C (F) signifies for covering (factor space) and first (second) letter signifies for CD (CP_2) and correspond to the spaces $(\hat{CD}\hat{\times}G_a)\times(\hat{CP}_2\hat{\times}G_b)$, $(\hat{CD}\hat{\times}G_a)\times\hat{CP}_2/G_b$, $\hat{CD}/G_a\times(\hat{CP}_2\hat{\times}G_b)$, and $\hat{CD}/G_a \times \hat{CP}_2/G_b$.

4. The groups G_i could correspond to cyclic groups Z_n. One can also consider an extension by replacing M^2 and S^2 with its orbit under more general group G (say tedrahedral, octahedral, or icosahedral group). One expects that the discrete subgroups of $SU(2)$ emerge naturally in this framework if one allows the action of these groups on the singular sub-manifolds M^2 or S^2. This would replace the singular manifold with a set of its rotated copies in the case that the subgroups have genuinely 3-dimensional action (the subgroups which corresponds to exceptional groups in the ADE correspondence). For instance, in the case of M^2 the quantization axes for angular momentum would be replaced by the set of quantization axes going through the vertices of tedrahedron, octahedron, or icosahedron. This would bring non-commutative homotopy groups into the picture in a natural manner.

About the phase transitions changing Planck constant

There are several non-trivial questions related to the details of the gluing procedure and phase transition as motion of partonic 2-surface from one sector of the imbedding space to another one.

1. How the gluing of copies of imbedding space at $M^2 \times CP_2$ takes place? It would seem that the covariant metric of CD factor proportional to $\hbar^2$ must be discontinuous at the singular manifold since only in this manner the idea about different scaling factor of CD metric can make sense. On the other hand, one can always scale the M^4 coordinates so that the metric is continuous but the sizes of CDs with different Planck constants differ by the ratio of the Planck constants.

2. One might worry whether the phase transition changing Planck constant means an instantaneous change of the size of partonic 2-surface in M^4 degrees of freedom. This is not the case. Light-likeness in $M^2 \times S^2$ makes sense only for surfaces $X^1 \times D^2 \subset M^2 \times S^2$, where X^1 is light-like geodesic. The requirement that the partonic 2-surface X^2 moving from one sector of H to another one is light-like at $M^2 \times S^2$ irrespective of the value of Planck constant requires that X^2 has single point of M^2 as M^2 projection. Hence no sudden change of the size X^2 occurs.
3. A natural question is whether the phase transition changing the value of Planck constant can occur purely classically or whether it is analogous to quantum tunneling. Classical non-vacuum extremals of Chern-Simons action have two-dimensional CP_2 projection to homologically non-trivial geodesic sphere S^2_I. The deformation of the entire S^2_I to homologically trivial geodesic sphere S^2_{II} is not possible so that only combinations of partonic 2-surfaces with vanishing total homology charge (Kähler magnetic charge) can in principle move from sector to another one, and this process involves fusion of these 2-surfaces such that CP_2 projection becomes single homologically trivial 2-surface. A piece of a non-trivial geodesic sphere S^2_I of CP_2 can be deformed to that of S^2_{II} using 2-dimensional homotopy flattening the piece of S^2 to curve. If this homotopy cannot be chosen to be light-like, the phase transitions changing Planck constant take place only via quantum tunnelling. Obviously the notions of light-like homotopies (cobordisms) are very relevant for the understanding of phase transitions changing Planck constant.

How one could fix the spectrum of Planck constants?

The question how the observed Planck constant relates to the integers n_a and n_b defining the covering and factors spaces, is far from trivial and I have considered several options. The basic physical inputs are the condition that scaling of Planck constant must correspond to the scaling of the metric of CD (that is Compton lengths) on one hand and the scaling of the gauge coupling strength $g^2/4\pi\hbar$ on the other hand.

1. One can assign to Planck constant to both CD and CP_2 by assuming that it appears in the commutation relations of corresponding symmetry algebras. Algebraist would argue that Planck constants $\hbar(CD)$ and $\hbar(CP_2)$ must define a homomorphism respecting multiplication and division (when possible) by G_i. This requires $r(X) = \hbar(X)\hbar_0 = n$ for covering and $r(X) = 1/n$ for factor space or vice versa.
2. If one assumes that $\hbar^2(X)$, $X = M^4$, CP_2 corresponds to the scaling of the covariant metric tensor g_{ij} and performs an over-all scaling of H-metric allowed by the Weyl invariance of Kähler action by dividing metric with $\hbar^2(CP_2)$, one obtains the scaling of M^4 covariant metric by $r^2 \equiv \hbar^2/\hbar_0^2 = \hbar^2(M^4)/\hbar^2(CP_2)$ whereas CP_2 metric is not scaled at all.
3. The condition that $\hbar$ scales as n_a is guaranteed if one has $\hbar(CD) = n_a\hbar_0$. This does not fix the dependence of $\hbar(CP_2)$ on n_b and one could have $\hbar(CP_2) = n_b\hbar_0$ or $\hbar(CP_2) = \hbar_0/n_b$. The intuitive picture is that n_b- fold covering gives in good approximation rise to $n_a n_b$ sheets and multiplies YM action action by $n_a n_b$ which is equivalent with the $\hbar = n_a n_b \hbar_0$ if one effectively compresses the covering to $CD \times CP_2$. One would have $\hbar(CP_2) = \hbar_0/n_b$ and $\hbar = n_a n_b \hbar_0$. Note that the descriptions using ordinary Planck constant and coverings and scaled Planck constant but contracting the covering would be alternative descriptions.

   This gives the following formulas $r \equiv \hbar/\hbar_0 = r(M^4)/r(CP_2)$ in various cases.

	$C-C$	$F-C$	$C-F$	$F-F$
r	$n_a n_b$	$\frac{n_a}{n_b}$	$\frac{n_b}{n_a}$	$\frac{1}{n_a n_b}$

Preferred values of Planck constants

Number theoretic considerations favor the hypothesis that the integers corresponding to Fermat polygons constructible using only ruler and compass and given as products $n_F = 2^k \prod_s F_s$, where $F_s = 2^{2^s} + 1$ are distinct Fermat primes, are favored. The reason would be that quantum phase $q = exp(i\pi/n)$ is in this case expressible using only iterated square root operation by starting from rationals. The known Fermat primes correspond to $s = 0, 1, 2, 3, 4$ so that the hypothesis is very strong and predicts that p-adic length scales have satellite length scales given as multiples of n_F of fundamental p-adic length scale. $n_F = 2^{11}$ corresponds in TGD framework to a fundamental constant expressible as a combination of Kähler coupling strength, CP_2 radius and Planck length appearing in the expression for the tension of cosmic strings, and the powers of 2^{11} was proposed to define favored as values of n_a in living matter [23] .

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1+i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that all the four p-adic length scales sith $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm) define scaled up copies of electro-weak and QCD type physics with ordinary value of $\hbar$ and that these physics are induced by dark variants of corresponding lower level physics leads to a prediction for the preferred values of

$r = 2^{k_d}$, $k_d = k_i - k_j$, and the resulting picture finds support from the ensuing models for biological evolution and for EEG [23] . This hypothesis - to be referred to as Mersenne hypothesis - replaces the rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant.

How Planck constants are visible in Kähler action?

$\hbar(M^4)$ and $\hbar(CP_2)$ appear in the commutation and anticommutation relations of various superconformal algebras. Only the ratio of M^4 and CP_2 Planck constants appears in Kähler action and is due to the fact that the M^4 and CP_2 metrics of the imbedding space sector with given values of Planck constants are proportional to the corresponding Planck. This implies that Kähler function codes for radiative corrections to the classical action, which makes possible to consider the possibility that higher order radiative corrections to functional integral vanish as one might expect at quantum criticality. For a given p-adic length scale space-time sheets with all allowed values of Planck constants are possible. Hence the spectrum of quantum critical fluctuations could in the ideal case correspond to the spectrum of $\hbar$ coding for the scaled up values of Compton lengths and other quantal lengths and times. If so, large $\hbar$ phases could be crucial for understanding of quantum critical superconductors, in particular high T_c superconductors.

A simple model for fractional quantum Hall effect

The generalization of the imbedding space suggests that it could possible to understand fractional quantum Hall effect [1] at the level of basic quantum TGD as integer QHE for non-standard value of Planck constant.

The formula for the quantized Hall conductance is given by

$$\begin{aligned} \sigma &= \nu \times \frac{e^2}{h} \ , \\ \nu &= \frac{n}{m} \ . \end{aligned} \tag{13.7.1}$$

Series of fractions in $\nu = 1/3, 2/5, 3/7, 4/9, 5/11, 6/13, 7/15...$, $2/3, 3/5, 4/7, 5/9, 6/11, 7/13...$, $5/3, 8/5, 11/7, 14/9...4/3, 7/5, 10/7, 13/9...$, $1/5, 2/9, 3/13...$, $2/7, 3/11...$, $1/7....$ with odd denominator have been observed as are also $\nu = 1/2$ and $\nu = 5/2$ states with even denominator [1] .

The model of Laughlin [16] cannot explain all aspects of FQHE. The best existing model proposed originally by Jain is based on composite fermions resulting as bound states of electron and even number of magnetic flux quanta [13] . Electrons remain integer charged but due to the effective magnetic field electrons appear to have fractional charges. Composite fermion picture predicts all the observed fractions and also their relative intensities and the order in which they appear as the quality of sample improves.

Before proposing the TGD based model of FQHE as IQHE with non-standard value of Planck constant, it is good to represent a simple explanation of IQHE effect. Choose the coordinates of the current currying slab so that x varies in the direction of Hall current and y in the direction of the main current. For IQHE the value of Hall conductivity is given by $\sigma = j_y/E_x = n_e ev/vB = n_e e/B = Ne^2/hBS = Ne^2/mh$, were m characterizes the value of magnetized flux and N is the total number of electrons in the current. In the Landau gauge $A_y = xB$ one can assume that energy eigenstates are momentum eigenstates in the direction of current and harmonic oscillator Gaussians in x-direction in which Hall current runs. This gives

$$\Psi \propto exp(iky) H_n(x + kl^2) exp(-\frac{(x+kl^2)^2}{2l^2}) \ , \quad l^2 = \frac{\hbar}{eB} \ . \tag{13.7.2}$$

Only the states for which the oscillator Gaussian differs considerably from zero inside slab are important so that the momentum eigenvalues are in good approximation in the range $0 \leq k \leq k_{max} = L_x/l^2$. Using $N = (L_y/2\pi) \int_0^{k_{max}} dk$ one obtains that the total number of momentum eigenstates associated with the given value of n is $N = eBdL_xL_y/h = n$. If ν Landau states are filled, the value of σ is $\sigma = \nu e^2/h$.

The interpretation of FQHE as IQHE with non standard value of Planck constant could explain also the fractionization of charge, spin, and electron number. There are $2 \times 2 = 4$ combinations of covering and factor spaces of CP_2 and three of them can lead to the increase or at least fractionization of the Planck constant required by FQHE.

1. The prediction for the filling fraction in FQHE would be

$$\nu = \nu_0 \frac{\hbar_0}{\hbar} \ , \quad \nu_0 = 1, 2, ... \ . \tag{13.7.3}$$

ν_0 denotes the number of filled Landau levels.

2. Let us denote the options as C-C, C-F, F-C, F-F, where the first (second) letter tells whether a singular covering or factor space of CD (CP_2) is in question. The observed filling fractions are consistent with options C-C, C-F, and F-C for which CD or CP_2 or both correspond to a singular covering space. The values of ν in various cases are given by the following table.

Option	$C-C$	$C-F$	$F-C$
ν	$\frac{\nu_0}{n_a n_b}$	$\frac{\nu_0 n_b}{n_a}$	$\frac{\nu_0 n_a}{n_b}$

(13.7.4)

   There is a complete symmetry under the exchange of CD and CP_2 as far as values of ν are considered.

3. All three options are consistent with observations. Charge fractionization allows only the options $C-C$ and $F-C$. If one believes the general arguments stating that also spin is fractionized in FQHE then only the option $C-C$, for which charge and spin units are equal to $1/n_b$ and $1/n_a$ respectively, remains. For $C-C$ option one must allow $\nu_0 > 1$.

4. Both $\nu = 1/2$ and $\nu = 5/2$ state has been observed [1, 9] . The fractionized charge is believed to be $e/4$ in the latter case [19, 17] . This requires $n_b = 4$ allowing only (C, C) and (F, C) options. $n_i \geq 3$ holds true if coverings and factor spaces are correlates for Jones inclusions and this gives additional constraint. The minimal values of (ν_0, n_a, n_b) are $(2, 1, 4)$ for $\nu = 1/2$ and $(10, 1, 4)$ for $\nu = 5/2$) for both $C-C$ and $F-C$ option. Filling fraction $1/2$ corresponds in the composite fermion model and also experimentally to the limit of zero magnetic field [13] . $n_b = 2$ would be inconsistent with the observed fractionization of electric charge for $\nu = 5/2$ and with the vision inspired by Jones inclusions implying $n_i \geq 3$.

5. A possible problematic aspect of the TGD based model is the experimental absence of even values of m except $m = 2$ (Laughlin's model predicts only odd values of m). A possible explanation is that by some symmetry condition possibly related to fermionic statistics (as in Laughlin model) both n_a and n_b must be odd. This would require that $m = 2$ case differs in some manner from the remaining cases.

6. Large values of m in $\nu = n/m$ emerge as B increases. This can be understood from flux quantization. One has $e \int BdS = n\hbar$. By using actual fractional charge $e_F = e/n_b$ in the flux factor would give for (C, C) option $e_F \int BdS = nn_a\hbar_0$. The interpretation is that each of the n_b sheets contributes one unit to the flux for e. Note that the value of magnetic field at given sheet is not affected so that the build-up of multiple covering seems to keep magnetic field strength below critical value.

7. The understanding of the thermal stability is not trivial. The original FQHE was observed in 80 mK temperature corresponding roughly to a thermal energy of $T \sim 10^{-5}$ eV. For graphene the effect is observed at room temperature. Cyclotron energy for electron is (from $f_e = 6 \times 10^5$ Hz at $B = .2$ Gauss) of order thermal energy at room temperature in a magnetic field varying in the range 1-10 Tesla. This raises the question why the original FQHE requires such a low temperature. A possible explanation is that since FQHE involves several values of Planck constant, it is quantum critical phenomenon and is characterized by a critical temperature. The differences of single particle energies associated with the phase with ordinary Planck constant and phases with different Planck constant would characterize the transition temperature.

13.7.2 Could the dynamics of Kähler action predict the hierarchy of Planck constants?

The original justification for the hierarchy of Planck constants came from the indications that Planck constant could have large values in both astrophysical systems involving dark matter and also in biology. The realization of the hierarchy in terms of the singular coverings and possibly also factor spaces of CD and CP_2 emerged from consistency conditions. The formula for the Planck constant involves heuristic guess work and physical plausibility arguments. There are good arguments in favor of the hypothesis that only coverings are possible. Only a finite number of pages of the Big Book correspond to a given value of Planck constant, biological evolution corresponds to a gradual dispersion to the pages of the Big Book with larger Planck constant, and a connection with the hierarchy of infinite primes and p-adicization program based on the mathematical realization of finite measurement resolution emerges.

One can however ask whether this hierarchy could emerge directly from the basic quantum TGD rather than as a separate hypothesis. The following arguments suggest that this might be possible. One finds also a precise geometric interpretation of preferred extremal property interpreted as criticality in zero energy ontology.

1-1 correspondence between canonical momentum densities and time derivatives fails for Kähler action

The basic motivation for the geometrization program was the observation that canonical quantization for TGD fails. To see what is involved let us try to perform a canonical quantization in zero energy ontology at the 3-D surfaces located at the light-like boundaries of $CD \times CP_2$.

1. In canonical quantization canonical momentum densities $\pi_k^0 \equiv \pi_k = \partial L_K/\partial(\partial_0 h^k)$, where $\partial_0 h^k$ denotes the time derivative of imbedding space coordinate, are the physically natural quantities in terms of which to fix the initial values: once their value distribution is fixed also conserved charges are fixed. Also the weak form of electric-magnetic duality given by $J^{03}\sqrt{g_4} = 4\pi\alpha_K J_{12}$ and a mild generalization of this condition to be discussed below can be interpreted as a manner to fix the values of conserved gauge charges (not Noether charges) to their quantized values since Kähler magnetic flux equals to the integer giving the homology class of the (wormhole) throat. This condition alone need not characterize criticality, which requires an infinite number of deformations of X^4 for which the second variation of the Kähler action vanishes and implies infinite number conserved charges. This in fact gives hopes of replacing π_k with these conserved Noether charges.
2. Canonical quantization requires that $\partial_0 h^k$ in the energy is expressed in terms of π_k. The equation defining π_k in terms of $\partial_0 h^k$ is however highly non-linear although algebraic. By taking squares the equations reduces to equations for rational functions of $\partial_0 h^k$. $\partial_0 h^k$ appears in contravariant and covariant metric at most quadratically and in the induced Kähler electric field linearly and by multplying the equations by $det(g_4)^3$ one can transform the equations to a polynomial form so that in principle $\partial_0 h^k$ can obtained as a solution of polynomial equations.
3. One can always eliminate one half of the coordinates by choosing 4 imbedding space coordinates as the coordinates of the spacetime surface so that the initial value conditions reduce to those for the canonical momentum densities associated with the remaining four coordinates. For instance, for space-time surfaces representable as map $M^4 \to CP_2$ M^4 coordinates are natural and the time derivatives $\partial_0 s^k$ of CP_2 coordinates are multivalued. One would obtain four polynomial equations with $\partial_0 s^k$ as unknowns. In regions where CP_2 projection is 4-dimensional -in particular for the deformations of CP_2 vacuum extremals the natural coordinates are CP_2 coordinates and one can regard $\partial_0 m^k$ as unknows. For the deformations of cosmic strings, which are of form $X^4 = X^2 \times Y^2 \subset M^4 \times CP_2$, one can use coordinates of $M^2 \times S^2$, where S^2 is geodesic sphere as natural coordinates and regard as unknowns E^2 coordinates and remaining CP_2 coordinates.
4. One can imagine solving one of the four polynomials equations for time derivaties in terms of other obtaining N roots. Then one would substitute these roots to the remaining 3 conditions to obtain algebraic equations from which one solves then second variable. Obviously situation is very complex without additional symmetries. The criticality of the preferred extremals might however give additional conditions allowing simplifications. The reasons for giving up the canonical quantization program was following. For the vacuum extremals of Kähler action π_k are however identically vanishing and this means that there is an infinite number of value distributions for $\partial_0 h^k$. For small deformations of vacuum extremals one might however hope a finite number of solutions to the conditions and thus finite number of space-time surfaces carrying same conserved charges.

If one assumes that physics is characterized by the values of the conserved charges one must treat the the many-valuedness of $\partial_0 h^k$. The most obvious guess is that one should replace the space of space-like 4-surfaces corresponding to different roots $\partial_0 h^k = F^k(\pi_l)$ with four-surfaces in the covering space of $CD \times CP_2$ corresponding to different branches of the many-valued function $\partial_0 h^k = F(\pi_l)$ co-inciding at the ends of CD.

Do the coverings forces by the many-valuedness of $\partial_0 h^k$ correspond to the coverings associated with the hierarchy of Planck constants?

The obvious question is whether this covering space actually corresponds to the covering spaces associated with the hierarchy of Planck constants. This would conform with quantum classical correspondence. The hierarchy of Planck constants and hierarchy of covering spaces was introduced to cure the failure of the perturbation theory at quantum level. At classical level the multivaluedness of $\partial_0 h^k$ means a failure of perturbative canonical quantization and forces the introduction of the covering spaces. The interpretation would be that when the density of matter becomes critical the space-time surface splits to several branches so that the density at each branches is sub-critical. It is of course not at all obvious whether the proposed structure of the Big Book is really consistent with this hypothesis and one also consider modifications of this structure if necessary. The manner to proceed is by making questions.

1. The proposed picture would give only single integer characterizing the covering. Two integers assignable to CD and CP_2 degrees of freedom are however needed. How these two coverings could emerge?

(a) One should fix also the values of $\pi_k^n = \partial L_K/\partial h_n^k$, where n refers to space-like normal coordinate at the wormhole throats. If one requires that charges do not flow between regions with different signatures of the metric the natural condition is $\pi_k^n = 0$ and allows also multi-valued solution. Since wormhole throats carry magnetic charge and since weak form of electric-magnetic duality is assumed, one can assume that CP_2 projection is four-dimensional so that one can use CP_2 coordinates and regard $\partial_0 m^k$ as un-knows. The basic idea about topological condensation in turn suggests that M^4 projection can be assumed to be 4-D inside space-like 3-surfaces so that here $\partial_0 s^k$ are the unknowns. At partonic 2-surfaces one would have conditions for both π_k^0 and π_k^n. One might hope that the numbers of solutions are finite for preferred extremals because of their symmetries and given by n_a for $\partial_0 m^k$ and by n_b for $\partial_0 s^k$. The optimistic guess is that n_a and n_b corresponds to the numbers of sheets for singular coverings of CD and CP_2. The covering could be visualized as replacement of space-time surfaces with space-time surfaces which have $n_a n_b$ branches. n_b branches would degenerate to single branch at the ends of diagrams of the generaled Feynman graph and n_a branches would degenerate to single one at wormhole throats.

(b) This picture is not quite correct yet. The fixing of π_k^0 and π_k^n should relate closely to the effective 2-dimensionality as an additional condition perhaps crucial for criticality. One could argue that both π_k^0 and π_k^n must be fixed at X^3 and X_l^3 in order to effectively bring in dynamics in two directions so that X^3 could be interpreted as a an orbit of partonic 2-surface in space-like direction and X_l^3 as its orbit in light-like direction. The additional conditions could be seen as gauge conditions made possible by symplectic and Kac-Moody type conformal symmetries. The conditions for π_0^k would give n_b branches in CP_2 degrees of freedom and the conditions for π_k^n would split each of these branches to n_a branches.

(c) The existence of these two kinds of conserved charges (possibly vanishing for π_k^n) could relate also very closely to the slicing of the space-time sheets by string world sheets and partonic 2-surfaces.

2. Should one then treat these branches as separate space-time surfaces or as a single space-time surface? The treatment as a single surface seems to be the correct thing to do. Classically the conserved changes would be $n_a n_b$ times larger than for single branch. Kähler action need not (but could!) be same for different branches but the total action is $n_a n_b$ times the average action and this effectively corresponds to the replacement of the $\hbar_0/g_K^2$ factor of the action with $\hbar/g_K^2$, $r \equiv \hbar/\hbar_0 = n_a n_b$. Since the conserved quantum charges are proportional to $\hbar$ one could argue that $r = n_a n_b$ tells only that the charge conserved charge is $n_a n_b$ times larger than without multi-valuedness. $\hbar$ would be only effectively $n_a n_b$ fold. This is of course poor man's argument but might catch something essential about the situation.

3. How could one interpret the condition $J^{03}\sqrt{g_4} = 4\pi\alpha_K J_{12}$ and its generalization to be discussed below in this framework? The first observation is that the total Kähler electric charge is by $\alpha_K \propto 1/(n_a n_b)$ same always. The interpretation would be in terms of charge fractionization meaning that each branch would carry Kähler electric charge $Q_K = ng_K/n_a n_b$. I have indeed suggested explanation of charge fractionization and quantum Hall effect based on this picture.

4. The vision about the hierarchy of Planck constants involves also assumptions about imbedding space metric. The assumption that the M^4 covariant metric is proportional to $\hbar^2$ follows from the physical idea about $\hbar$ scaling of quantum lengths as what Compton length is. One can always introduce scaled M^4 coordinates bringing M^4 metric into the standard form by scaling up the M^4 size of CD. It is not clear whether the scaling up of CD size follows automatically from the proposed scenario. The basic question is why the M^4 size scale of the critical extremals must scale like $n_a n_b$? This should somehow relate to the weak self-duality conditions implying that Kähler field at each branch is reduced by a factor $1/r$ at each branch. Field equations should posses a dynamical symmetry involving the scaling of CD by integer k and $J^{0\beta}\sqrt{g_4}$ and $J^{n\beta}\sqrt{g_4}$ by $1/k$. The scaling of CD should be due to the scaling up of the M^4 time interval during which the branched light-like 3-surface returns back to a non-branched one.

5. The proposed view about hierarchy of Planck constants is that the singular coverings reduce to single-sheeted coverings at $M^2 \subset M^4$ for CD and to $S^2 \subset CP_2$ for CP_2. Here S^2 is any homologically trivial geodesic sphere of CP_2 and has vanishing Kähler form. Weak self-duality condition is indeed consistent with any value of $\hbar$ and impies that the vacuum property for the partonic 2-surface implies vacuum property for the entire space-time sheet as holography indeed requires. This condition however generalizes. In weak self-duality conditions the value of $\hbar$ is free for any 2-D Lagrangian sub-manifold of CP_2.

   The branching along M^2 would mean that the branches of preferred extremals always collapse to single branch when their M^4 projection belongs to M^2. Magnetically charged light-light-like throats cannot have M^4 projection in M^2 so that self-duality conditions for different values of $\hbar$ do not lead to inconsistencies. For spacelike 3-surfaces at the boundaries of CD the condition would mean that the M^4 projection becomes light-like geodesic. Straight cosmic strings would have M^2 as M^4 projection. Also

CP_2 type vacuum extremals for which the random light-like projection in M^4 belongs to M^2 would represent this of situation. One can ask whether the degeneration of branches actually takes place along any string like object $X^2 \times Y^2$, where X^2 defines a minimal surface in M^4. For these the weak self-duality condition would imply $\hbar = \infty$ at the ends of the string. It is very plausible that string like objects feed their magnetic fluxes to larger space-times sheets through wormhole contacts so that these conditions are not encountered.

Connection with the criticality of preferred extremals

Also a connection with quantum criticality and the criticality of the preferred extremals suggests itself. Criticality for the preferred extremals must be a property of space-like 3-surfaces and light-like 3-surfaces with degenerate 4-metric and the degeneration of the $n_a n_b$ branches of the space-time surface at the its ends and at wormhole throats is exactly what happens at criticality. For instance, in catastrophe theory roots of the polynomial equation giving extrema of a potential as function of control parameters co-incide at criticality. If this picture is correct the hierarchy of Planck constants would be an outcome of criticality and of preferred extremal property and preferred extremals would be just those multi-branched space-time surfaces for which branches co-incide at the the boundaries of $CD \times CP_2$ and at the throats.

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Part III

NUMBER THEORETICAL MODELS FOR GENETIC CODE AND ITS EVOLUTION

Chapter 14

Could Genetic Code Be Understood Number Theoretically?

14.1 Introduction

I have developed several models for genetic code with motivation coming from the belief that there might be some deeper number theoretical structure involved. The model based on Combinatorial Hierarchy was discussed in the chapter "Genes and Memes". In this chapter two further models are developed. The chapter begins with a discussion of a model relying on exact A-G symmetry and almost exact T-C symmetry of the genetic code with respect to the third nucleotide. The idea is that genetic code has emerged in some sense as a product of 1-code and 2-code via symmetry breaking. This symmetry breaking is also a central element of both the second model discussed in this chapter and the number theoretic model developed in the next chapter. Second idea is that there is some kind of variational principle mathematically analogous to the second law of thermodynamics involved.

Unfortunately, the physical model developed for the pre-biotic evolution of the genetic code does not fully support the proposed symmetry breaking scenario. The 2-code in the physical model trivial in the sense that it is induced by RNA conjugation for RNA doublets whereas 1-code is deducible directly from wobble rules and is non-deterministic. Symmetry breaking of the physical model has a beautiful interpretation in terms of fundamental physics but the realization of the symmetry breaking is not quite what has been assumed in these three models and also in the model based on Combinatorial Hierarchy discussed in the chapter "Genes and Memes". Despite this the models deserve to be represented.

Since the number theoretic model is the basic topic of this chapter, it is perhaps in order to describe the basic observations leading to the model. The number of DNA triplets is 64. This inspires the idea that DNA sequence could be interpreted as an expansion of an integer using 64 as the base. Hence given DNA triplet would represent some integer in {0,1....,63} (sequences of I Ching symbols give a beautiful representation of numbers in 64 base).

The observation which puts bells ringing is that the number of primes smaller than 64 is 18. Together with 0, and 1 this makes 20: the number of aminoacids!

14.1.1 Questions

The finding just described stimulates a whole series of questions.

Do aminoacids correspond to integers in the set $S = \{primes < 64\} \cup \{0, 1\}$. Does aminoacid sequence have an interpretation as a representation as a sequence of integers consisting of 0, 1 and products of primes $p = 2, ..., 61$? Does the aminoacid representing 0 have an interpretation as kind of period separating from each other structural units analogous to genes representing integers in the sequence so that we would quite literally consists of sequences of integers? Do 0 and 1 have some special biological properties, say the property of being biologically inert both at the level of DNA and aminoacids?

Does genetic code mediate a map from integers 0,...,63 to set S such that 0 and 1 are mapped to 0 and 1? If so then three integers $2 \leq n \leq 63$ must correspond to stopping sign codons rather than primes. What stopping sign codon property means at the level of integers? How the map from integers 2,...,61 to the primes $p = 2, ..., 61$ is determined?

14.1.2 The chain of arguments leading to a number theoretical model for the genetic code

The following chain of arguments induced to large part by concrete numerical experimentation leads to a model providing a partial answer to many of these questions.

1. The partitions of any positive integer n can be interpreted in terms of number theoretical many boson states. The partitions for which a given integer appears at most once have interpretation in terms of fermion states. These states could be identified as bosonic and fermionic states of Super Virasoro representation with given conformal weight n or even better, with the states of conformal weight n created by U(1) Kac Moody generators so that basically a breaking of Kac Moody symmetry would be in question.

2. The generalization of Shannon entropy by replacing logarithms of probabilities with the logarithms of p-adic norms of probabilities allows to have systems with negative entropy and thus positive negentropy. The natural requirement is that n corresponds to such prime $p \leq 61$ that the negentropy assigned to n is maximal in some number theoretic thermodynamics. The resulting correspondence $n \to p(n)$ would naturally determine the genetic code.

3. One can assign to the bosonic and fermionic partitions a number theoretic thermodynamics defined by a Hamiltonian. Purely bosonic and fermionic thermodynamics are defined by corresponding partition functions Z_B and Z_F whereas supersymmetric option is defined by the product $Z_B \times Z_F$.

4. The simplest option is that Hamiltonian depends only on the number r of the integers in the partition. The dynamics would be in a well defined sense local and would not depend on the sizes of summands at all. The thermodynamical states would be degenerate with degeneracy factors given by total numbers $d_I(n,r)$ of partitions of type $I = B, F$. The invariants known as rank and crank define alternative candidates for basic building blocks of Hamiltonian.

5. Ordinary exponential thermodynamics based on, say $e^{-H/T} = q_0^{r-1}$, q_0 a rational number, produces typically unrealistic genetic codes for which most integers are mapped to small primes $p \leq 11$ and many primes are not coded at all. The idea that realistic code could result at some critical temperature fails also.

6. Quantum criticality and fractality of TGD Universe inspire the idea that the criticality is an inherent property of Hamiltonian rather than only thermodynamical state. Hence Hamiltonian can depend only weakly on the character of the partition so that all partitions contribute with almost equal weights to the partition function.

   Fractality is achieved if Boltzmann factors are given by $e^{-H/T} = (r + r_0)^{n_0}$ so that $H(r) = log(r + r_0)$ serves as Hamiltonian and n_0 corresponds to the inverse temperature. The super-symmetric variant of this Hamiltonian yields the most realistic candidates for the genetic code and one might hope that a number theoretically small perturbation not changing the divisors $p \leq 61$ of partition function but affecting the probabilities could give correct degeneracies.

   Numerical experimentation suggests however that this might not be the case and that simple analytic form of Hamiltonian is too much to hope for. A simple argument however shows that $e^{-H/T} = f(r)$ could be in quantum critical case be deduced from the genetic code by fixing the 62 values of $f(r)$ so that the desired 62 correspondences $n \to p(n)$ result. The idea about almost universality of the genetic code would be replaced with the idea that quantum criticality allows to engineer almost arbitrary genetic code. In this case the model becomes predictive if the condition that $S_{tot} = \sum_n S_{p(n)}(n)$ is minimized (negentropy maximization) with the constraint that each prime is coded and one could consider the possibility that $f(n)$ and $n \to p(n)$ is determined by this condition.

7. Genetic code has an almost unbroken symmetry in the sense that DNA triplets for which last nucleotide is A or G code for same aminoacid. For T and C this symmetry is slightly broken. This implies that the number of DNAs coding given aminoacid is almost always even. A very general number theoretic counterpart for this symmetry as a symmetry of partition function in the set 59 integers containing other than stopping codons. This symmetry must have fixed point and this is enough to explain why there is only single aminoacid coded by odd number DNAs besides singlets.

A natural guess is that the map of codons to integers is given as a small deformation of the map induced by the map of DNA codons to integers induced by the identification of nucleotides with 4-digits 0,1,2, 3 (this identification depends on whether first, second, or third nucleotide is in question). This map predicts approximate $p(n) = p(n + 1)$ symmetry having also a number theoretical justification. One can deduce codon-integer and aminoacid-prime correspondences and at (at least) two Boltzmann weight distributions $f(n)$ consistent with the genetic code and Negentropy Maximization Principle constrained by the degeneracies of the genetic code.

14.1.3 What is the physical counterpart of the number theoretical thermodynamics?

The partitions of any positive integer n can be interpreted in terms of number theoretical many boson states. The partitions for which a given integer appears at most once have interpretation in terms of fermion states. The states could be identified as bosonic and fermionic states of Super Virasoro representation with given conformal weight n or even better, with the states of conformal weight n created by U(1) Kac Moody generators so that basically a breaking of Kac Moody symmetry would be in question.

The obvious question concerns about the identification of the system in question. For instance, could it be associated with the light-like boundaries of magnetic flux quanta which are key actors in TGD based model of topological quantum computation [81] ? If so, then each DNA triplet would correspond to a portion of magnetic flux quantum characterized by a conformal weight n determined by the DNA triplet in question. If there is single flux quantum parallel to the DNA strand, the value of n would be constant only along the portion of length corresponding to single DNA triplet. This non-conservation of conformal weight along light-like boundary is quite possible due to the breaking of strict classical non-determinism in TGD Universe having interpretation as a space-time correlate of quantum non-determinism.

With this identification one might perhaps interpret the integer determined by a given gene as a code for a topological quantum computer program using 64-base instead of 2-base. Since the boundaries of the magnetic flux tubes associated with DNA double strands are light-like, they can be interpreted either as states or as dynamical evolutions. Therefore the light-like boundary of the flux tube associated with DNA strand could be interpreted either as a code of a quantum computer program or as a running quantum computer program [81] .

14.2 The first model for the evolution of the genetic code

The exact A-G symmetry and almost exact T-C symmetry of the memetic codons with respect to third nucleotide suggest that genetic code factorizes in a good approximation to a product of codes associated with DNA doublets and singlets. This suggests factorization also at the level of pre-amino-acids. Perhaps DNAs triplets have resulted as a symbiosis of singlets and doublets whereas amino-acids might have been developed via a symbiosis of 2 molecules coded by 4 DNA singlets and 10 molecules coded by 16 DNA doublets.

In this section a formal model for the evolution of the genetic code based on the approximate factorization of the genetic code into a product code formed by doublet and singlet codes is discussed. Also physical model for the evolution of the genetic code is briefly discussed. Product code as such predicts degeneracies approximately but fails at the level of detailed predictions for DNA-amino-acid correspondences. A "volume preserving" flow in discrete DNA space is needed to produce realistic DNA-amino-acid correspondences. This flow has the general tendency to cluster amino-acids to connected vertical stripes inside the 4-columns appearing as elements of the 4×4 code table, whose elements are labeled by the first two bases of DNA triplet. One can invent an information maximization principle providing a quantitative formulation for this tendency. The physical model for the evolution modifies the vision about RNA world [168, 158] .

14.2.1 Does amino-acid structure reflect the product structure of the code?

The exact A-G symmetry and the almost exact T-C symmetry of our genetic code supports approximate 2×10 structure such that 16 DNA doublets and 4 DNA singlets code for 10 *resp.* 2 "pre-amino-acids" which combine to form the real amino-acids. The 3×7 decomposition of the number 21 of amino-acids plus stopping sign suggests 3×7 decomposition of the genetic code. This decomposition is however not favored by the symmetries of the genetic code and will not be discussed in the sequel.

The coding of amino-acids involves tRNA binding with amino-acids and this means that the structure of amino-acids need not reflect the product structure of the genetic code and it might be that only the structure of tRNA reflects the product structure. The study of the amino-acid geometric structure does not reveal any obvious structural 3×7-ness or 2×10-ness. One can however wonder whether this kind of structures might be present at more abstract level and present only in the interactions of tRNA and amino-acids. As will be found, pre-amino-acids correspond most naturally to RNA sequences so that the product decomposition is realized trivially.

14.2.2 Number theoretical model for the genetic code

The study of the genetic code allows to deduce the process leading to the breaking of the product symmetry and T-C symmetry.

Approximate reduction to a product code

The dependence of the amino-acid coded by DNA on the third codon of DNA triplet is weak. This inspires the guess that triplet code might have evolved as a fusion of doublet code and singlet codes.

This should be reflected in its structure. The decomposition $20 = 2 \times 10$ for real amino-acids suggest that singlet code maps four bases to 2 'pre-amino-acids' such that A and G resp. T and C are mapped to same pre-amino-acid, and 16 doublets to 10 'pre-amino-acids'. The exact A-G symmetry and almost exact T-C symmetry of our genetic code support this interpretation.

Product code hypothesis is very strong since the degeneracies of the product code are products of the degeneracies for the composite codes so that the number n_{AB} of DNA triplets coding a given amino-acid having the product form 'AB', to be referred as the degeneracy of the amino-acid, is given by the product

$$n_{AB} = n_A \times n_B$$

of the degeneracies of the 'pre-amino-acids' A and B. Here A and B can refer to $(A, B) = (3, 7)$ or $(A, B) = (2, 10)$ respectively.

The number $N_{AB}(n)$ of amino-acids with given degeneracy n is given by the formula

$$N_{12}(n) = \sum_{n_1 \times n_2 = n} N_1(n_1) N_2(n_2) \quad ,$$

where $N_1(n_1)$ resp. $N_2(n_2)$ is the number of pre-amino-acids with the degeneracy n_1 resp. n_2.

For 2×10 case singlet sector allows only single candidate for the code since the genetic code has exact A-G symmetry and almost exact T-C symmetry with respect to the last base. Thus A and G code for the first pre-amino-acid and T and C the second one. A breaking of the T-C symmetry is needed to obtain realistic code.

Our genetic code as result of symmetry breaking for 2×10 product code

As found, there are two cases to be considered: 3×7 T-C asymmetric and 2×10 T-C symmetric product code. The approximate T-C symmetry favors strongly 2×10 option and 3×7 will be considered only briefly in a separate subsection. On basis of degeneracies alone it is not possible to distinguish between these codes and 3×7 code was in fact the first guess for the product code.

In case of 2×10 code the decomposition of 16 DNA doublets giving almost the degeneracies of our genetic code is (3322 111 111).

$$(2 \oplus 2) \times (3 \oplus 3 \oplus 2 \oplus 2 \oplus 6 \times 1)$$

This gives

n	1	2	3	4	6
N(prod)	0	12	0	4	4
N(real)	2	9	2	5	3

Table 5: The numbers $N(n)$ of amino-acids coded by n DNAs for unperturbed 2×10 product code and for the real genetic code for 2×10 option.

It is important to notice that the multiplets appear as doubled pairs corresponding to A-G and T-C symmetries. One generalized amino-acid (which cannot correspond to stopping sign) is lacking and must result by a symmetry breaking in which one amino-acid in the code table is transformed to a new one not existing there. Alternatively three amino-acids are transformed to stopping signs.

It is easy to find the deformation yielding correct degeneracies by removing DNAs from the DNA-boxes defined by various values of degeneracies to other boxes and adding them to other boxes. The rule is simple: taking m DNAs from a box containing n DNAs creates a box with $n - m$ DNAs and annihilates one n-box:

$$N(n) \to N(n) - 1 \quad , \quad \textit{and } N(n-m) \to N(n-m) + 1 \quad .$$

If one adds k of these DNAs to r-box one has

$$N(r) \to N(r) - 1 \quad , \quad N(r+k) \to N(r+k) + 1 \quad .$$

The operation which is not allowed is taking the entire content of a DNA box defined by amino-acid and adding it to other boxes since this would mean that the amino-acid in question would not be coded by any DNA. Thus the number of boxes can only grow in this process.

Realistic degeneracies are obtained by a rather simple operation.

1. Take from one 6-plet two amino-acid and move the first of them to 2-plet to get $N(6) = 3$, $N(4) = 5$, $N(3) = 1 < 2$, $N(2) = 11 > 9$ and move the second one to hitherto non-existing singlet to get $N(1) = 1$.
2. Move one DNA from some doublet to second doublet to get triplet and singlet to get $N(1) = 2$, $N(2) = 9$ and $N(3) = 2$.

This operation gives correct degeneracies only and it turns out that correct symmetry structure requires additional operations.

Failures of the product structure and the symmetry breaking as volume preserving flow in DNA space

A slightly broken product structure allows to understand the degeneracies of our genetic code relatively easily. It however leads also to wrong predictions at the level of DNA-amino-acid correspondence.

1. Exact product structure predicts that all 4-columns XYU, $U = A, G, T, C$ appearing as elements of the code table labelled by first and second bases of DNA triplet should have similar amino-acid structure. For 2×10 code the prediction is that all 4-columns should have $AABB$ structure and this prediction breaks down only for $AAAA$ type 4-columns.
2. For 2×10 code a given amino-acid should be coded either by DNA pairs of form (XYA, XYG) or of form (XYC, XYT). This is not the case. A given amino-acid tends to appear as connected vertical stripes inside the elements of the 4×4 table (4-columns). For instance, all 4-columns of form $AAAA$ (A=leu, val, ser, pro, thr, ala, arg, gly) and 3-column ile break the prediction of the product code.
3. In the case of 2×10 2n-plet formed by (XYA,XYG)-pairs is accompanied always by an 2n-plet formed by (XYT,XYC) pairs. By studying the degeneracies of the code one can get idea about how good these predictions are.

It seems that the breaking of the product symmetry tends to form connected vertical clusters of amino-acids inside a given element of the 4×4 code table but that one cannot regard stripes longer than 4 elements as connected structures. The 2×10 structure is favored by approximate T-C symmetry, and one can imagine that relatively simple flow in DNA space could yield the desired condensation of the amino-acids to form connected vertical stripes. The most general flow is just a permutation of DNAs and obviously preserves the degeneracies of various amino-acids. There are 64! different permutations but A-G and T-C symmetries reduce their number to 32!.

The idea about discrete volume preserving flow in DNA space can be made more precise. A-G and T-C gauge symmetries suggest the presence of a discrete symplectic structure. Perhaps one could regard 16×4 DNAs as 16 points of 4-dimensional discrete symplectic space so that the canonical symmetries of this space (volume preserving flows) acting now as permutations would be responsible for the exact A-G gauge invariance and approximate T-C gauge invariance. This brings in mind the canonical symmetries of CP_2 acting as $U(1)$ gauge transformations and acting as almost gauge symmetries of the Kähler action.

A natural guess is that the DNAs coding same amino-acid tend to be located at the same column of the 4×4 code table before the breaking of the product symmetry. If this is the case then only vertical flows need to be considered and A-G and T-C symmetries imply that their number is $8!^4$ corresponding to the four columns of the table.

The table 6c) summarizes our genetic code. It is convenient to denote the rows consisting of A-G resp. T-C doublets by X_1 and X_2. For instance, A_1 corresponds to the highest row phe-phe, ser-ser, tr-tyr, cys-cys and G_2 to the row leu-leu, pro-pro, gln-gln, arg-arg.

1. The simplest hypothesis is 2×10 option is realized and that the flow permutes entire rows of the code table consisting of A-G and T-C doublets. From the table below it is clear that there is a G-C symmetry with respect to the first nucleotide broken only in the third row. This kind of primordial self-conjugacy symmetry would not be totally surprising since first and third nucleotides are in a somewhat similar position.
2. There are 3 6-plets leu, ser, and arg, and it is easy to see that one cannot transform them to the required form in which all 6-plets are on A-G or T-C row alone using this kind of transformation. For instance, one could require that leu doublets correspond to T-C doublets before the symmetry breaking. This is achieved by permuting the G_1 row with the C_2 row. Since A_2 contains also ser-doublet, also ser must correspond to T-C type 6-plet, and since arg is contained by G_2 row, also arg must correspond to T-C type 6-plet. Thus there would be 4 T-C type 6-plets but the product code gives only 2 of them.
3. The only manner to proceed is to allow mixing of suitable 6-plet of A-G type and 4-plet of T-C type in the sense that A-G doublet from 6 is moved to T-C doublet inside 4-plet and T-C doublet in 4-plet is moved to A-G doublet inside 6-plet. The exchange of AG_2 (ser doublet) and TG_1 (trh-doublet) represents this kind of permutation.

The tables below summarize the three stages of the construction.

1. Table 6a): Code table before the flow inducing the breaking of the product symmetry

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	thr	asn	thr	T
	leu	thr	asn	thr	C
G	val	ala	glu	gly	T
	val	ala	glu	gly	C
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	ser	stop	ser	A
	ile	ser	stop	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	leu	pro	his	arg	A
	leu	pro	his	arg	G

2. Table 6b): The code table after the action of the flow inducing the breaking of product symmetry

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	thr	T
	leu	ser	stop	thr	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

3. Table 6c): The code table after the T-C symmetry breaking

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	stop	T
	leu	ser	stop	trp	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	ile	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

At the last stage the T-C symmetry breaking giving rise to bla-trp and ile-met doublets occurs.

1. thr 6-plet is transformed to 4-plet by replacing thr-thr in AC_2 by bla-trp. trp is the missing amino-acid.
2. TA_2 met-doublet is transformed to ile-met so that the realistic genetic code results.

One might argue that symmetry breaking permutations $G_1 - C_2$ and $AG_2 - TG_1$ should permute amino-acids with a similar chemical character. A similar constraint applies to T-C symmetry breaking. By studying the chemical structure of the amino-acids, one finds that this is satisfied to a high degree.

1. The permutations val-leu and ala-pro exchange amino-acids with non-polar (hydrophobic) side groups. The permutations glu-his and gly-arg exchange polar (hydrophilic) amino-acid with a polar amino-acid which is also basic. Ser and thr are both non-polar amino-acids.
2. Ile and met are both non-polar so that ile$\rightarrow$ met replacement satisfies the condition.
3. The objection is that the side group for trp is non-polar but polar for thr. Interestingly, the code table decomposes to two connected regions corresponding to non-polar/polar side groups at the left/right such that the non-polar trp located inside the polar region is the only black sheep whereas thr naturally belongs to the polar region. As will be found trp is also otherwise singular case.

The information maximization principle determining the "volume preserving flow"

The interaction between the DNA singlets and doublets is the physical explanation for the breaking of the product symmetry. This interaction involves two parts: the flow and T-C symmetry breaking. The flow is analogous to the formation of connected vertical stripes of amino-acids in DNA space: kind of condensation process in which different phases represented by amino-acids tend to condense to form regions consisting of at most 4-units of type XYU, $U = A, G, T, C$. Obviously this means continuity and thus also symmetry analogous to that emerging when (amino-acid) gases condense to a liquid state: the breaking of the product symmetry is the price paid for this additional symmetry. It turns out to be possible to formulate a variational principle consistent with the proposed flow in the direction of the columns of the code table and defining the dynamics of the condensation.

What this means that one can assign an information measure to the code table such that the volume preserving flow in question maximizes this information measure.

1. Information measure is assumed to be local in the sense that it decomposes into a sum of information measures associated with the elements C_{AB}, $A, B \in \{A, G, T, C\}$, of the 4×4 code table (elements are 4-element columns). In the physical analogy this means that the condensed droplets of various amino-acids can have at most the size of single 4-element column.
2. Consider the element C_{AB}. Let the multiplet associated with the amino-acid a_k contain $n(k, AB)$ amino-acids and let $i(k, AB)$ tell the number of the disjoint parts to which the amino-acids a_k in the 4-plet AB split. The number of these disjoint multiplets can be $0, 1, 2$. Let the i:th region contain $n(k, AB, i)$ amino-acids a_k. The meaning of the equations

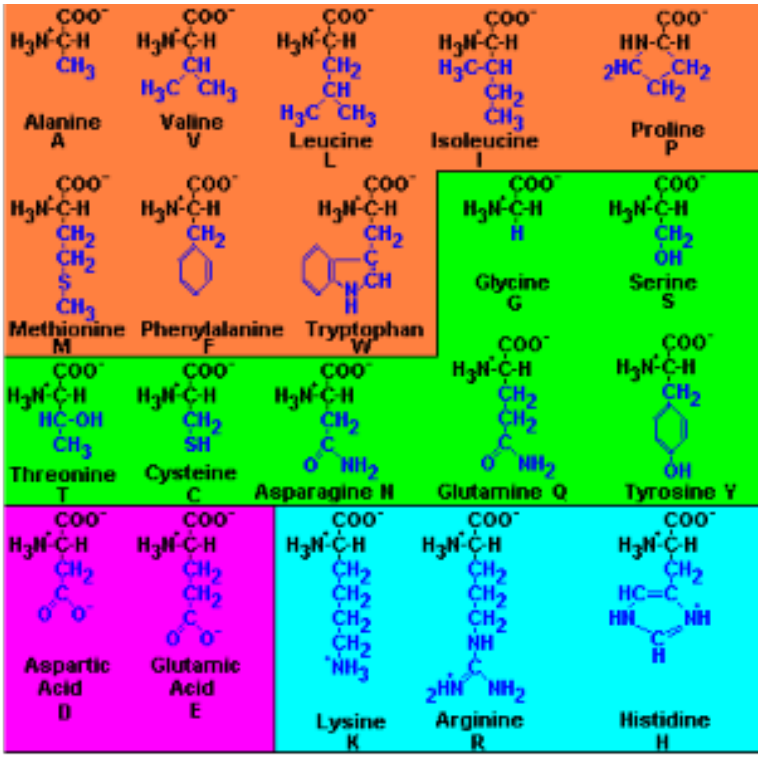

Figure 14.1: The chemical structure of amino-acids. The first group (ala,. ..) corresponds to non-polar amino-acid side groups, the remaining amino-acids to polar side groups. The two lowest groups correspond to acidic (asp, glu) and basic side groups.

$$\sum_{i=1}^{i(k,AB)} n(a_k, AB, i) = n_k(AB) \quad ,$$

$$\sum_{AB} n_k(AB) = n_k \quad ,$$

$$\sum_k n_k = 64$$

is obvious.

Assign to the i:th connected region containing $n(k,i,AB)$ identical amino-acids a_k probability

$$p(k,i,AB) = \frac{n(k,i,AB)}{64} \quad ,$$

to the element AB the total probability

$$p(k,AB) = \sum_{i=1}^{i(k,A,B)} p(k,i,AB) \quad ,$$

and to the entire table the probability

$$p_k = \sum_{AB} p(k,AB) = \frac{n(k,AB)}{64} \quad .$$

The sum of the probabilities associated with various amino-acids satisfies

$$\sum_k p_k = 1 \quad .$$

The information measure associated with amino-acid a_k element AB is defined as

$$I(k,AB) = \sum_{i=1}^{i(k,A,B)} p(k,i,AB) \times log[p(k,i,AB)] \ ,$$

Note that this number is non-positive always. The total information associated with the amino-acid a_k in code table is defined as

$$I(k) = \sum_{AB} I(k,AB) \ .$$

The total information of the code table is defined as the sum of the information measures associated with various amino-acids:

$$I = \sum_{k} I(k) \ .$$

This information measure is maximized (which means the minimization of the absolute value of the measure since one can speak of the minimization of entropy) by the vertical flow satisfying the previous constraints, and thus satisfying the constraints that the numbers a_k of various amino-acids are fixed and $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries are respected. There is a direct analogy with thermodynamical equilibrium with fixed particle numbers and symmetry. The equilibrium is characterized by the chemical potentials associated with the amino-acids. There is no temperature type parameter now.

The variational principle indeed favors the formation of vertically connected regions consisting of $n = 2, 3$ or 4 amino-acids. By construction the variational principle does not tell anything about larger regions. In particular, it is more favorable for 4 amino-acids in a given column (say ser in the second column of the table) to be contained by single element than by 2 elements since the information measure would be $-1/16log(1/16)$ for two disjoint doublets and $-1/16log(1/8)$ for singlet 4-plet in same element and thus smaller in absolute value. In the similar manner the AAAB decomposition of singlet element instead of say AABA is favored.

The deviations from the standard code as tests for the basic symmetries of the model

The deviations of the genetic codes from the standard code [95] provide a testing ground for the postulated symmetries of the genetic code and might also help to deduce the alien codes.

The deviations from universality of the start codon (coding for met) and stop codons are very rare. With two exceptions all known deviations from the standard code are located in the first and fourth columns of the code table. For the first exceptional case the codon is ATC in the third column and codes for both stopping sign and pyrrolysine, which is an exotic amino-acid. It is somewhat a matter of taste whether one should say that the universality of the third column is broken or not since, depending on context, ATC codes stopping sign or pyrrolysine. Second exceptional case corresponds to the use of two stop codons to code amino-acids and this necessarily breaks the universality of the third column in T-C 2-subcolumns. No violations of the predicted A-G symmetry and the universality of the second column of the code table are known.

The deviations from the standard code [95] provide valuable hints when one tries to deduce information about the alien codes.

1. Consider first the mitochondrial genes.
   i) Mitochondrial codon ACT from animals and micro–organisms (but not from plants) codes trp instead of stopping sign.
   ii) Most animal mitochondria use TAT to code met instead of ile.
   iii) Yeast mitochondria use GAX codons to code for thr instead of leu.

2. The violations of the universality are very rare for nuclear genes. A few unicellular eukaryotes have been found that use one or two of three stop codons to code amino-acids instead. The use of two stop codons to code amino-acids necessarily violates the universality of the third column but need not break the universality for the imbedding of amino-acid space to DNA space.

3. There are also two non-standard amino-acids: selenocysteine and pyrrolysine.
   i) Selenocysteine is encoded by ACT (fourth column) coding stopping sign normally. Interestingly, ACT codes also stopping sign and the translation machinery is somehow able to discriminate when selenocysteine is coded instead of stop. This codon usage has been found in certain Archaea, eubacteria, and animals. This deviation means that the number of amino-acids is 21 or 20 depending on context. This conforms with the view that number 21 indeed has a deep number theoretical meaning and that one can regard stopping sign formally as amino-acid.
   ii) In one gene found in a member of the Archaea, exotic amino-acid pyrrolysine is coded by ATC, which corresponds to the lower stopping sign in the code table. This case represents the only deviation from universality of the third column of the code table but even in this case also stopping sign is coded. How the translation machinery knows whether to code pyrrolysine or to stop translation is not yet

known. TGD would suggest that electromagnetic signaling mechanisms ('topological light rays') might be involved.

14.3 Basic ideas and concepts underlying second model of genetic code

In the following the basic ideas and concepts are summarized.

14.3.1 Genetic code from the maximization of number theoretic information?

One of the earlier ideas about genetic code was that genetic code maximizes some kind of information measure [29, 20, 21] . In that context ordinary entropy was used. The discovery of number theoretic variants of Shannon entropy based on p-adic norm allows however a modified approach.

14.3.2 Genetic code from a minimization of a number theoretic Shannon entropy

The idea about entropy minimization determining genetic generalizes to the idea that the map $n \to p(n)$ from integers representing DNA to primes representing aminoacids maximizes some kind of information measure.

Identification of ensembles

There is a natural candidate for the ensemble. This ensemble is defined by the partitions of n to sums of integers identified in terms of many-boson states. Each partition of an integer would correspond to a physical state. For Virasoro representations encountered in conformal field theories this is indeed the case. One can also consider partitions subject to some additional conditions. For instance, one could require that same integer appears at most once or that only odd integers appear in the partition (these options are in fact equivalent).

These two ensembles correspond to bosonic and fermionic systems and states in question correspond to the bosonic and fermionic states of given conformal weight n in Super Virasoro reprsentation. Supersymmetric alternative would be based on the product of bosonic and fermionic partitition functions so that entropy would be the sum of the bosonic and fermionic contributions. In the sequel all these options will be studied and supersymmetric option turns out to be the most promising one.

In the bosonic case the partition numbers are conveniently calculated by using the recurrence relation [5]

$$d_B(n,r) = P(n,r) = P(n-1,r-1) + P(n-r,r) \quad , \quad P(n,1) = 1 \quad . \tag{14.3.1}$$

In the fermionic case the numbers $Q(n,k)$ of partitions of n to a sum of integers such that same integer does not appear twice characterize simplest models. These numbers are obtained from the formula [5]

$$d_F(n,r) = Q(n,r) = P(n - \left(\begin{array}{c} r \\ 2 \end{array} \right), r) \quad . \tag{14.3.2}$$

These formulas allow a highly effective numerical treatment when Boltzmann weights depend on r only.

Identification of information measures

There is also a good guess for the information measure as the p-adic entropy S_p obtained by replacing the argument logarithm of a rational valued probability p_k appearing in Shannon entropy with the logarithm of its p-adic norm $|p_k|_p$. If the probabilities of partitions are same and given by $1/d_I(n)$, $I = B, F$, where $d_I(n)$ is the total number of partitions, one would have

$$S_{I,p}(n) = -\sum_1^{d_I(n)} \frac{1}{d_I(n)} log(|\frac{1}{d_I(n)}|_p) = -log(|\frac{1}{d_I(n)}|_p) \quad , \quad I = B, F \quad . \tag{14.3.3}$$

The simplest model obviously corresponds to a high temperature limit in thermodynamics. $S_{I,p}(n)$ can be expressed also in a form which is a convenient starting point for finite temperature thermodynamics with Hamiltonian given by the number r of integers in the partition.

$$\begin{aligned} S_{I,p}(n) &= -\sum_{r=1}^{n} p_I(n,r) log(|\frac{1}{d_I(n)}|_p) \ , \\ p_I(n,r) &= \frac{d_I(n,r)}{d_I(n)} \ , \ d_I(n) = \sum_{r=1}^{n} d_I(n,r) \ , \ I = B, F \ . \end{aligned} \tag{14.3.4}$$

$p_I(n,r)$ is the total probability that partition has r summands.

What makes number theoretical thermodynamics so fascinating is that p-adic entropies can be negative so that they can become genuine information measures. Indeed, if $d_I(n)$ is divisible by p the p-adic norm of $d_I(n)$ can become smaller than one and its contribution to the entropy is negative. Hence the maximization of $S_{I,p}$ as a function of p assigning to n a unique prime $p(n)$ is natural in the case of genetic code. Furthermore, if $S_{I,p}(n)$ zero or positive, n does not carry information and is an excellent candidate for the stopping sign codon.

It is possible to deduce the correspondence $n \to p(n)$ by using simple number theoretical arguments. If the number $d_I(n)$ of partitions is divisible by p, n might be mapped to p since the logarithm of $1/d_I(n)$ receives a large negative contribution tending to make the number theoretic entropy negative. It is easy to see that the largest power of prime appearing in $d_I(n)$ determines $p(n)$ in the case that $d_I(n)$ is divisible by some primes $p \leq 61$. At high temperature limit any prime $p \leq 61$ yields the same value of $S_{I,p}(n)$.

14.3.3 High temperature limit for bosonic, fermionic, and supersymmetric thermodynamics

The tables below represent the bosonic and fermionic partition numbers and the prediction of high temperature limit of number theoretical thermodynamics in the bosonic, fermionic, and supersymmetric cases.

High temperature limit does not predict a realistic genetic code.

1. The decompositions of $d(n)$ to primes contain all primes < 64 except 37 and 61. 23 is not allowed by the rule determining the value $p(n)$. In fermionic case $d(n)$ is divisible by 61 for $n = 24$ and by 37 for $n = 28, 20, 47, 62$.

2. For $n = 13$ and $n = 36$ for which $d(n)$ is prime larger than 61 so that it is not possible to assign any unique prime to them ($n = 13$ seems to deserve its bad reputation!), p-adic entropy and thus also information vanishes. A possible interpretation is that these two zero information integers correspond to stopping sign codons. In the general case integers coding $p = 2$ are good candidates for stopping codons since minimization of entropy favors $p = 2$ when the partition function fails to be divisible by any prime $p \leq 61$.

3. The primes p smaller than 13, in particular $p = 11$, which would be coded by as many as 19 DNAs, are strongly over-represented. The over-representation of small integers might reflect the three congruences $p(4 + 5d) \ mod \ 5 = 0$, $d(5 + 7r) \ mod \ 7 = 0$, and $d(6 + 11r) \ mod \ 11 = 0$ found by Ramanujan for which quite recently a proof and generalization has been found [26] .

4. For both fermionic and supersymmetric partition functions primes 41 and 43 fail to be coded and there is strong over-abundance of $p = 2$. An amusing numerical coincidence is that $d_F(20) = 64$ holds true.

n	$d_B(n)$	$p_B(n)$	$d_F(n)$	$p_F(n)$	$p_{BF}(n)$
0	1	1	1	0	0
1	1	1	1	1	1
2	2	2	1	1	2
3	3	3	2	2	3
4	5	5	2	2	5
5	7	7	3	3	7
6	11	11	4	2	11
7	3×5	5	5	5	5
8	2×11	11	6	3	11
9	$2 \times 3 \times 5$	5	8	2	2
10	$2 \times 3 \times 7$	7	10	5	3
11	$2^3 \times 7$	2	12	2	2
12	7×11	11	15	5	11
13	101 (prime)	?	18	3	3
14	$3^3 \times 5$	3	22	11	3
15	$2^4 \times 11$	2	27	3	3
16	$3 \times 7 \times 11$	11	32	2	2
17	$3^3 \times 11$	3	38	19	3
18	$5 \times 7 \times 11$	11	46	23	23
19	$2 \times 5 \times 7^2$	7	54	3	7
20	$3 \times 11 \times 19$	19	64	2	2
21	$2^3 \times 3^2 \times 11$	11	76	2	2
22	$2 \times 3 \times 167$	3	89(prime)	?	3
23	5×251	5	104	13	13
24	$3^2 \times 5^2 \times 7$	5	122	61	61
25	$2 \times 11 \times 89$	11	142	11	11
26	$2^2 \times 3 \times 7 \times 29$	29	165	29	29
27	$2 \times 5 \times 7 \times 43$	43	192	2	2
28	$2 \times 11 \times 13^2$	13	222	37	13
29	$5 \times 11 \times 83$	11	256	2	2

Table 1. The table represents the partition numbers $d_B(n)$ and $d_F(n)$ as well as the primes $p_B(n)$,$p_F(n)$, $p_{BF}(n)$ resulting from the minimization of the p-adic entropy $S_{I,p}(n)$, $I = B, F, BF$ as a function of n for $n < 30$.

n	$d_B(n)$	$p_B(n)$	$d_F(n)$	$p_F(n)$	$p_{BF}(n)$
30	$2^2 \times 3 \times 467$	2	296	2	37
31	$2 \times 11 \times 311$	11	340	17	17
32	$3 \times 11^2 \times 23$	11	390	13	11
33	$3^2 \times 7^2 \times 23$	7	448	2	7
34	$2 \times 5 \times 1231$	3	512	2	2
35	$3 \times 11^2 \times 41$	11	585	13	11
36	17977(prime(	?	668	2	2
37	$7 \times 11 \times 281$	11	760	19	19
38	$5 \times 11^2 \times 43$	11	864	2	11
39	$3^4 \times 5 \times 7 \times 11$	3	982	2	3
40	$2 \times 3 \times 7^2 \times 127$	7	1113	53	7
41	$3 \times 7 \times 11 \times 193$	11	1260	3	7
42	$2 \times 11 \times 2417$	11	1426	31	31
43	$3^4 \times 11 \times 71$	3	1610	23	7
44	$5^2 \times 31 \times 97$	31	1816	2	31
45	$2 \times 41 \times 1087$	41	2048	2	2
46	$2 \times 3 \times 73 \times 241$	3	2304	2	2
47	$2 \times 7^2 \times 19 \times 67$	7	2590	37	7
48	$3 \times 7 \times 7013$	7	2910	5	3
49	$5^2 \times 11 \times 631$	5	3264	2	2
50	$2 \times 11 \times 9283$	11	3658	59	59
51	$3 \times 11^2 \times 661$	11	4097	17	11
52	$3 \times 7 \times 11 \times 23 \times 53$	53	4582	29	53
53	$3^2 \times 7 \times 5237$	3	5120	2	2
54	$5 \times 7 \times 11 \times 17 \times 59$	59	5718	3	59
55	$2^2 \times 7 \times 71 \times 227$	7	6378	3	2
56	$11 \times 47 \times 1019$	47	7108	47	47
57	$2 \times 3 \times 102359$	3	7917	29	29
58	$2^2 \times 5 \times 11 \times 3251$	11	8808	2	2
59	$2^2 \times 5 \times 11 \times 19 \times 199$	19	9792	2	2
60	$17 \times 139 \times 409$	17	10880	2	17
61	$3 \times 5 \times 7 \times 11 \times 971$	11	12076	2	11
62	$2^2 \times 11 \times 13 \times 2273$	13	13394	37	37
63	$3 \times 113 \times 4441$	3	14848	2	2
64	$2 \times 5 \times 11 \times 71 \times 223$	11	16444	11	11
65	2×1006279	2	18200	5	5

Table 2. The table represents the partition numbers $d_B(n)$ and $d_F(n)$ as well as the primes $p_B(n)$,$p_F(n)$, $p_{BF}(n)$ resulting from the minimization of the p-adic entropy $S_{I,p}(n)$, $I = B, F, BF$ as a function of n for $30 \leq n \leq 65$. Note that for bosonic case $p = 37$ and 61 are not coded whereas for supersymmetric case $p = 41$ and 43 are not coded.

n	1	2	3	4	6
N	2	9	2	5	3

Table 3: The numbers $N(n)$ of amino-acids coded by n DNAs.

14.4 Could finite temperature number theoretic thermodynamics reproduce the genetic code?

The number theoretical ansatz in its simplest form fails. It is however possible to modify the measure associated with the partitions, which can be regarded as $T \to \infty$ limit of thermodynamics. Some kind of conserved quantity playing the role of Hamiltonian and distinguishing between different partitions should be introduced.

p-Adic thermodynamics implies that the counterpart of Boltzmann exponent $exp(-H/T)$ should be rational. One manner to guarantee this is to assume Boltzmann weight has the form q_0^{-H/T_r} for some rational number q_0 assuming that H/T_r is integer valued. A stronger condition is that q_0 is integer. With natural conventions both Hamiltonian and the inverse of the reduced temperature T_r are integer valued. For $T_r = 1/k$ the counterpart of the ordinary temperature would be $T = k/log(q_0)$. Thus q_0 would partially characterize

the number theoretical temperature of DNA-aminoacid system and varying temperature would allow the possibility of several codes. The genetic code indeed involves small variations [29, 21] . The Hamiltonian should depend on the number r of integers in the partition and possibly n, perhaps also on more refined properties of the partition.

The finite temperature need not as such be enough to guarantee a reasonable genetic code. On purely statistical grounds one expects that small primes appear very frequently as divisors of integer valued reduced partition function and over- abundance of small primes is expected. Detailed calculations in low temperature phase confirm this prediction.

Physical intuition suggests that there could exists something analogous to a critical temperature in the sense that large long range fluctuations for ordinary criticality correspond to large degeneracies for large primes. The challenge would be to find this critical phase expected to be located somewhere between high temperature phase and low temperature phases with $(r_0 > 1, s_0 = 1)$ and thus characterized by $r_0 > s_0 > 1$. The attempts to realize this program have not led to a success, and it seems that it is not only particular thermodynamical state of the system which should be critical, but the very Hamiltonian defining the number theoretical thermodynamics as the quantum criticality of TGD Universe indeed suggests.

14.4.1 How to choose the Hamiltonian?

Hamiltonian as a function of the number of summands in the partition?

The most symmetric positive definite Hamiltonian one can imagine is $H(n, r) = H(r) = r$ thermodynamically equivalent with $H(r) = r - 1$. The independence of the Hamiltonian on n conforms with the idea that the dynamics is local in the sense that only the number r of integers in the partition matters and that the value n of the individual integer is irrelevant. Dynamics would be same for all values of n and in this sense universal.

A possible interpretation for $H(r)$ is in terms of the breaking of conformal symmetry allowing to distinguish between states characterized by the same eigenvalue n of the Virasoro generator L_0 and generated by the products $\prod_k L_{n_k}$ of Virasoro generators. This Hamiltonian is certainly the most natural starting point because it possesses maximal symmetries and is also computationally tractable.

For the corresponding thermodynamics temperature corresponds to a rational $q = r/s > 1$ and Boltzmann weights are given by the exponents q^r. It turns out difficult to find realistic looking genetic codes for this thermodynamics. Unless q is near unity only lowest values of r contribute and the general tendency is that the spectral power concentrates at small primes ≤ 11. This can be understood from the fact that small primes are the most probable divisors of random integers. The only hope seems to be that there exists a critical temperature at which large long range fluctuations correspond to large degeneracies for large primes.

The most general thermodynamics allows arbitrary function $exp(H/T) = f(r, T)$ of r having positive integers as values. An especially natural choice is $f(r) = (r+r_0)^n$ corresponding to Hamiltonian $H = log(r+r_0)$ and temperature $T = 1/n$ so that one has

$$exp(-H/T) \quad = \quad (r + r_0)^{n_0} \quad , \quad n_0 = \pm 1, \pm 2, ... \quad , \quad r_0 = 0, 1, 2, ... \quad . \tag{14.4.1}$$

so that a second integer valued parameter creeps in. Note that the thermodynamics is invariant under the scalings $(r + r_0) \to \lambda \times (r + r_0)$.

For $n \geq 0$ the formula for $S_p(n)$ is computationally very attractive but $n_0 > 0$ corresponds to negative temperatures or negative values of $H(r)$. It is of course not clear whether the sign of temperature is really important since the number of states is finite. The general vision that rational valued entanglement coefficients correspond to negative entropy and are associated with bound states would suggest that H has interpretation as the analog of negative of binding energy and is therefore negative.

For $n_0 < 0$ the numerical calculations are somewhat intricate due to the emergence of factorials up to 63! in the calculation of p-adic norms of partition coefficients. The factors $1/(r + r_0)^{n_0}$ tend to divide from the partition function prime factors $r_0 + 1$ away and this means that for small values of r_0 the primes $pr_0 + 1 \leq 61$ rarely divide it. Hence an entropic phase is in question for $r_0 < 61$ and numerical calculations demonstrate that only few $p > 2$ are coded. One might hope that the situation changes for $r_0 > 61$ and should resemble that for $n_0 > 0$. Numerical calculations show that this is not the case. The outcome is a complete spontaneous magnetization in the sense that only $p = 2$ is coded. This can be understood from the fact that entropy is minimum for $p = 2$. The safe conclusion seems to be that $n_0 > 0$ phase is the only option possibly reproducing the genetic code for a properly chosen Hamiltonian.

The polynomial rather than exponential thermodynamics would conform with the quantum criticality and fractality of TGD Universe. The nice feature of the logarithmic Hamiltonian is that it describes inherently critical system since the thermodynamical weights are slowly varying functions of r and therefore thermal fluctuations are large. Therefore there are hopes of achieving criticality, perhaps for all values of n for $n_0 > 0$.

These optimistic expectations turn out to be correct. Numerical calculations for $n_0 > 0$ bosonic case demonstrate that the concentration of spectrum to small primes is not anymore present, all primes can be

coded in some cases, and qualitatively reasonable looking genetic codes are obtained with degeneracies smaller than 8. The next improvement is super-symmetry which leads to more realistic candidates for genetic code with small parameter values. It is quite possible that the requirement that the realistic genetic code results exactly fixes the Hamiltonian completely and that some kind of symmetry breaking is required to get the correct code.

Hamiltonian as a function of the rank of the partition?

There are also more complex candidates for the Hamiltonian if one allows Hamiltonian to have different values for partitions having the same value of r. Already Dyson introduced the notion of rank of a partition of type (n,r) as the difference

$$R(n,r,n_{max}) \quad = \quad n_{max} - r \quad , \tag{14.4.2}$$

where n_{max} is the largest integer appearing in the partition [26] .

Rank divides the partitions into equal sized classes and the number of them obviously appears as a factor in $d(n)$. The notion of rank allows to prove the congruences $d(4+5d) \ \ mod \ \ 5 = 0$ and $d(5+7r) \ \ mod \ \ 7 = 0$ discovered by Ramanujan but fails for $d(6+11r) \ \ mod \ \ 11 = 0$ as found by Dyson [14] . Dyson speculated the existence of a more complex invariant which he christened crank.

Rank is not positive definite as the study of simplest examples demonstrates. A simple manner to get a non-negative Hamiltonian is based on the so called group number defined as rank modulo $n+1$:

$$G(n,r,n_{max}) \quad = \quad R(n,r,n_{max}) \ \ mod \ \ n+1 \quad , \tag{14.4.3}$$

and having values only in the set $\{0,...,n\}$. The modulo arithmetics has the effect of producing double degeneracy of partitions with same group number. The numbers $N(p)$ coding given prime satisfy $N(p) \geq 2$ for the real genetic code and this might be due to the modular arithmetics (the exponential thermodynamics based on rank predicts typically $N(p) = 1$ or 0 for $p > 11$).

Hence one could consider the Boltzmann weights

$$\begin{aligned} exp(-H/T) \quad &= \quad q^{kH(n,r,n_{max})} \quad , \\ kH(n,r,n_{max}) \quad &= \quad G(n,r,n_{max}) \quad . \end{aligned} \tag{14.4.4}$$

For this option partitions $(r,n_2...n_r)$ are favored for positive temperatures since $R=0$ in this case and at low temperature limit the finding of genetic code reduces to the identification of the largest prime power factors of the number of partitions of n of type $(r,n_2...n_r)$. Note that ground state degeneracy results whereas for $H=r$ the ground state is singly degenerate at low temperature limit. The study of small values of n shows that this thermodynamics is not very interesting since the number of partitions of this kind is rather small. For large primes this would mean that they cannot be coded.

The inherently critical option corresponds to

$$exp(-H/T) \quad = \quad (G(n,r,n_{max}) + g_0)^k \quad , \tag{14.4.5}$$

with integer valued temperature k. For $g_0 = 0$ the partitions of type $(r,n_2...n_r)$ would have zero thermodynamical weights for $k > 0$ and infinite conformal weight for $k < 0$.

Hamiltonian as the function of the crank of the partition?

Quite recently Mahlburg [26] represented an ingenious proof of a theorem generalizing the famous regularities of partitions discovered by Ramanujan and followers (for a popular representation of what is involved see the article [14]). The proof is based on the identification of the invariant anticipated by Dyson.

The reason why a function of crank is a promising candidate for Hamiltonian is following.

A partial explanation for why primes $p \leq 11$ are so abundant at infinite temperature limit is that $d(n)$ is divisible by $5,7,11$ for $n = 4+5k$, $n = 5+7k$, and $n = 6+k11$ respectively so that these primes are strong competitors in negentropy maximization race for a large number of values of n (19 for $p=5$, 8 for $p=7$, 5 for $p=11$).

Crank, denote it by C, decomposes the partitions to subsets for which numbers of elements are divisible by $5,7$ *resp.* 11 in these three cases. The expression for $S_p(n)$ in the case of polynomial thermodynamics can be written as

$$\begin{aligned} S_p(n) &= \sum_i N(n,i)C^k(i)log(|\frac{C^k(i)}{Z(n)}|_p) \ , \\ Z(n) &= \sum_i N(n,i)C^k(i) \ , \end{aligned} \tag{14.4.6}$$

It is clear that 5,7, 11 appearing as divisors in both $N(n,i)$ and $Z(n)$ cancel each other and there is no large contribution to negentropy from these primes. This contribution is actually tamed also for other Hamiltonians defining polynomial dynamics.

14.4.2 Could supersymmetric $n_0 > 0$ polynomial thermodynamics determine the genetic code?

The numerical experimentation excludes exponential thermodynamics whereas exponential thermodynamics produces qualitatively reasonable looking genetic codes for $n_0 > 0$ whereas for $n_0 < 0$ most of the spectral power is concentrated at $p = 2$. For small values of n_0 and r_0 purely bosonic thermodynamics fails to reproduce codes satisfying the necessary conditions $D(p) > 0$ and $D(p) < 7$ satisfied by the real genetic code. Super symmetric variant with $S_p(n) = S_{B,p}(n) + S_{F,p}(n)$ however yields several codes satisfying this condition when Hamiltonian is taken to be $exp(H/T) = (r + r_0)^{n_0}$, r the number of summands in the partition.

Basic conditions

The basic conditions on the degeneracies are following:

1. 3 values of n should correspond to stopping codons due to their non-positive or negative entropy. Non-positive entropy is certainly the logical option since the notion of zero information codon does not seem to be reasonable. Numerical computations demonstrate that negative entropies are rather rare whereas $S_p(n) = 0$ occurs rather often. The reason is that if partition function is not divisible by any $p \leq 61$ then the smallest prime $p \leq 61$ not dividing any of the numerators of Boltzmann weights minimizes information and gives $S_p(n) = 0$. These observations suggest that $S_p(n) \leq 0$ condition should be used as a criterion for stopping codon property.
2. The degeneracies $D(p)$ satisfy $D(p) > 1$ if one has $(0,1) \to (0,1)$ so that 0 and 1 correspond to the two aminoacids coded by single DNA.
3. Complete hit means that the numbers $N(k)$ of DNAs coding $D = k \in \{2,3,4,5,6\}$ real aminoacids (as distinguished from stopping sign) should be $(9,1,5,0,3)$. This condition combined with the condition $N(stop) = 3$ allows an automatic search of candidates for codes.

Results

For polynomial thermodynamics the range $n_0 \in \{1,5\}, r_0 \in \{0,5\}$ is scanned. For exponential thermodynamics the range studied is $r_0 \in \{1,5\}, s_0 \in \{1,5\}$. B,F, and BF variants are studied applying the two alternative criteria for the stopping codon and requiring that exactly 3 stopping codons result.

1. $S \leq 0$ as a criterion for the stopping codon

a) Polynomial thermodynamics.

i) Numerical experimentation shows that the number of stopping codons increases rapidly with the values of (n_0, r_0) for polynomial thermodynamics so that only small parameter values seem to be worth of considering.

ii) For cases B and F no solutions are found. BF allows single solution. This code corresponds to $(n_0, r_0) = (2,4)$ having degeneracies

$$(D(2), D(3), ..., D(61)) = (4,4,9,3,7,6,2,2,1,1,4,1,3,1,2,2,3,4) \ .$$

The numbers of DNAs associated with the degeneracies (1,2,3,4,5,6) are

$$(N(1), N(2), N(3), N(4), N(5), N(6)) = (6,4,3,3,0,1)$$

to be compared with the degeneracies

$$(2,9,1,5,0,3)$$

of the real code. If 3 DNAs from 9-plet ($p = 5$) and 1 DNA from 7-plet ($p = 11$) are shifted to 4 1-plets, and 1 DNA from 3-plet is shifted to 3-plet, correct degeneracies result. A modification of r_0 by adding the product of primes $p \leq 61$ with $p \notin \{5, 11\}$ would affect the degeneracies associated with 5 and 11.

b) Exponential thermodynamics.

There are no solutions for F and BF. B gives solution $(r_0, s_0) = (5, 3)$ with degeneracies

$$(9, 1, 3, 1, 5, 2, 3, 2, 4, 4, 4, 2, 3, 2, 2, 3, 1, 8) \quad .$$

From this solution it is possible to construct the real genetic code by shifting 3 codons from 9-plet to 3 1-plets, one codon from 3-plet to a second 3-plet, and 2 codons from 8-plet to 5-plet and 3-plet.

2. $S < 0$ as a criterion for the stopping codon

1. Polynomial thermodynamics.
   For F and BF no solutions are found. B gives single solution $(n_0, r_0) = (3, 1)$. The degeneracies are $(3, 2, 11, 6, 3, 1, 5, 1, 5, 6, 4, 1, 2, 1, 1, 2, 2, 3)$ and quite far from those of the real genetic code.
2. Exponential thermodynamics.
   No solutions are found.

The conclusion is that BF for $S_p < 0$ criterion for stopping codon is the most realistic one and might produce by a small deformation the real genetic code.

14.4.3 Could small perturbations of Hamiltonian cure the situation?

The troubling outcome of calculations is that no realistic code is found for the simplest Hamiltonian. The obvious guess is that one should study small perturbations of the Hamiltonian. There are two kinds of small perturbations. The perturbations of the first kind are small in the real sense but can induce dramatic changes of the genetic code by affecting the p-adic norms of $Z(n)$. The perturbations of the second kind are small in the number theoretical sense but as a rule affect strongly the values of the real probabilities.

Small perturbations in the real sense

The perturbations which are small in the real sense would simply modify $f(r)$ by few units. They would however dramatically affect the p-adic norms of $Z(n)$ and induce thorough changes in the genetic code. In order to proceed in a rational manner some additional assumptions are necessary and therefore this approach will be left in the next subsection where the maximization of the total negentropy of the genetic code is introduced as a variational principle allowing to fix the Hamiltonian as a small perturbation reducing the values of $f(r) = r$ of the Boltzmann weight. It seems that this approach is the more promising one.

Number theoretically small perturbations

The small values of n_0 and r_0 plus unsuccessful searches for $n_0 > 5$ encourage to ask whether the real code result from the semi-realistic codes via a small perturbation of Hamiltonian changing only the partition function Z in number theoretical sense.

The simplest situation is achieved if perturbations do not distinguish between partitions with the same value of r. The number theoretical generalization for the notion of symmetry of action principle suggests that perturbations should leave invariant the prime power factors p^k of Z for $p \leq 61$ but affect them for $p > 61$. This would affect only the probabilities of individual partitions and the positive contributions to $S_p(n)$ coming from the numerators of Boltzmann weights. This might be enough to affect the situation in the case that two primes p_1 and p_2 have nearly the same value of $S_p(n)$ in the original situation. What would be needed that three singly (and thus rarely) coded primes would become doubly coded by this kind of fine tuning.

More precisely, the Boltzmann weight associated with r transforms in $H(r) \to H(r) + \Delta H(r)$ as $B(r) = exp(-H(r)/T) \to B(r) \times (1 + \Delta H(r)/T)$. From this it is clear that the p-adic norm of the contribution of r to the partition function is unaffected if $H(r)$ is divisible by a sufficiently high powers of all primes $2 \leq p \leq 61$: this by the way defines what the notion of small perturbation means number theoretically. Obviously this kind of symmetries exist and since large powers of p in $\Delta H(r)$ modify dramatically the probabilities $p(n, r)$, it is indeed possible to affect the degeneracies associated with various aminoacids.

The simplest perturbation corresponds to the addition of a sufficiently high power of the product $P = \prod_{p \leq 61} p$ to $r_0 : r_0 \to r_0 + P^k$. The p-adic norms appearing as arguments of logarithms would remain invariant. Boltzmann weights would be identical in an excellent approximation as for infinite temperature limit so that the probabilities $p(n, r)$ would reduce to $p(n, r) \simeq d(n, r)/d(n)$. The model would result via the replacement of $p(n, r) \to d(n, r)/d(n)$ from the original model.

It turns out that this replacement does not solve the problem in the range $(n_0 \in \{1,5\}, r_0 \in \{0,5\}$: no codes with 3 stopping sign codons are found. One cannot of course exclude the possibility that larger values of n_0 and r_0 might provide a solution.

A more general trial would assume that the perturbation modifies the p-adic norms of Boltzmann weights but leaves the norms of partition function invariant.

Should one break the symmetry between partitions with same r?

A more radical modification results if the perturbation distinguishes between partitions with different values of r. It is however not clear whether integer valued perturbation can be small in number theoretic sense. Rank and crank distinguish between partitions with same r.

The most radical option is to replace r with a new invariant. If rank and crank define the entire Hamiltonian, they divide partitions into equivalence classes by combining partitions with different values of r to single equivalence class so that the situation changes dramatically. The knowledge about the numbers of partitions in corresponding equivalence classes plus values of these invariants would make it easy to check whether either of them could reproduce the real genetic code.

14.4.4 Could one fix Hamiltonian $H(r)$ from negentropy maximization?

Numerical calculations suggests that number theoretically small modifications might not be the correct manner to find a correct genetic code: the codes having the correct number of stopping codons and coding for all primes differ simply too much from the real code. Even if such a code could be found one can argue that it is only a skillful exercise in the modular arithmetics. Numerical difficulties are also obvious since powers of the product $P = 2 \times 3.... \times 61$ must be added to $f(r)$.

For the perturbations of $f(r) = r$ which are small in the real sense numerical control is not lost but with physicist's intuition in the number theory the modifications of the genetic code are completely unpredictable. The reduction of $f(r)$ by a single unit for single sufficiently small value of r could change the whole biology! In order to study them one should have additional principle allowing to get grasp of the problem.

The great principles of physics are variational principles and Negentropy Maximization Principle is the basic principle in TGD inspired theory of consciousness [44] . Quantum criticality predicts a Universe able to engineer itself and this suggests that the Hamiltonian $H(r)$ determining the genetic code could be a result of "genetic engineering" maximizing the total negentropy of the genetic code.

Could one engineer $H(r)$ from the real genetic code in the case of polynomial thermodynamics?

The most general hypothesis would be that the 62 values of $f(r) = exp(-H(r)/T)$ are completely free positive integers and look whether it is possible to find a Hamiltonian reproducing the genetic code. The naive idea is that since the number of integers $f(r)$ is the same as the values of n, a judicious choice of $f(r)$ could allow to assign to a given n arbitrary $p(n)$ or make it a stopping sign codon. If each r is shifted by the same sufficiently large power of $P = \prod_{p \leq 61} p$, the probabilities for partitions are in an excellent approximation identical in the case of polynomial thermodynamics so that the situation would reduce to a mere modular arithmetics.

One could start from $n = 2$ and proceed by increasing n and determining the value of $f(r = n)$ at n:th step from the requirement that the desired value of p results. What seems obvious is that the value of the partition function $Z(n) = \sum_{r=1}^{n} d(n,r) f(r)$ can be fixed to have an arbitrary prescribed value and thus also the $k_p(Z(n))$ giving the negative contribution to the entropy can be fixed to a desired value. This leaves still some freedom to arrange the value of $k_p(d(n,n)f(n)) = k_p(f(n))$ making possible fine tuning in the n:th numerator contributing to the entropy. The entropies $S_p(n+1)$ and $S_p(n)$ would be related by the condition

$$\begin{aligned} \frac{S_p(n+1) - S_p(n)}{log(p)} &= -k_p(Z(n+1)) + k_p(Z(n)) \\ &+ \sum_{r=1}^{n} \left[d(n+1,r) - d(n,r) \right] k_p(f(r)) + k_p(f(n+1)) \quad . \end{aligned} \tag{14.4.7}$$

The modular arithmetics is of course different from real analysis and the situation might not be so simple as it looks. On the other hand, if this picture is correct, one might interpret the freedom to construct the genetic code almost at will as the fruit of quantum criticality making possible genetic engineering.

Maximization of the total negentropy of the genetic code as a manner to fix the Hamiltonian

The basic objection to this approach is that it is not predictable. It is however possible to introduce a natural variational principle. The maximization of the total negentropy $N_{tot} = -\sum_n S_{p(n)}(n)$ of the genetic code subject to the constraint that all primes are coded and there are 3 stopping codons would in principle allow to fix the function $f(r)$ uniquely.

The maximization of the total negentropy allows to conclude that large (small) prime powers correspond to large (small) DNA multiplets. For instance, if only first powers of p appear, 9 doublets would correspond to $p = 2, ..., 23$, triplet to $p = 29$, five 4-plets to $p = 31, ..., 47$, and 3 6-plets to $p = 53, 59, 61$. Furthermore, since the value of $Z(n)$ increases with n, and thus also the probability that it has large prime power factors, one expects that large values of n should correspond to large values of p. Hence the the orderings of multiplet sizes, primes powers p^k appearing as factors of $Z(n)$, and integers n should correlate strongly.

Is there then any bound on the exponents of powers p^k appearing in $Z(n) = \sum_r d(n,r)f(r)$? If not, then the variational principle does not work. For instance, one might think that ones has

$$f(n+1) = \sum_{r=1}^{n} d(n+1,r) + mp^k \quad ,$$

where k is an arbitrarily large power of p so that $Z(n+1) = mp^k$ holds true and gives an unbounded contribution to $k_p(Z(n+1))$. Only $p(n+1, n+1)$ would differ significantly from zero and would be near 1 but this does not give any restriction. It would seem that there must exist some natural bound on the values of $f(r)$ to stabilize the variational principle.

The most natural option is modulo n+1 arithmetics based on the assumption that Boltzmann factors depend on both n and r and one has $f(n,r) \leq n$ at level n. Boltzmann factors would formally restrict the partition of any integer $m > n$ to partitions of n. This would make the problem numerically more tractable. With this assumption the model for $f(r) = r$ would correspond to the maximum value of $Z(n)$. There would be $61! \sim 5 \times 10^(83)$ alternatives to be scanned but reasonable assumptions should reduce considerably this number.

One can imagine two kinds of additional assumptions.

1. If the genetic code has resulted as a product of singlet and doublet codes then one could argue that also $n = 4$ and $n = 16$ should maximize their total negentropy and code for all primes $p < n$ as real or stopping codons.

2. A much stronger additional assumption that a genetic code coding all primes $p \leq n$ results for every value of n does not work since it implies that highest primes are coded only once.

Consider the situation for the smallest values of n in the bosonic case. For $n = 2$ $f(r) = r$ implies $Z(2) = 3$ giving $p(2) = 3$ favored by local negentropy maximization and $S(2) = -log(3)$. $f(2) = 1$ would give $p(2) = 2$ and $S(2) = -log(2)$. For $n = 3$ to $f(r) = r$ would give $Z(3) = 6$ giving $p(2) = p(3) = 3$ and $S(3) = -log(3) + log(2)/3$ and $S_{tot} = -2log(3) + log(2)/3$. This corresponds to the maximum of total negentropy for 4-code. The code is consistent with the proposal that $2n$ and $2n + 1$ code for the same aminoacid for $n < 61$ explaining the fact that almost all aminoacids are coded by an even number of codons. The absence of stop codon does not allow this code as a genuine singlet code. For $(f(1), f(2), f(3)) = (1, 2, 2)$ with $(Z(2), Z(3)) = (3, 5)$ one would have $n(2) = 3$ and $n = 3$ would represent stopping codon.

For larger values of n a convenient starting point would be $f(n) = n$ and direct checking of values $f(n) = n - k$ for not too large values of k to find a value of Z corresponding to a large prime power. This would give a precise content to what a small perturbation of the Hamiltonian $H(r) = log(r)$ in real sense means in practice. Perturbation would be small only in sense of real analysis and number theoretic effects would be rather dramatic for perturbations at small values of r. Also the notion of a small perturbation of a given genetic code makes also sense. If $f(r)$ is changed only for the values of r near to $r = 63$, only the degeneracies of the aminoacids coded by largest integers and thus having largest degeneracies are affected.

Bosonic Hamiltonian maximizing negentropy subject to constraints coming from the real genetic code

The direct computational search of genetic codes maximizing the total negentropy without any assumptions about genetic code besides non-degeneracy requires a considerable computational power. It is much easier to search for $n \to p(n)$ assignments maximizing the negentropy subject to the constraint that the assignment is consistent with the genetic code.

The reason is that one can imagine a very simple method giving hopes of finding an assignment $n \to f(n)$, $1 \leq f(n) \leq n$ consistent with the genetic code. The basic observation is the variation of $f(n)$ in the allowed range allows always to achieve the condition $Z(n)\ mod\ p = 0$ for $p \leq n$. This gives reasonable hopes that

the nearest prime $p \leq n$ maximizes $Z(n)$. Of course, it can happen that some prime $p > n$ divides $Z(n)$ or some large power of small prime divides $Z(n)$. The optimistic guess for the assignment is simple to construct by starting from $n = 63$ and by proceeding downwards in this manner. One might argue that the ansatz is too conservative. With some good luck it might be possible to assign 6-plets to quite many large primes since the probability $P(n,p)$ to find a value of $f(n)$ guaranteing $Z(n)$ mod $p = 0$ for p slightly larger than n is $P(n,p) = n/p$ and near to one. The assignment of 2-plets and stopping to small primes also helps to maximize the total negentropy.

Computational testing of various ansätze based on guesses for stopping codons required to correspond to as small integers as possible is rather straightforward when one starts from a simple guess deduced by the strategy above and described in table 4 below. The strategy is following.

1. It is easy to deduce the map $n \to p(n)$ for $n \leq 13$. For larger values of n prime divisors larger than that implied by the ansatz produce trouble so that the natural strategy is to look whether stopping codons could correspond to integers above $n = 14$ and near to it.

2. The larger the values n of integers corresponding to stopping codons are, the larger the numbers of values $f(n(stop))$ satisfying the criterion for the stopping codon are. The criterion is the indivisibility of $Z(n(stop))$ by any $p \leq 61$ so that prime values of $Z(n(stop))$ certainly satisfy the constraint for $n(stop) > 7$. This increases the hopes that the constraints from the real code can be satisfied. The smallest values of $n(stop)$ for which the constraints can be satisfied for all values of n are $n(stop) \in \{14, 15, 17\}$. The computation proceeds simply by checking whether any combination of candidates for these three stopping codons satisfies is consistent with the genetic code.

In the sequel considerations are restricted to the bosonic partition function but the generalization to the supersymmetric case is straightforward. The table below represents the ansatz which served as a starting point for the calculations.

n in range	is coded to	multiplet
63-61	61	3
60-59	59	2_1
58-53	53	6_1
52-47	47	6_2
46-43	43	4_1
42-41	41	2_2
40-37	37	4_2
36-31	31	6_3
30-29	29	2_3
28-25	23	4_3
24-21	19	4_4
$\{20-18, 16\}$	17	4_5
17		*stop*
15-14		*stop*
13-12	12	2_4
11-10	11	2_5
9-8	7	2_6
7-6	2	2_7
5-4	5	2_8
3-2	3	2_9

Table 4. The $n \to p(n)$ correspondence whose deformation produces an $n \to f(n)$ correspondence consistent with the real genetic code.

Maps $n \to p(n)$ consistent with the real code can be found by a numerical experimentation starting from the simple guess summarized by Table 4 above and changing the assignments in a obvious manner in the case that some relatively small n yields a large prime factor. In this manner for instance $p = 61$ multiplet can be completed to a 6-plet. The table below represents such a map. From the table it is clear that $p(n) = p(n+1)$ symmetry is only slightly broken and can be understood as a direct consequence of the mechanism assigning to given n the desired prime $p \sim n$.

n in set	is coded to p	multiplet
$\{63-60, 52, 27\}$	61	6_1
$\{59, 57\}$	59	2_1
$\{58, 56-53, 51\}$	53	6_2
$\{50, 49, 31\}$	47	3
$\{48-44, 33\}$	43	6_3
$\{43, 28, 26, 24\}$	23	4_1
42-41	41	2_2
40-37	37	4_2
36-32	31	4_3
30-29	29	2_3
25-21	19	4_4
$\{20, 19, 18, 16\}$	17	4_5
$\{17, 15, 14\}$		$stop_3$
13-12	13	2_4
11-10	11	2_5
9-8	7	2_6
7-6	2	2_7
5-4	5	2_8
3-2	3	2_9

Table 5. The $n \to p(n)$ correspondence maximizing the total negentropy with a constraint for multiplicities coming from the real genetic code.

The Boltzmann weights for the $n \to p(n)$ correspondence represented in the table are given in the array below.

n	1	2	3	4	5	6	7	8	9	10	11	12
$f(n)$	1	2	3	2	2	2	1	4	6	5	1	12
n	13	14	15	16	17	18	19	20	21	22	23	24
$f(n)$	7	12	12	3	16	4	13	19	9	18	21	18
n	25	26	27	28	29	30	31	32	33	34	35	36
$f(n)$	22	11	6	1	6	23	19	17	15	22	34	5
n	37	38	39	40	41	42	43	44	45	46	47	48
$f(n)$	11	32	32	25	41	28	10	37	35	25	11	39
n	49	50	51	52	53	54	55	56	57	58	59	60
$f(n)$	1	11	24	22	2	5	47	39	9	25	1	48
n	61	62	63									
$f(n)$	21	15	20									

14.4.5 Could the symmetries of the genetic code constrain number theoretical thermodynamics?

The number theoretic approach alone leaves completely open the correspondence between DNA triplets and integers n and only the comparison of a code predicting correctly the degeneracies of various aminoacids with the real genetic code allows to deduce information about this correspondence. For instance, 0,1 DNAs and aminoacids can be identified immediately.

The model for prebiotic evolution [41, 29] relies on the fact that the genetic code has an almost exact symmetry: the third nucleotide of the codon has symmetry under A-G exchange and slightly broken symmetry under T-C exchange and an interesting possibility is that this symmetry could be understood at the number theoretical level. Certainly it cannot be a property of the map mapping DNA triplets to integers alone.

What exact A-G symmetry and almost exact T-C symmetry could mean number theoretically?

The most natural interpretation for A-G and T-C symmetries of last nucleotide of codon is that the third 4-digit of the DNA triplet interpreted as a number in the set $\{0, 63\}$ represented in 4-base do not matter much. The symmetry for T-C is slightly broken and this gives 64-20 code instead of $64 \to N \leq 16$ code. Real mathematics would suggest that these 4-digit corresponds to zeroth power of 4 whereas 2-adic arithmetics suggests that it corresponds to the second power of 4.

The characteristic feature of the genetic code is that the degeneracies come in pairs which can be understood in terms of A-G symmetry. There are 3 6-plets, 5 4-plets, 9 2-plets and 1 3-plet of aminoacids and one 3-plet of stopping codons besides the 2 singlets assignable to 0 and 1. That almost all multiplets contain even number of DNAs reflects the additional approximate T-C symmetry.

Even degeneracies must correspond to an approximate symmetry of the partition function. This kind of symmetry could be produced by hand by expressing the partition function as a product of partition functions $Z(n)$ and $Z(f(n))$, where $n \to f(n)$ represents the symmetry but numerical experimentation shows that this does not work. The reason is that for a given n the primes associated with n and $f(n)$ compete and product partition function selects winners from these pairs reducing the degeneracies of the losers so that spectral power tends to get peaked. Hence the product model works only if the symmetry is already there in the sense that the largest prime power factor for $Z(n)$ and $Z(f(n))$ correspond to same prime p.

Suppose that 3 codons correspond to stopping codons. Suppose that there exist a symmetry $n \to f(n)$, not necessary reflection, acting on remaining codons with the property that the largest prime power dividing $Z(n)$ and $Z(f(n)$ corresponds to the same p. Since the number of these codons is odd, the map $n \to f(n)$ must have a fixed point. Obviously the degeneracies are even for primes coded by non-fixed points and odd for those coded by fixed points and the structure of genetic code is consistent with this prediction.

Quite generally, for the reduction of the code to a maximal subset of integers $2 \leq n \leq 63$ not containing $f(n)$ for any n, one would have 11 singlets, 5 2-plets, and 3 3-plets in the set of even integers, or briefly

$$29 = 10 \times \mathbf{1} \oplus 5 \times \mathbf{2} \oplus 3 \times \mathbf{3} \quad .$$

The fixed point $n = f(n)$ would cocde the aminoacid (ile) coded by 3 DNAs.

A reasonable candidate for the symmetry is suggested by the preceding construction reproducing the degeneracies of the genetic code correctly and predicting that n and $n + 1$ tend to code the same aminoacid.

A further input is the information provided by the deviations from the universality of the genetic coded to be discussed later. The deviations from the universality typically involve stopping codons and in the proposed construction it is easy to perform small modifications of the code for values of n near 63. Hence it is natural to test the stronger assumption $2n$ and $2n + 1$ code for the same p for $2 \leq n < 60$ and that $n = 61, 62, 63$ act as stopping codons so that $n = 60$ would correspond to the fixed point coding for ile.

An objection against this hypothesis is that a lot of negentropy is lost if large integers are forced to act as stopping codons. Also the successful construction of the genetic code table starting from the A-G and T-C symmetries of the code table leads to the assignment of the stopping codons to relatively small integers. In this construction the assignment of stopping codons to large values of n codons would also make more difficult to assign large multiplets to large primes.

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	stop	T
	leu	ser	stop	trp	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	ile	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

Table 6. Genetic code.

How close is the correlation between the map from DNA triplets to integers and the map $n \to p(n)$?

The number theoretical model alone does not fix the map between DNA triplets and integers although it poses constraints on this correspondence. A-G symmetry and almost T-C symmetry of the code table however suggest a labelling of the codons which in good approximation could determine *codon* $\to n$ map.

1. A-G and T-C symmetries suggests that the numbering of genetic codons using 4-base representations, that is as sequences of integer triplets (n_1, n_2, n_3), $0 \leq n_i \leq 3$ in 4-base such that each integer labels the four bases. The correspondence can be different for the different members of the triplet. The natural correspondence would be such that (n_1, n_2, n_3) interpreted as 4-digit representation of n gives the map in a reasonable approximation.

2. The correspondence $(T, C, A, G) \leftrightarrow (0, 1, 2, 3)$ for the third nucleotide turns out to be most realistic one from the point of view of $n \to p(n)$ correspondence. A-G and T-C symmetries suggests that n_3 is mapped almost as such to the third 4-digit of n apart from symmetry breaking due to the complications caused by the insertion of 0 and 1 to the code table.

3. The previous example for the genetic code suggests that $n = 14, 15$ correspond to stopping codons. Negentropy Maximization Principle favors doublets for small integers. Since the third column of the code table contains only doublets, it should correspond to small integers. These constraints are satisfied under two conditions. First, n_1 labels the rows of the table with the correspondence $(T, C, A, G) \leftrightarrow (0, 1, 2, 3)$ along the rows of the table so that first and second and third and fourth columns are permuted. Secondly, n_2 must label the entries formed by 4-sub columns of the table and one must have $(C, T, G, A) \leftrightarrow (0, 1, 2, 3)$ for so that n_2 increases from bottom to top.

4. The two stopping codons ATT and ATC would would correspond to $n = 14, 15$ as in the example discussed above. Stopping codon ACT would correspond to $n = 30$ ($n = 17$ in the example). Encouragingly, ser corresponds to $\{63, 62, 61, 60, 22, 23)\}$ coding very naturally $p = 61$. Also in the example discussed 61 belongs to 6-plet.

5. The correspondence between codons (n_1, n_2, n_3) and integers n cannot be given exactly by the representation of n in 4-base since 0 and 1 do not correspond to ACC coding trp (0 or 1) but would correspond to $(1, 3, 3) = 31$. TAC coding met (1 or 0) would correspond to $(2, 1, 3) = 39$. The map from codons to integers with minimal symmetry breaking is obtained from the 4-digit coding of n by shifting 0 and 1 to the positions of 31 and 39. For $n(codon) < 29$ this induces the map $n = n(codon) + 2$. For $41 > n(codon) > 29$ the map is $n = n(codon) + 1$, and for $n(codon) > 41$ the map is $n = n(codon)$. Table 7. lists the resulting number theoretic code in the bosonic case and its correspondence with DNA triplets and aminoacids for this option. It is clear that the risky assignments $n \to p(n)$ are associated with ser and pro.

	A	G	T	C	
A	phe (46,43)	ser(62,61)	tyr(16,17)	cys(31,29)	A
	phe(47,43)	ser(63,61)	tyr (17,17)	cys(32,29)	G
	leu (44,41)	ser (61,61)	stop (14)	stop(30)	T
	leu (45,41)	ser(62,61)	stop(15)	trp(0/1)	C
G	leu(42,41)	pro(58,59)	his(12,13)	arg(28,23)	A
	leu (43,41)	pro(59,59)	his(13,13)	arg(29,23)	G
	leu(40,41)	pro(56,59)	gln(10,11)	arg(26,23)	T
	leu (41,41)	pro(57,59)	gln(11,11)	arg(27,23)	C
T	ile (38,37)	thr(54,53)	asn(8,7))	ser(24,61)	A
	ile(39,37)	thr(55,53)	asn (9,7)	ser(25,61)	G
	ile (37,37)	thr(52,53)	lys (6,2)	arg(22,23)	T
	met (1/0)	thr(53,53)	lys (7,2)	arg(23,23)	C
C	val(35,31)	ala(50,47)	asp(4,5)	gly(20,19)	A
	val(36,31)	ala(51,47)	asp(5,5)	gly(21,19)	G
	val(33,31)	ala(48,47)	glu(2,3)	gly(18,19)	T
	val (34,31)	ala(49,47)	glu(3,3)	gly(19,19)	C

Table 7. Genetic code with the proposed correspondences between DNA triplets with integers n and aminoacids with primes $p(n)$. For instance, $ala(50, 47)$ tells that CGA is mapped to $n = 50$ and ala corresponds to the prime $p = 47$.

1. Numerical testing in the bosonic case

It is straightforward to test the proposed $n(codon) \to n$ map by numerical computations. They are done for both bosonic and supersymmetric case. In the bosonic case correspondence cannot be realized as such. $n = 29$ corresponding to 6^{th} arg is the source of problems and by a trial and error one ends up with a slightly modified $p \to n(p)$ correspondence allowing two solutions for Boltzmann weights $f(n)$ represented in Table 8

below. The requirement that the small deviations from the standard code are realizable as small deviations of $f(n)$ without affective genetic code leaves only $f_1(n)$ into consideration (as will be found in the next section).

n	1	2	3	4	5	6	7	8	9	10	11	12	13
model	0	3	3	5	5	2	2	7	7	11	11	13	13
real	0	3	3	5	5	2	2	7	7	11	11	13	13
$f_1(n)$	1	2	3	2	2	2	1	4	6	5	1	12	7
$f_2(n)$	1	2	3	2	2	2	1	4	6	5	1	12	7
n	14	15	16	17	18	19	20	21	22	23	24	25	26
model	0	0	17	17	19	19	19	19	23	23	61	61	23
real	0	0	17	17	19	19	19	19	23	23	61	61	23
$f_1(n)$	4	8	6	10	12	12	3	5	12	11	15	17	7
$f_2(n)$	4	12	2	6	12	12	7	5	16	11	15	17	7
n	27	28	29	30	31	32	33	34	35	36	37	38	39
model	23	23	0	29	29	23	31	31	31	31	37	37	43
real	23	23	0	29	29	23	31	31	31	31	37	37	37
$f_1(n)$	7	6	21	28	20	27	33	33	21	21	15	36	30
$f_2(n)$	3	6	21	24	24	31	33	33	17	17	15	32	26
n	40	41	42	43	44	45	46	47	48	49	50	51	52
model	37	41	41	41	41	41	41	43	47	47	47	47	53
real	41	41	41	41	41	41	43	43	47	47	47	47	53
$f_1(n)$	13	6	18	23	12	27	28	44	24	33	14	23	52
$f_2(n)$	9	10	18	23	12	31	32	5	20	29	6	23	10
n	53	54	55	56	57	58	59	60	61	62	63		
model	53	53	53	59	61	59	59	59	61	61	61		
real	53	53	53	61	59	59	59	59	61	61	61		
$f_1(n)$	29	26	25	56	10	49	9	10	4	27	49		
$f_2(n)$	5	48	45	41	14	56	15	27	8	35	22		

Table 8. $n \to p(n)$ correspondence allowing two different Boltzmann weights $f_1(n)$ and $f_2(n)$ consistent with the real genetic code obtained by a small modification of the correspondence $n \to p(n)$ implied by the map $n(codon) \to n$ discussed above. This correspondence is also shown in the table for comparison purposes.

2. Numerical testing in the supersymmetric case

One might hope that the replacement of the bosonic partition function with the super-symmetric one might allow an exact realization of the simplest $n(codon) \to n$ correspondence. The multiplication of Z_B by Z_F does not destroy any divisors already present so that the effect might be small. It however turns out that the proposed ansatz fails already at $n = 10$ since Z_F equals to prime $p = 23$ giving higher negentropy than $p = 11$-factor of Z_B. One can try to continue by a modification of the ansatz but the troubles continue and are basically due to the large prime power factor of Z_F. Hence it seems that bosonic ansatz is the only realistic one. Fermionic ansatz is certainly non-realistic since the number of non-vanishing elements of $d_F(n, r)$ is as small as 10 even for $n = 63$.

14.5 Confrontation of the model with experimental facts

The proposed model of genetic code means that we would rather literally consist of sequences of numbers with DNA representing sequences in base 64 and aminoacid sequences represented as products of primes $2 \leq p \leq 61$ and separated by zeros. What this predicts depends on how literally we take this interpretation.

14.5.1 Basic facts about aminoacids

Amino-acids can be classified into three groups.
i) The first class contains 8 hydrophobic non-polar amino-acids with non-polar neutral side-chain. They are leu (6), ala (4), val (4), pro (4), ile (3), phe (2), met (1), trp (1) (numbers in parenthesis tell the number of DNAs coding the aminoacid in question).
ii) Second class consists of 7 hydrophilic polar amino-acids with polar neutral side-chain: ser (6), gly (4), thr (4), cys (2), asp (2), gln (2), tyr(2).

iii) The third class consists of polar hydrophilic acidic amino-acids with charged side chain: asp (2), glu (2) and hydrophilic basic amino-acids arg (6), lys (2), his (2): 5 altogether.

As already noticed, met and trp representing 0 and 1 should belong to the group of non-polar neutral aminoacids and indeed do so. Also the aminoacid representing a fixed point of symmetry $n \to f(n)$ (ile) (if such a symmetry indeed exists) would belong to this group. It is worth of noticing that each group contains single aminoacid coded by 6 DNAs.

14.5.2 Could the biological characteristics of an aminoacid sequence be independent on the order of aminoacids?

The representation of an integer as a product of primes does not depend on the order of factors. Unless the aminoacid sequence does not inherit the natural order of DNA triplets somehow, the biological properties of portions of aminoacid sequences separated by zeros would be invariant under the permutations of aminoacids: the permutation of aminoacids would be analogous to a permutation of bosons. The prediction is extremely strong and certainly testable and might have been observed long ago if indeed true. Professional biologist could probably immediately kill this option.

14.5.3 Are the aminoacids and DNAs representing 0 and 1 somehow different?

The aminoacid representing 0 would most naturally separate different structural and/or functional units and both 0 and 1 could represent a biologically inert aminoacid. Also other interpretation might of course be imagined. The aminoacids representing 0 and 1 would be met coded by TAC and trp coded by ACC, not necessarily in this order.

Do met and trp then have some special properties distinguishing them as 1 and 0?

1. Consider first chemical structure. Both are neutral and non-polar aminoacids, which can be regarded as a basic prerequisite for biological inertness. Met is the only aminoacid containing $CH_2 - S - CH_3$ side chain (cys contains $CH_2 - S - H$ side chain and there are no other aminoacids containing sulphur). Trp in turn is the only aminoacid containing two cyclic chains.

   This kind of arguments must be however taken with a big grain of salt as the following argument shows. Proline differs from all other amino-acids in that the neutral group $H_3N^+ - COO^- - C - H$ group is replaced by a charged $H_2N - COO^- - C - H$ group and is therefore a reasonable looking candidate for 0: pro is however coded by 4 DNAs which would correspond to 2 n and $n + 2$ DNAs with $2 \leq n \leq 31$.

2. At the level of biological function there is indeed a deep difference. The DNA triplet coding for met acts almost universally (for deviations see [95]) as a starting codon which conforms with the identification of met as an aminoacid representing either 0 or 1 (literally the first aminoacid!) and having no other biological significance than telling where in a more complex structure consisting of aminoacid sequences a structural basic element coded by single gene begins.

14.5.4 The deviations from the standard code as tests for the number theoretic model

One can take two different attitudes concerning the deviations from the universality of the code.

Since the deviations occur in mitochondrial genomes and in nuclear genomes of some unicellular eukaryotes, one could argue that in these cases the code need not have achieved full negentropy maximization and that NMP model does not apply. Even if NMP applies, one can argue that the maps $n(codon) \to n$, $n \to f(n)$, and even $n \to p(n)$ correspondence can differ dramatically from that for the nuclear genome.

Second attitude would be that these codes correspond to different local maxima of total negentropy and that the codes correspond to small perturbations of nuclear $n(codon) \to n$, $n \to f(n)$ correspondences.

The deviations from the standard genetic code [95] allow to test between these options, in particular the genetic variant of Negentropy Maximization Principle predicting that small perturbations of $f(n)$ inducing small perturbations of genetic code can affect only large values of n. Numerical experimentation suggest that small perturbations of $n(codon) \to n$, $n \to f(n)$ correspondences are not in question.

Violations of universality for nuclear genes are consistent with the number theoretical model

The violations of the universality [95] are very rare for nuclear genes. A few unicellular eukaryotes have been found that use one or two of three stop codons to code amino-acids instead. The use of two stop codons to code amino-acids necessarily violates the universality of the third column of the code table.

These violations would be consistent with the hypothesis that the two stopping codons ATA and ATG correspond to large values of n (most naturally 62 and 63) but do not force this model. For the codes represented in Table 8 however ATA and ATG however correspond to $n = 14, 15$ so that the modification of the code occurs at rather small values of n and the modifications of $f(n)$ at these values radiate their effect to all higher values of $f(n)$ via the coupling $Z(n) = \sum_{r=1}^{n} d(n,r)f(r)$ and this effect is large in number theoretical sense. Hence small perturbations of $n \to f(n)$ and $n(codon) \to n$ correspondences might not be enough and even $n \to p(n)$ correspondence might need a modification. A detailed numerical computation is required to check whether the model can reproduced the modified codes with some assignment $f(n)$ of Boltzmann weights.

The mitochondrial deviations related to codons representing 0, 1, and stopping sign

For the mitochondrial genes the situation is more complex. There are several kinds of deviations and first kind of deviations related to codons representing 0, 1, and stopping sign.

1. Deviations

Consider first the exceptions associated with stopping codons and codons representing usually 0 and 1 in the proposed model.

1. Mitochondrial codon ACT from animals and micro–organisms (but not from plants) codes trp instead of stopping sign. The problem is that trp corresponds to singly coded aminoacid and should represent either 0 or 1.

2. Most animal mitochondria use TAT in the first column of the code table to code met instead of ile coded usually 3 times. Also this is troublesome since met should correspond to $n = 0$ and be coded only once.

Since both trp and met correspond to 0 and 1 in either order in the model, the question what it means that DNA not representing 0 or 1 codes for 0 or 1. The working hypothesis is that met codes for $p = 1$ whereas trp codes for 0 acting as a codon separating two functional units of aminoacid sequence and being in this sense almost equivalent with stopping codon.

1. Does the notion of $p = 1$ codon make sense?

The condition $S_{p(n)}(n) = 0$ is the most general manner to define effective $p = 1$ codon whereas stopping codon would has positive entropy. This requires that for effective $p = 1$ codons $Z(n)$ is divisible by $p(n)$ and gives a negative contribution to $S_{p(n)}(n)$ but despite this $S_{p(n)}$ is vanishing or positive.

Perhaps it is not a accident that the triply coded ile corresponds to the exceptional multiplet with odd degeneracy. As proposed, single odd degeneracy could be understood if the partition function has an approximate symmetry $n \to f(n)$ such that the DNA coding the third ile corresponds to a fixed point of this symmetry. The fixed point codon would code for 1 in the sense proposed rather than for ile.

In the proposed model $p = 37$ corresponds to ile and the ile transforming to met in yeast mitochondria is coded by $n = 37$. Numerical search demonstrates that $p(37) = 13$ instead of $p(37) = 37$ provides 3 modifications of $f_1(n)$ and 4 modifications of $f_2(n)$ for which $p = 1$ condition is satisfied. The solutions $f_{11}(n)$ and $f_{21}(n)$ are identical with $f_1(n)$ and $f_2(n)$. Obviously this solution is unique.

n	27	28	29	30	31	32	33	34	35	36	37	38	39
p(n)	23	23	0	29	29	23	31	31	31	31	13	37	43
$f_{11}(n)$	7	6	21	28	20	27	33	33	21	21	21	30	24
$f_{12}(n)$	7	6	21	28	20	27	33	33	21	21	22	29	23
$f_{13}(n)$	7	6	21	28	20	27	33	33	21	21	30	21	15
$f_{21}(n)$	3	6	21	24	24	31	33	33	17	17	9	38	32
$f_{22}(n)$	3	6	21	24	24	31	33	33	17	17	10	37	31
$f_{23}(n)$	3	6	21	24	24	31	33	33	17	17	21	26	20
$f_{24}(n)$	3	6	21	24	24	31	33	33	17	17	22	25	19
n	40	41	42	43	44	45	46	47	48	49	50	51	52
p(n)	37	41	41	41	41	41	41	43	47	47	47	47	53
$f_{11}(n)$	13	6	24	23	18	27	28	44	24	27	14	23	46
$f_{12}(n)$	13	6	25	23	19	27	28	44	24	26	14	23	45
$f_{13}(n)$	13	6	33	23	27	27	28	44	24	18	14	23	37
$f_{21}(n)$	9	10	12	23	6	31	32	5	20	35	6	23	16
$f_{22}(n)$	9	10	13	23	7	31	32	5	20	34	6	23	15
$f_{23}(n)$	9	10	24	23	18	31	32	5	20	23	6	23	4
$f_{24}(n)$	9	10	25	23	19	31	32	5	20	22	6	23	3
n	53	54	55	56	57	58	59	60	61	62	63		
p(n)	53	53	53	59	61	59	59	59	61	61	61		
$f_{11}(n)$	29	26	25	56	10	49	15	10	4	27	55		
$f_{12}(n)$	29	26	25	56	10	49	16	10	4	27	56		
$f_{13}(n)$	29	26	25	56	10	49	24	10	4	27	3		
$f_{21}(n)$	5	48	45	41	14	56	9	27	8	35	16		
$f_{22}(n)$	5	48	45	41	14	56	10	27	8	35	17		
$f_{23}(n)$	5	48	45	41	14	56	21	27	8	35	28		
$f_{24}(n)$	5	48	45	41	14	56	22	27	8	35	29		

Table 9. $n \to p(n)$ correspondence allowing three different Boltzmann weights $f_{1i}(n)$ and 4 different Boltzmann weights $f_{2i}(n)$ as perturbations of $f_1(n)$ and $f_2(n)$. $f_{11} = f_1$ and $f_{21} = f_2$ implies that these "perturbations" are unique and correspond to $p(37) = 13$ instead of $p(37) = 37$. The table lists only the rows for which deviation from $f_1(n)$ and $f_2(n)$ occurs.

3. What coding of $p = 0$ could mean?

What it means that $n > 0$ codes instead of stopping sign for 0 is more difficult to interpret unless 0 indeed effectively represents an aminoacid (trp) separating functionally independent units of aminoacid sequence effectively coded by separate genes and stopping sign in this sense. One might think that code has evolved like a computer program via modularization so that in the advanced form of the code DNA sequences code only for the basic building aminoacid sequences rather than their composites separated by exotic aminoacids. Other deviations are consistent with the genetic variant of Negentropy Maximization Principle.

The anomalous behavior of yeast mitochondria

Yeast mitochondria use GAX codons in the first column to code for thr (coded by 4 codons usually) instead of leu (coded by 6 codons usually). For the $n \to p(n)$ correspondences motivated by the mapping $n(codon) \to n$, the deviation would mean that the integers $n = 40 - 43$ code for $p = 53$ (thr) besides n in the range 52-55. A rough modular arithmetics based estimate for the probability that this occurs for single codon is roughly n/p for $n < p$ so that the total probability for this to occur would be $P = 40 \times 41 \times 42 \times 43/53^4 \simeq .38$. It turns out that $n = (40, 41, 42, 43)$ fails to code for $p = 53$. Thus mitochondrial code and nuclear code for yeast should have slightly different $n(codon) \to n$ correspondence. The modification

$$\begin{aligned} p(40, 41, 42, 43, 44, 45, 46, 47) = &\quad (41, 41, 41, 41, 41, 41, 43, 43) \\ \to &\quad (53, 53, 41, 53, 53, 43, 43, 41) \end{aligned}$$

is consistent with negentropy maximization. This means that the permutations $(42 \leftrightarrow 44)$ and $(45 \leftrightarrow 47)$ distinguish the map $n(codon) \to n$ from that for the nuclear code. The modification is given in the table below.

n	1	2	3	4	5	6	7	8	9	10	11	12	13
nuclear	0	3	3	5	5	2	2	7	7	11	11	13	13
$f_2(n)$	1	2	3	2	2	2	1	4	6	5	1	12	7
n	14	15	16	17	18	19	20	21	22	23	24	25	26
nuclear	0	0	17	17	19	19	19	19	23	23	61	61	23
$f_2(n)$	4	12	2	6	12	12	7	5	16	11	15	17	7
n	27	28	29	30	31	32	33	34	35	36	37	38	39
nuclear	23	23	0	29	29	23	31	31	31	31	37	37	43
$f_2(n)$	3	6	21	24	24	31	33	33	17	17	15	32	26
n	40	41	42	43	44	45	46	47	48	49	50	51	52
nuclear	37	41	41	41	41	41	41	43	47	47	47	47	53
yeast	53	53	41	53	53	43	43	41	47	47	47	47	53
$f_2(n)$	9	10	18	23	12	31	32	5	20	29	6	23	10
$f(n)$	13	2	18	22	10	3	36	42	14	29	4	20	7
n	53	54	55	56	57	58	59	60	61	62	63		
nuclear	53	53	53	59	61	59	59	59	61	61	61		
yeast	41	59	41	61	41	59	59	59	61	61	61		
$f_2(n)$	5	48	45	41	14	56	15	27	8	35	22		
$f(n)$	53	53	53	59	61	59	59	59	61	61	61		

Table 9. $n \to p(n)$ correspondence allowing single distribution $f(n)$ of Boltzmann weights consistent with the genetic code of yeast mitochondria obtained by a small modification of the correspondence $n \to p(n)$ implied by the map $n(codon) \to n$ discussed above. The $n \to f(n)$ correspondence results as a modification of $n \to f_2(n)$ for nuclear genetic code so that this option is favored by universality. Only the rows of $n \to p(n)$ and $n \to f(n)$ correspondences differing from those for the nuclear code are given in the table. The correspondences for nuclear genetic code are also shown in the table for comparison purposes.

The deviations associated with exotic aminoacids and stopping sign codons

There are also two non-standard amino-acids: selenocysteine and pyrrolysine.

1. Selenocysteine is encoded by ACT (fourth column) coding stopping sign normally. Interestingly, ACT codes also stopping sign and the translation machinery is somehow able to discriminate when selenocysteine is coded instead of stop. This codon usage has been found in certain Archaea, eubacteria, and animals. This deviation means that the number of amino-acids is 21 or 20 depending on context.
2. In one gene found in a member of the Archaea, exotic amino-acid pyrrolysine is coded by ATC, which corresponds to the lower stopping sign in the code table. This case represents the only deviation from universality of the third column of the code table but even in this case also stopping sign is coded. How the translation machinery knows whether to code pyrrolysine or to stop translation is not yet known.

   These deviations are consistent with the number theoretical models discussed in [41, 29] for which number 21 indeed has a deep number theoretical meaning and assuming that stopping sign can be regarded formally as an amino-acid. In the recent model a reasonable looking interpretation of the exotic aminoacids is as variants of stopping sign in some sense. For instance, the resulting aminoacid sequences could consist of separate functional units separated by selenocysteine/pyrrolysine.

To sum, all deviations challenging the number theoretic model discussed in this chapter are associated with mitochondrial genome only and involve stopping sign codons, codons representing 0 and 1 and exotic aminoacids.

14.5.5 Model for the evolution of the genetic code and the deduction of $n \to p(n)$ map from the structure of tRNA

In [29] a detailed model for the evolution of the genetic code is developed. The hypothesis is that recent DNA-aminoacid code evolved from a code mapping RNA triplets to RNA triplets with the mediation of pre-RNA catching RNA molecules from environment and bringing them to the growing RNA sequence. Aminoacids served originally as catalyzers of the reaction but at some stage began attach to the growing RNA sequence after which RNA sequence become un-necessary and only aminoacid sequence remained.

In the recent framework tRNA would represent the mapping of integers represented by RNA as sequences in 64 base to RNAs representing sequences of primes. Genetic coded literally mapped RNA representing integer $0 \leq n \leq 63$ to an RNA representing the prime $p(n)$. The map $n \to p(n)$ could be determined up to a permutation of the 18 primes $2 \leq p \leq 61$ and permutations of integers mapped to same p (not

larger than 6) from the structure of the recent tRNA since tRNA molecules could still contain RNA pairs representing $n(p)-p$ pairs. That mRNA-RNA correspondence at the level of tRNA would represent $n \to p(n)$ correspondence means that there is no need to ponder the problem how to assign to a given aminoacid the corresponding prime p: tRNA-aminoacid correspondence would be determined by biochemistry.

14.5.6 Genetic code as a product of singlet and doublet codes?

The model of the genetic code applies to any number n of DNAs and maps the numbers $n = 0, 1...n-1$ to $\{0,1\} \cup \{primes\ p \leq n-1\}$. In [29] a model for the genetic code resulting via a symmetry breaking from the product of codes associated with 16 DNA doublets and 4 DNA singlets was considered. At the level of DNAs the product code is very natural and the almost symmetries of the genetic code with respect to the last codon support the idea.

The product structure at the level of aminoacids is however not at all manifest and seems to be absent. This is what the number theoretical model predicts. The primes associated with the product of singlet and doublet codes have no natural composition into products of primes associated with singlet and doublet codes. Nor is the number of these primes product of numbers of primes associated with singlet and doublet codes.

14.6 Exponential thermodynamics does not work

In the following various unsuccessful attempts to understand genetic code in terms of exponential thermodynamics using Hamiltonian $H(r) = r$ are summarized.

14.6.1 What can one conclude about p-adic temperature associated with the genetic code in the case of exponential thermodynamics?

Ordinary thermodynamics suggests that also in the case of exponential thermodynamics temperature should be non-negative. This would boil down to basic requirement $q_0 = r_0/s_0 > 1$ characterizing the genetic temperature. This condition has been however dropped in computations since it is not mathematically necessary in the case of finite state system.

The work with exponential thermodynamics is restricted to the bosonic case. As already found, the fermionic high temperature limit is extremely unrealistic. One important requirement is that also the primes 37 and 61 can appear as divisors in the generalization of $d(n)$ to be discussed. For the remaining primes the most conservative, and probably unrealistic, assumption would be that the arguments of the logarithms appearing in S_p are unaffected so that only the reduction of large r contributions would reduce the degeneracies of over-represented primes. It seems that for small over-represented primes the norms of logarithms must be affected.

The requirement that all entropies $S_{p(n)}(n)$ associated are negative poses strong conditions on q_0, and this might not be possible for all n. The entropic or zero entropy integers could correspond to stopping sign codons.

1. Conditions on q_0

Writing $q_0 = r_0/s_0 > 1$ one can express S_p and assuming $H = r-1$ and $T_r = 1$ in terms of integers alone:

$$\begin{aligned} S_p(n) &= \sum_{r=1}^{n} p(n,r)\left(\frac{r_0}{s_0}\right)^{-r+1} log(|\frac{r_0^{n-r+1}s_0^{r-1}}{\hat{d}(n)}|_p) \ , \\ \hat{d}(n) &= \sum_{r=1}^{n} \hat{d}(n,r) \ , \\ \hat{d}(n,r) &= r_0^{n-r+1}s_0^{r-1}d(n,r) \ . \end{aligned} \tag{14.6.1}$$

The use of different representation for $p(n,r)$ and the argument of logarithm is especially convenient in the numerical calculation of entropy since modular arithmetics can be applied to deduce the argument of logarithm.

To make the representation more fluent, introduce the set $\mathcal{Q}_R$ as subset of primes $p \in \mathcal{P} = \{2,3,...,61\}$ by excluding primes in the set $\mathcal{R} \subset \mathcal{P}$. It turns out that $\mathcal{Q} = P \setminus \mathcal{R}$ condition is too restrictive and hence the subscript $_R$ is added to the definition. The minimal choice for $\mathcal{R}$ is $\mathcal{R}_{min} = \{37, 61\}$ but also 23 is a reasoanable candidate for an element of $\mathcal{R}$. More explicitly,

$$\mathcal{Q}_{max} = \mathcal{P} \setminus \mathcal{R}_{min} = \{2,3,5,7,11,23,17,19,23,29,31,41,43,47,53,59\} \ .$$

Define also integer X_Q as the product of primes in $\mathcal{Q}$:

$$X = \prod_{p_k \in \mathcal{Q}} p_k \ . \tag{14.6.2}$$

Consider now the conditions on q_0 in more detail.

1. Every prime $2 \leq p \leq 61$ must divide $\hat{d}(n)$ for some values of $n(p)$ in order that the prime in question has integers n mapped to it. This has two implications. First, the arguments of the logarithms appearing in the entropy should remain invariant for all primes in $\mathcal{Q}$ to guarantee that no prime is lost. Secondly, for each prime $q \in \{23, 31, 61\}$ there should exist n_q such that $\hat{d}(n)$ is divided by q and q corresponds to the largest prime power of prime in $\hat{d}(n)$.
2. Stopping sign codons correspond to zero information integers n not containing $p \leq 61$ in their decomposition to primes. Assume that $n = 13$ and 36 remain such primes so that $\hat{d}(13)$ and $\hat{d}(36)$ remain indivisible by $p \leq 61$. Also a third similar integer must emerge in finite temperature thermodynamics.

2. Conditions for primes in $\mathcal{Q}$

Consider now these conditions for primes in $\mathcal{Q}$.

1. The p-adic norms of $\hat{d}(n, r)$ and $\hat{d}(n)$ are same as those of $d(n, r)$ and $d(n)$ if the conditions

$$r_0 \ mod \ p = 1 \ , \quad s_0 \ mod \ p = 1 \tag{14.6.3}$$

   hold true. This guarantees that logarithms appearing in S_p are unaffected.
2. These conditions could hold for all primes in $\mathcal{Q}$ and can be satisfied by the ansatz:

$$\begin{aligned} r_0 &= 1 + R_0 X \ , \ s_0 = 1 + S_0 X \ , \\ X &= \prod_{p_k \in \mathcal{Q}} p_k \ . \end{aligned} \tag{14.6.4}$$

   Note that one must have $R_0/S_0 > 1$ in order to have a positive temperature T.
3. The condition $\mathcal{Q}_R = \mathcal{P} \setminus \mathcal{R}$ is un-necessarily restrictive. One can also consider the situation in which one drops some over-represented small primes from X. The dropping of say $p = 7$ and $p = 11$ could make possible the representability of 23 appearing as a factor in $d(32) = 3 \times 11^2 \times 23$ and $d(33) = 3^2 \times 7^2 \times 23$. In fact, the dropping of all small primes $p \leq 11$ might cure at single stroke the over-representability problem. They are probably not lost totally since they have a considerable probability to appear as factors in $\hat{d}(n)$.

3. Conditions for primes in $\mathcal{R}$

Consider next the situation for a prime $q \in \mathcal{R}$, say $\mathcal{R}_{min} = \{37, 61\}$. The task is to deduce conditions on the integers (R_0, S_0).

1. There must exist at least one n_q such that $\hat{d}(n_q)$ is divisible by q:

$$\begin{aligned} \hat{d}(n_q) &= mod \ q = 0 \ , \ q \in \mathcal{R} \ , \\ \hat{d}(n_q) &= \sum_{r=1}^{n_q} \hat{d}(n_q, r) \ , \\ \hat{d}(n_q, r) &= (1 + R_0 X)^{n_q - r + 1} (1 + S_0 X)^{r-1} d(n_q, r) \ , \\ X &= \prod_{p_k \in S} p_k \ . \end{aligned} \tag{14.6.5}$$

   S_0 and R_0 satisfying these conditions for some n_q can be found by a direct numerical search.

2. For each n_q there must exist at least one r_q satisfying the condition

$$\hat{d}_{n_q r_q} \ mod \ q \neq 0 \ , \quad q \in \mathcal{R} \ . \tag{14.6.6}$$

These conditions are very general and allow many solutions (R_0, S_0).

i) For $\mathcal{R}_{min} = \{37, 61\}$ and $\mathcal{Q}_{max} = \mathcal{Q}_{R_{min}}$ one can use the conditions $X_Q = X_{min} \ mod \ 37 = 7$ and $X_{min} \ mod \ 61 = 1$ to reduce conditions to a numerically more tractable form

$$\begin{aligned} \sum_{r=1}^{n_{37}} (1+7R_0)^{n_{37}-r+1}(1+7S_0)^{r-1} d(n_{37}, r) \ mod \ 37 &= 0 \ , \\ \sum_{r=1}^{n_{61}} (1+R_0)^{n_{61}-r+1}(1+S_0)^{r-1} d(n_{61}, r) \ mod \ 61 &= 0 \ . \end{aligned} \tag{14.6.7}$$

ii) If one drops the over-represented small primes $p \leq 11$ from X one obtains $X_Q = X_{min} \ mod \ 37 = 27$ and $X_{min} \ mod \ 61 = 40$. In this case conditions are obtained from previous ones by the replacement $(7, 1) \to (27, 40)$.

iii) For $\mathcal{R} = \{23, 37, 61\}$ one would have $X_R \ mod \ 23 = 10$, $X \ mod \ 37 = 22$ and $X \ mod \ 61 = 2$ and one would have the conditions

$$\begin{aligned} \sum_{r=1}^{n_{23}} (1+10R_0)^{n_{37}-r+1}(1+10S_0)^{r-1} d(n_{37}, r) \ mod \ 23 &= 0 \ , \\ \sum_{r=1}^{n_{37}} (1+22R_0)^{n_{37}-r+1}(1+22S_0)^{r-1} d(n_{37}, r) \ mod \ 37 &= 0 \ , \\ \sum_{r=1}^{n_{61}} (1+2R_0)^{n_{61}-r+1}(1+2S_0)^{r-1} d(n_{61}, r) \ mod \ 61 &= 0 \ . \end{aligned} \tag{14.6.8}$$

14.6.2 Low temperature limit of exponential thermodynamics

The case $s_0 = 1$ ($S_0 = 0$) corresponds to integer valued q_0 and to the low temperature limit of number theoretical thermodynamics characterized by R_0 alone. In this case only $r = 1$ partition contributes significantly to $S_p(n)$ and one expects that the genetic code is determined by the decomposition of the probability $p(r = 1) = r_0^n / \hat{d}(n)$ to prime factors. The positive contribution to information comes from $\hat{d}(n)$ so that in practice this is of primary interest.

The deduction of primes minimizing $S_p(n)$ can be done conveniently by separating the calculation of the exponents of the p-adic norms from the calculation of probabilities. The calculation of the probabilities from their basic formulas is convenient due to the rapid convergence of the exponents $(1 + R_0 X)^{-r+1}$ $r = 1$ term indeed gives an excellent approximation to $S_p(n)$ so that the decomposition of $\hat{d}(n)$ to primes determines $p(n)$ completely unless $d(n, r)$ compensates for the exponential decrease. This might of course mean that the assumption $S_0 = 1$ is not realistic. The study of the low temperature limit in detail can however provide valuable information about a more realistic model.

The overall idea is simple.

1. The primes in $\mathcal{R}_{min} = \{37, 61\}$ must divide $\hat{d}(n)$ for some values of n and these give conditions on R_0.
2. Sum of the over-represented small primes $n \leq 11$ can be dropped from Q and thus from X_Q to see whether $\hat{d}(n)$ is not anymore divisible by these primes so often.

The computational algorithm for finding candidates for realistic genetic codes uses the fact that the number N of DNA triplets coding given aminoacid is never large than 6 for the real genetic code.

1. Form an array of plausible looking choices of X labelling the models to be studied.
2. Calculate the allowed values of R_0 for a given model X and arrange them to a vector.
3. Calculate the components of the vector $p(n)$ for allowed values of R_0 for given X one by one. Keep count of the number of occurrence $N_n(i) = N(p(i))$ of prime $p(i)$ $i = 1, , ..18$ for given (X, R_0) as n increases. If the number $max\{N_i, i = 1, .., 18\}$ exceeds 6, stop the further scanning of n values as useless and start to test the next value of R_0.

Preliminary calculations suggest that the predictions of low temperature thermodynamics do not differ in an essential manner from those of high temperature thermodynamics. The problem is still posed by the over abundance of small primes. The reason is that in the decomposition of integer small primes are most abundant whereas large primes are rare. The probability that small prime p divide random integer is $P = 1/p$. $p = 11$ seems to be the boundary between under-represented primes and over-represented primes. Typically about 40 integers code for primes $p \leq 11$.

14.6.3 How to find the critical temperature in exponential thermodynamics?

The challenge is to understand whether and how $S_0 > 0$ could cure the situation and whether there exists something analogous to a critical temperature in the sense that large long range fluctuations for ordinary criticality correspond to large degeneracies for large primes. From the point of view the association of a number theoretical critical temperature to genetic code would be rather natural since in TGD framework living systems indeed are quantum critical systems. and genetic code should be be something completely exceptional.

The following arguments give some glimpse about what criticality might mean.

1. For $r_0 \sim s_0$ near criticality the probabilities $p(n,r) = r_0^{n-r} s_0^r p(n,r)/\hat{d}(n)$ are of same order of magnitude so that all values of r contribute significantly to $S_p(n)$ as in the case of infinite temperature limit. Individual contributions are however relatively small for large values of $\hat{n}$.
2. In the argument of logarithm the small primes appearing as factors of $r_0^{n-r} s_0^(r-1) p(n,r)$ tend to compensate the small primes dividing $\hat{d}(n) = \sum_r r_0^{n-r} s_0^(r-1) d(n,r)$ so that only a small number of terms with negative entropy remains and the small value of $p(n,r)$ means that overall contribution is small.

The cautious conclusion is that at criticality r_0 and s_0 should be near to each other. There are however tight constraints. For instance, for $s_0 = 1$ r_0 cannot be divisible by primes $2 \leq p \leq 61$ since in this case the partition functions would not be divisible by any of these primes and corresponding aminoacids would not be coded at all. There one must have $r_0 \geq 67, s_0 \geq 67$ in order to not lose the primes from the partition function.

The preliminary computations with small values of r_0 and s_0 near shows that realistic looking degeneracies result except for $p = 2$ whose degeneracy is of order 40 typically: it seems that the spectral power is shifted from primes $p \leq 11$ to $p = 2$. The very special character of $p = 2$ suggests a possible remedy. Perhaps the integers 0,1,2 should be mapped to themselves by genetic code and only odd primes compete in the variational principle. This would however mean that the number of aminoacids coded by single DNA would be 3 rather than the observed 2 consistent $(0,1) \to (0,1)$ hypothesis. This option can work only if one maps some other DNAs than 0 (1) to 0 (1). This could make sense only in the case that all primes give $S_p(n) = 0$ for some n. It turns out that the dropping of $p = 2$ only shifts the spectral power to $p = 3$ for checked small values of (r_0, s_0). It seem that if the idea of criticality is not enough unless one has clear idea about what makes (r_0, s_0) critical.

The first TGD inspired model for genetic code was based on the Combinatorial Hierarchy $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$ starting from $M(1) = 2$ and giving Mersenne primes $3, 7, 127, 2^{127} - 1$. $M_7 = 127$ corresponds to genetic code. This inspires the idea that perhaps $(r_0 = M_7, s_0 = 1)$ might be worth of checking. The parameter values $r_0 = 127, s_0 = 1$ indeed yield the first example for which the spectral power for primes $p \leq 11$ is reasonably small and equal to 17. 22 units of spectral power however concentrates on $p = 2^5 - 1 = 31$, the Mersenne prime below M_7! many primes are lacking from the spectrum. In any case, it would seem possible to distribute the spectral power outside the small prime region but it is clear that genetic code would be number theoretically something extremely special of realized in this manner.

For $s_0 > 1$ spectral power again concentrates on $p = 2$. Since M_{127} corresponds to the Mersenne assigned to the memetic code, natural curiosity leads to check what happens in this case. All spectral power concentrates to $p = 2$ in this case: this is nothing but 2-adic spontaneous magnetization! It seems that this phenomenon occurs quite generally for very large values of r_0.

There might be something wrong with the program making the modulo arithmetics. For even values of r_0 partition function should be odd and $p = 2$ would give positive contribution to entropy. The general finding is that $p = 2$ is highly degenerate. This is possible only if the partition function fails to be divisible for primes $2 \leq p \leq 61$ for very many values of n. Even this does not help for $r_0 = 2^n$ since in this case $p > 2$ gives non-positive entropy for all values of n.

14.7 Appendix

The appendix sums up some computational aspects of the model and represents the models for doublet and singlet genetic codes as toy models.

14.7.1 Computational aspects

Calculation of partition numbers $d(n,r)$

The basic problem in the calculation of partition numbers $p(n,r)$ is the presence of partitions containing same integer several times. This problem can be circumvent by arranging the integers in the partition in decreasing order so that one has $n_1 \geq n_2 ... \geq n_r$. Using this ordering the calculation of partition numbers $d(n,r)$

$$d(n,r) = \sum_{k=1}^{n-r+1} d(n-k, r-1|k) \ , \tag{14.7.1}$$

where $d(n,r|k)$ denotes the number of partitions for which the first number n_1 satisfies $n_1 \leq k$. The formula states that the ordered r-partitions of n decompose as $(k, n_1, ...n_{r-1})$, $k \leq n-r-1$ such that $r-1$-partition $(n_1, ..., n_{r-1})$ satisfies $n_1 \leq k$ by the ordering assumption.

What one must calculate are the numbers $d(n-k, r|k)$ and this can be done recursively

$$d(n,r|k) = \sum_{k_1 \leq k} d(n-k_1, r-1|k_1) \ . \tag{14.7.2}$$

The basic data item besides these formulas is $d(1,1) = 1$. Also $d(n,n) = 1$ and $d(n,1) = 1$ can be used.

The algorithm becomes time consuming for $n > 50$ and larger partition numbers are conveniently calculated by using the recurrence relation [5]

$$P(n,k) = P(n-1, k-1) + P(n-k, k) \ . \tag{14.7.3}$$

The numbers $Q(n,k)$ of partitions of n to integers such that same integer does not appear twice are obtained from the formula [5]

$$Q(n,k) = P(n - \binom{k}{2}, k) \ . \tag{14.7.4}$$

Numerical treatment of $n_0 < 0$ polynomial thermodynamics

The numerical treatment of $n_0 < 0$ polynomial thermodynamics is somewhat tricky and deserves a separate discussion. For definiteness the consideration is restricted to $H = log(r + r_0)$ case with $T = 1/n_0$. The generalization to other critical Hamiltonians is trivial.

For $n_0 = -m < 0$ case the entropy has the expression

$$\begin{aligned} S_p(n) &= \sum_{r=1}^{n} p(n,r) \left[m log(|\frac{(n+r_0)}{r_0!(r+r_0)}|_p) \right] - log(|Z(n)|_p) \\ &= \left[\sum_{i=r_0+2}^{n+r_0} k_p(i) - \sum_r p(n,r) k_p(r+r_0) \right] m log(p) - log(|Z(n)|_p) \\ Z(n) &= \sum_{r=1}^{n} \left[\frac{(n+r_0)!}{r_0!(r+r_0)} \right]^m d(n,r) \ . \end{aligned} \tag{14.7.5}$$

Here $k_p(n)$ is defined by the p-adic norm $|n|_p = p^{k_p}$. The integers appearing as coefficients of $d(n,r)$ in Z are very large and this causes numerical difficulties since factorials are represented precisely as integers only up to 21! and mod operation gives zero above this limit.

In order to calculate the p-adic norm of Z one must perform modulo p^k operations for Z by doing it separately for each summand and summing the resulting expressions. The problem is that the modulo p^k operation for the products involved does not reduce it to a small integer when p is large and one is forced to do the sum of large integers.

The solution of the problem is provided by finite field arithmetics. Start with the expression of $Z(n)$ written as

$$Z(n) = \sum_{r=1}^{n} \frac{1}{(r+r_0)^m} d(n,r) \ . \tag{14.7.6}$$

Since the calculation of p-adic norm involves only repeated modulo p operations to check whether the result vanishes modulo p, and if it does, a subsequent division by p, it suffices to interpret the factors $(1/(r+r_0)^m$ as elements of finite field $G(p,1)$.

1. If the condition $r+r_0 \; mod \; p \neq 0$ holds true, all denominators are non-vanishing. This is the case when $r_0+1 \leq p \leq n+r_0$ holds true. In this case it suffices to calculate the inverses $(r+r_0)_p^{-1}$ of $r+r_0$ in $G(p,1)$ and replace $Z(n)$ with

$$\hat{Z}(n) = \sum_{r=1}^{n} \left[(r+r_0)_p^{-1}\right]^m d(n,r) \quad . \tag{14.7.7}$$

   The resulting expression is free of overflow problems and its p-adic norm can be calculated without difficulties.

2. When the condition $r+r_0 \; mod \; p \neq 0$ fails to be satisfied poles appear at $r=r_k=kp-r_0$, $k_{min}=[(1+r_0)/p]+1 \leq k \leq k_{max}=[(n+r_0)/p]$, where $[x]$ denotes nearest integer smaller than x. Note that the problem is not encountered for $r_0 > 60$. The trick is to express Z in the form

$$\begin{aligned}
Z(n) &= \frac{1}{X} \times \hat{Z}(n) \quad , \\
\hat{Z}(n) &= \sum_{r \neq kp-r_0} X \times \left[(r+r_0)_p^{-1}\right]^m \times d(n,r) \\
&+ \sum_{k=k_{min}}^{k_{max}} X_k \times d(n, kp-r_0) \quad , \\
X &= \prod_k (r_k+r_0)^m = \prod_{i=k_{min}}^{k_{max}} (ip)^m = \left(\prod_{i=k_{min}}^{k_{max}} i \right)^m p^{m(k_{max}-k_{min})} \quad , \\
X_k &= \frac{X}{(r_k+r_0)^m} = \left(\frac{\prod_{i=k_{min}}^{k_{max}} i}{k} \right)^m \times p^{m(k_{max}-k_{min}-1)} \quad .
\end{aligned} \tag{14.7.8}$$

   This expression involves only relatively small integers and overflow problems are avoided.
   $k_p(X)$ can be expressed in the form

$$k_p(X) = m \left[\sum_{k_{min}}^{k_{max}} k_p(k) - k_{max} + k_{min} \right] \quad . \tag{14.7.9}$$

To sum up, the expression for $S_p(n)$ reduces in $(n_0=-m<0, r_0)$ case to the form

$$\begin{aligned}
\frac{S_p(n)}{log(p)} &= \left[\sum_{i=r_0+2}^{n+r_0} k_p(i) + \sum_{k_{min}}^{k_{max}} k_p(k) - k_{max} + k_{min} - \sum_{r=1}^{n} p(n,r) k_p(r+r_0) \right] m \\
&- k_p(\hat{Z}(n)) \quad , \\
\hat{Z}(n) &= \sum_{r \neq kp-r_0} X \left[(r+r_0)_p^{-1}\right]^m d(n,r) + \sum_{k=k_{min}}^{k_{max}} X_k \times d(n, kp-r_0) \quad , \\
X &= \left(\prod_{i=k_{min}}^{k_{max}} i \right)^m p^{m(k_{max}-k_{min})} \quad , \\
X_k &= = \left(\frac{\prod_{i=k_{min}}^{k_{max}} i}{k} \right)^m \times p^{m(k_{max}-k_{min}-1)} \quad , \\
k_{min} &= [(1+r_0)/p]+1 \quad , \quad k_{max}=[(n+r_0)/p] \quad .
\end{aligned} \tag{14.7.10}$$

In the nonsingular case 1) $X=1$ and $X_i=0$ holds true.

In practice $r \neq r_k$ terms do not contribute to $k(\hat{Z}(n))$ unless all $d(n,kp-r_0)$ happen to be divisible by a large power of p. The highest power of $p \leq 61$ appearing in $d(n,r)$ is 4 for $n \leq 63$. For the sake of generality and safety it is however better to keep also these contributions in the formula.

14.7.2 Number theoretic model for singlet and doublet codes as a toy model

The model of the genetic code applies to any number n of DNAs and maps the numbers $n = 0, 1...n-1$ to $\{0,1\} \cup \{primes\ p \leq n-1\}$. In [29] a model for the genetic code resulting via a symmetry breaking from the product of codes associated with 16 DNA doublets and 4 DNA singlets was considered. At the level of DNAs the product code is very natural and the almost symmetries of the genetic code with respect to last codon support the idea.

Singlet code

In the case of singlet code the requirement that at least single stopping sign codon exists, implies that either $p = 2$ or $p = 3$ fails to be coded. This would conform with the idea that $n = 3 = -1\ mod\ 4$ represents automatically stopping sign and 3 aminoacids would be coded. Fermionic entropy vanishes identically with this assumption.

It is perhaps instructive to consider the singlet codes at low temperature limit of exponential thermodynamics for $(r_0 > 1, s_0 = 1)$ to get some grasp of the situation. Singlet code gives $(\hat{d}(1), \hat{d}(2), \hat{d}(3)) = (1, 1+r_0, 1+r_0+r_0^2)$. The probabilities $p(n,r)$ are $p(n,r) = r_0^{n-r}/\hat{d}(n)$ and entropy can be written as

$$S_p(n) = -\frac{r_0^m}{1+r_0+..+r_0^n}\sum_{m=1}^{n} log(|\frac{r_0^m}{1+r_0+...+r_0^n}|_p)\ . \tag{14.7.11}$$

For $r_0 = 2$ *resp.* $r_0 = 3$ one has $(\hat{d}(1), \hat{d}(2), \hat{d}(3)) = (1, 3, 7)$ and $(\hat{d}(1), \hat{d}(2), \hat{d}(3)) = (1, 4, 13)$. For $r_0 = 2$ the code is $(0, 1, 2, 3) \to (0, 1, 3, stop)$ with $n = 3$ having vanishing entropy and thus naturally acting as stopping codon. $p = 2$ is not coded. For $r_0 = 3$ the code is $(0, 1, 2, 3) \to (0, 1, 2, stop)$. $p = 3$ is not coded.

Allowing $s_0 > 1$ does not allow to circumvent these problems. In this case the formula for entropy reads as

$$S_p(n) = -\frac{1}{s_0^n + r_0 s_0^{n-1}..+r_0^n}\sum_{m=1}^{n} r_0^m s_0^{n-m} log(|\frac{r_0^m s_0^{n-m}}{s_0^n + r_0 s_0^{n-1}..+r_0^n}|_p)\ . \tag{14.7.12}$$

For $(r_0 = 3, s_0 = 2)$ the denominator is not divisible by 2 or 3 so that all codons possess vanishing or negative information. The conclusion is that the mapping of $3 = -1 mod 4$ to stopping codon is the only consistent option.

For polynomial thermodynamics with Boltzmann weights given by $(r + r_0)^{n_0}$ there is a large number of parameter combinations giving single stopping codon which is always $n = 2$.

Doublet codes

Doublet code should map the integers $0, 1..., 14(15)$ to primes $0, 1, 2, 3, 5, 7, 11, 13$. The inspection of the tables 1 and 2 shows that at infinite temperature limit $p = 13$ fails to coded for both B,F, and BF and also $p = 7$ for F. $n = 13$ is not coded to a unique prime for B. The parameter values are restricted to the range $(n_0, r_0) \in (\{1,5\}, \{0,5\})$ in the polynomial case and to the range $(r_0, s_0)(\{1,5\}, \{1,5\})$ in the exponential case. The findings support the view that polynomial thermodynamics is the only viable approach.

1. Stopping sign codons as codons with $S_p < 0$

For finite temperature thermodynamics the conditions used are that least one stopping codon having by definition $S_p < 0$ exists and all primes $p \leq 13$ must be coded.

1. For finite temperature polynomial thermodynamics the cases F and BF allow no solutions whereas B allows four solutions $((n_0, r_0) = (1,5), (2,1),$
   $(2,5), (3,3))$.
2. For exponential thermodynamics neither, B, F, nor BF allow solutions.

2. Stopping sign codons as $n = 15$ codon or codons with $S_p < 0$

One could argue that since $n = 15$ corresponds to -1 in modulo 16 mathematics, it should code for stopping sign. If so, the situation changes.

1. Polynomial thermodynamics.

   In BF case $(n_0, r_0) = (1, 1)$ provides in the range $(n_0, r_0) \in (\{1, 5\}, \{0, 5\})$ the only example of a genetic code for which all primes $p \leq 13$ are coded. One can say that supersymmetric option fixes the code uniquely in this parameter range. F allows no solutions. B allows 4 solutions $((n_0, r_0) = (1, 2), (2, 1), (2, 5), (3, 3))$.

2. Exponential thermodynamics

   Neither B, F, nor BF type thermodynamics allow solutions.

n	$d_B(n)$	$p_B(n)$	$d_F(n)$	$p_F(n)$	$p_{BF}(n)$
0	1	1	1	0	0
1	1	1	1	1	1
2	2	2	1	1	2
3	3	3	2	2	3
4	5	5	2	2	5
5	7	7	3	3	7
6	11	11	4	2	11
7	3×5	5	5	5	5
8	2×11	11	6	3	11
9	$2 \times 3 \times 5$	5	8	2	2
10	$2 \times 3 \times 7$	7	10	5	3
11	$2^3 \times 7$	2	12	2	2
12	7×11	11	15	5	11
13	101 (prime)	?	18	3	3
14	$3^3 \times 5$	3	22	11	3
15	$2^4 \times 11$	2	27	3	3

Table 10. The table represents the partition numbers $d_B(n)$ and $d_F(n)$ as well as the primes $p_B(n)$,$p_F(n)$, $p_{BF}(n)$ resulting from the minimization of the p-adic entropy $S_{I,p}(n)$, $I = B, F, BF$ as a function of n for $n < 16$.

Books related to TGD

[1] Prebiotic Evolution in Many-Sheeted Space-Time. In *Genes and Memes*. Onlinebook. http://tgd.wippiespace.com/public_html/cbookII/cbookII.html#prebio, 2000.

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Chapter 15

Unification of Four Approaches to the Genetic Code

15.1 Introduction

A proposal unifying four approaches to genetic code is discussed.

The first approach is introduced by Pitkänen [33, 29] and is geometric: genetic code is interpreted as an imbedding of the amino-acid space to DNA space possessing a fiber bundle like structure with DNAs coding for a given amino-acid forming a discrete fiber with a varying number of points. Also Khrennikov has proposed an analogous approach based on the identification of DNAs coding for a given amino-acid as an orbit a discrete flow defined by iteration of a map of DNA space to itself [22] .

Second approach starts from the 5-adic approach of Dragovich and Dragovich [11] . Codons are labeled by 5-adic integers n which have no non-vanishing 5-digits so that the n is in the range $[31, 124]$. The observation of Pitkänen that the number of primes in the range $[31, 124]$ is 20 makes the labeling of amino-acids by primes in this range suggestive. The identification of the conjugation $k \to 5 - k$ as DNA conjugation is however re-interpreted as the symmetry with respect to third letter leaving for all codons the coded amino-acid invariant in the case of vertebrate mitochondrial code. This inspires an additional condition on the geometric code: if possible, one of the integers n projected to p equals to $p(n)$. This condition fails only for the primes 53,79,101,103 for which some of 5-digits vanishing in 5-ary expansion.

The third approach is based on the generalization of the basic idea of the so called divisor code proposed by Khrennikov and Nilsson [24] . The requirement is that the number of factors for integer n labeling one of DNAs, call it n_d coding for a given amino-acid is the total number of codons coding for the amino-acid, its degeneracy. Therefore a given amino-acid labeled by prime p with no non-vanishing 5-digits is coded by DNAs labeled by p itself and by n_d. The two conditions fix the code to a high degree when one requires that all known variants of the code can be produced. A group theoretic and physical interpretation for the origin of the divisor code is proposed.

The fourth approach is a modification of the earlier 4-adic number theoretic thermodynamics approach of Pitkänen.

1. 5-adic thermodynamics involving a maximization of number theoretic negentropy $N_p(n) = -S_p(n) > 0$(!) [44, 19] as a function of p-adic prime p labeling amino-acids assigns a unique prime to the codon. If no prime in the range divides S_p, the codon is identified as a stopping codon carrying no information. The maximization criterion reduces to the condition that $p(n)$ corresponds to the largest prime power divisor of the partition function.

2. With a motivation coming from the symmetries of the code, the number theoretic thermodynamics is assigned with the partitions P of the integer $n_{2)}$ determined by the first two letters of the codon (16 integers belonging to the range $[6, 24]$). The integer valued number theoretic Hamiltonian $h(P) \in Z_{25}$ appearing in the Boltzmann weight $5^{h(P)/T_5}$ is assumed to depend on the number r of summands for the partition only. $h(r)$ is assumed to be tailored by evolution so that it reproduces the code.

3. The effect of the third nucleotide is described in terms of 5-adic temperature $T_5 = 1/n$, $n \in [0, 24]$: the variation (also temporal) of this temperature explains the existence of variants of genetic code and its temporal variation the observed context sensitivity of the codon-amino-acid correspondence for some variants of the code [29] , [95] .

A numerical calculation scanning over $N \sim 10^{30}$ candidates for $h(r)$ allows only 11 Hamiltonians and with single additional symmetry inspired condition there are 2 solutions which differ only for 5 largest values of r.

Due to the limited computational resources available only 24 percent of the available candidates have been scanned and the naive expectation is that the total number of Hamiltonians is about about 45 unless one poses additional conditions.

15.2 Unifying various approaches to the genetic code

The understanding of genetic at deeper level has gained increasing attention: mention only the proposals of Khrennikov [22, 23] , Pitkänen [33, 29, 19] , and Dragovich and Dragovich [11] . Quite recently Khrennikov and Nilsson introduced the idea of divisor code [24] . The idea is inspired by the observations that the numbers of divisors of integers in the range $[1, 20]$ are rather near to degeneracies of amino-acids for the genetic code. The attempts to realize this idea as such were however not successful and this led to a generalization of the basic idea of the divisor code and stimulated the attempt to combining four different approaches to the genetic code to single unified approach.

15.2.1 Geometric approach to the genetic code

The geometric approach of Pitkänen [33, 29, 19] was inspired by the basic hypothesis of TGD [5, 4, 3] that space-times can be regarded as 4-surfaces $X^4 \subset H = M^4 \times CP_2$ of 8-dimensional imbedding space H. The idea was to replace H by the discrete space of integers labeling the 64 DNA triplets and X^4 by the discrete space of 20 amino-acids [29] . Thus genetic code imbeds amino-acid space with points labeled by integers n_A to the DNA space labeled by some subset of integers (not necessarily $0 \leq n \leq 63$) such that the DNAs coding for a given amino-acid A form a discrete fiber like structure. One could also assume that one of the integers $n(DNA)$ labeling one of DNAs coding for A satisfies $n(DNA) = n(A)$ if possible.

As a matter fact, there exists the algebraic-geometric theory for codes based on the identification of code as a subset of subspace of G_p^k where G_p is finite field [16] . If the points of this subset are labeled by some subset of integers m, the inclusion induces the code as a map $m \to n(m)$ where $n(m)$ consists of k G_p valued numbers. This concept of code does not apply to genetic code but the generalization is obvious: assign to the imbedding a bundle structure assigning to each point $n(m)$ a fiber consisting of points of G_p^k.

[25] [22] has proposed identification of codons coding for given amino-acid as an orbit of a discrete flow in the space of codons. It is possible to interpret DNA space as a bundle with fibers identified as orbits of the flow acting as a discrete group Z_n of symmetries in the fiber. The imbedding of amino-acid space to DNA space in the case of 5-adic code is however not quite equivalent with this view since four primes labeling amino-acids do not label codons.

15.2.2 4-adicity and 5-adicity as possible realizations of the symmetries of the genetic code

An important physical constraint on any model is the fact that for the mitochondrial code codons have exact A-C and G-U symmetries with respect to the last codon. For eukaryote code this symmetry is broken only by two codons (Stop-Trp and Ile-Met pairs). A natural origin for this symmetry would be the formation of the 3-codons via fusion of 2-codons and 1-codons as suggested in the model of prebiotic evolution proposed in [29] .

One can consider two mathematical models for this symmetry.

1. 4-adic model of Pitkänen [19] assumes the labeling of the codons using 4-adic numbers $n = n_0 + n_1 4 + n_3 16$, $n_i \in Z_4$ such that codons with $i = 0, 2$ and $1, 3$, which are 4-adically close to each other, correspond to symmetry related pairs. Also the model of Khrennikov and Kozyrev based on the identification of DNA space as 8×8 diadic plane (chess board!) starts from 4-adicity [23] and interprets genetic code as a locally constant map from DNA space to amino-acid space. The number of primes $p < 64$ is 18 which leads to the idea that integers $n = 0, 1$ and the primes $p < 64$ code for amino-acids. Note however that 4-adicity as a strict symmetry needs to be assumed only for the third nucleotide.

2. For the 5-adic labeling of the codons suggested Dragovich and Dragovich [11] codons are labeled by integers $n_0 + n_1 5 + n_2 5^2$ with $n_i \neq 0$ and vary in the range $[31, 124]$. The observation that the number of primes in this range is 20 inspires the hypothesis that that the primes in question label amino-acids. 5-adicity in the weakest sense means 5-adicity with respect to the third nucleotide so that either the codons $(n, n+50)$ or codon pairs $(n, n+25)$ and $(n, n+75)$ code for the same amino-acid in the case of vertebrate mitochondrial code. There are three primes pairs $(p, p_1 = p + 50)$ [(47,97),(53,103),(59,109)] so that $n \to n + 50$ symmetry is not consistent with the labeling of amino-acids by primes. Hence only $(n, n+25)$ and $(n, n+75)$ option meaning that A-C and G-U pairs correspond to pairs of even and odd integers is acceptable and that the conjugation $n_3 \to 5 - n_3$ cannot correspond to DNA conjugation, which was the original motivation for the 5-adicity, but to the A↔C and G↔U symmetries.

15.2.3 Number theoretical thermodynamics and genetic code

The original thermodynamical model for the genetic code developed by Pitkänen [19] is based on 4-adic labeling of codons. The model assumes that the number theoretical thermodynamics associated with the partitions of integers n labeling codons assigns to a given codon a unique prime labeling the amino-acid coded by DNA as the prime p for which the number theoretic negentropy $S_p = -\sum_k p_k log_p(|p_k|_p) log(p)$ is maximum: here $|x|_p$ denotes p-adic norm. S_p satisfies basic axioms of Shannon entropy but can be also negative so that its negative becomes a genuine measure of information [44, 19] . Stopping codons would correspond to DNAs for which no prime in the allowed range of primes exists. A possible physical justification could be a breaking of conformal symmetry so that the states of given conformal weight $n = \sum n_i$ associated with the states $\prod L_{n_i}|n = 0\rangle$ are have different number theoretic "energies" depending only on the number r of integers n_i in the partition.

One can consider two variants of the number theoretical thermodynamics.

1. In the 4-adic case $n = 0$ and $n = 1$ amino-acids and codons correspond to DNAs labeled by same integers and are thus in a special role. The number theoretical thermodynamics [19] is able to reproduce the genetic code and its variants by assuming that the integer valued Boltzmann weights of the thermodynamics are integers in a suitable range tailored by evolution in order to maximize the number theoretical negentropy. Boltzmann weights are assumed to be arbitrary integers in some range rather than powers of some prime so that genuine p-adic thermodynamics for some prime is not in question.

2. The 5-adic thermodynamics is favored by the fact that there are no special amino-acids now ($n = 0$ and $n = 1$). Preliminary calculations suggests that the 5-adic thermodynamics can be reduced to that for the 2-codons defined by the first two nucleotides labeled by integers $n_{2)} = n_0 + n_1 5$, $n_i \neq 0$ belonging to the range $[6, ..., 24]$. The integer valued Hamiltonian $h(P)$ for the thermodynamics of partitions P of $n_{2)}$ and defining Boltzmann weights $5^{h(P)}$ would depend only on the number r of summands in the partition P of n as $n = \sum_{k=1}^{r} n_k$. The dependence of the coded amino-acid on the third letter of the codon would be coded by the integer valued inverse of the 5-adic temperature $T_5 = 1/n$. A-C and G-U symmetries would correspond to the symmetry $T_5(r, k) = T_5(r, 5 - k)$ and the breaking of these symmetries would be due to the variation of temperature. The temporal variation of T_5 would explain the fact that for some variants of code same codon can code for either an amino-acid or stopping sign [19] , [95] .

15.2.4 Group theoretic interpretation of the divisor code

The basic question is why the product decompositions of integer n characterizing one of the DNAs coding for a given amino-acid labeled by prime would determine the number of DNAs coding for the amino-acid. The original suggestion was that explanation is group theoretical. The fundamental role of discrete subgroups of rotation group in quantum TGD [83, 27] suggests that finite subgroups $H \subset G$ of $G \subset SU(2)$ are involved with the code. Finite symmetry groups are indeed naturally associated with codes and the first observation is that product decompositions of integer n correspond naturally to the decompositions of an Abelian group G order n to products of subgroups with orders r and s, $n = r \times s$.

The hypothesis is that integer n characterizing the amino-acid corresponds to the order of G and that the factor pairs (r, s) of $n = rs$ correspond to its subgroups $H_r \times H_s \subset G$. The codons coding for amino-acid characterized by n would correspond to a normal sub-groups of G in general case and to any subgroup in the Abelian case. The simplest identification of G is as the cyclic group Z_n. That the product decompositions (r, s) and (s, r), $r \times s = n$ must be counted as separate can be understood if a wave function invariant under $Z_r = Z_n/Z_s$ characterizes the codon labeled by (r, s). Z_n would naturally act as a symmetry group in the discrete fiber of the fiber bundle defined by the DNA space and defining a discrete flow in the fiber. The p-adic prime p assigned to the amino-acid could in turn characterize the p-adicity of corresponding space-time sheet [47] .

The physical interpretation suggested by TGD and to be discussed later is that the wave functions of (say) free electron pairs (possibly Cooper pairs) defined in the set of points defined by the orbit of $Z_n \subset G_a$ are invariant under the subgroup of $Z_r = Z_n/Z_s \subset Z_n$ for DNA labeled by (r, s), $r \times s = n$. Thus the codons coding for an amino-acid having Z_n as a symmetry group would be characterized by wave functions for free electron pairs transforming under representations of Z_n and remaining invariant under $Z_r \subset Z_n$ and thus reducing to representations of Z_s. Note that $r = 1$ corresponds to all irreps of Z_n and $r = n$ to singlets under Z_n.

15.2.5 Divisor code

The idea of divisor code discussed in [24] is inspired by the following observations.

1. Consider the number $N(n)$ of integer divisors for integers n in the range $[1, 21]$ corresponding to amino-acids with stopping sign counted as amino-acid.

2. Denote the number of integers $n \leq 21$ for which the number of divisors is k by $B(k)$. Also stopping sign is counted as an amino-acid and $n = 0$ corresponds to amino-acid also. This number $N(k)$ varies in the range $[1, 6]$. $B(k)$ has the values $(1, 8, 2, 5, 1, 3)$ where k runs from 1 to 6.
3. Denote by $A(k)$ the number of amino-acids coded by k DNA codons. $A(k)$ has the values $2, 9, 2, 5, 0, 3$.

The spectrum of $A(k)$ is very similar to that of $B(k)$ and this raises the question whether one could understand genetic code as a divisor code in the sense that the degeneracy of amino-acid would be dictated by the number of the integers $1 \leq n \leq 21$ coding it. One might also ask whether the amino-acids which are abundant and thus important are coded by integers with a large number of divisors. Also one can ask whether the divisor structure possibly correlates with the structure of the amino-acid.

Divisor code in this form would be only approximate and one can wonder could try to imagine some simple symmetry breaking mechanism. In this respect the crucial observations might be following.

1. The number of DNAs needed to realize divisor code would be 70 instead of 64. One must drop 6 codons and by choosing them suitably one might hope of getting correct degeneracies.
2. The most natural manner to break the symmetry is to drop the 4 codons from the codons coding for 5-plet which would thus become 1-plet. 5-plet corresponds to integer $n = 16$ and its product compositions $(16, 1), (1, 16), (2, 8), (8, 2), (4, 4)$ correspond to the DNAs coding for it. $(4, 4)$ would naturally correspond to singlet.
3. By dropping 2 codons from some 4-plet one obtains 2-plet and correct degeneracies. One candidate for 4-plet corresponds to $n = 8$ and its product decompositions $(1, 8), (8, 1), (2, 4), (4, 2)$. By dropping two of these one obtains correct degeneracies. It might that power of 2 property of $n = 8$ and $n = 16$ somehow relates to 2-adicity and to the special role of these amino-acids.
4. A possible interpretation is in terms of symmetry based on cyclic group $Z(n)$ serving as a symmetry of DNA codons coding for amino-acid labeled n. Z_n allows decompositions $Z_n = Z_{n_1} \times Z_{n_2}$, $n = n_1 \times n_2$ and if the representations are invariant under Z_{n_2} and thus reduce to those of Z_{n_1} codons coding for a given amino-acid correspond to the product decompositions. Symmetry breaking would be due to the lacking 6 codons and would mean that only Z_4 invariant states would be realized for Z_{16} and Z_1 and Z_8 of Z_2 and Z_4 invariant states are realized for $n = 8$. $n = 4$ could correspond to triplet of stopping codons so that powers of 2 would be in special role for vertebrate code suggesting 4-adicity. 4-adicity is also suggests by the almost exact A-G and T-C symmetries of the last nucleotide.

15.2.6 Topological interpretation of the divisor code in TGD framework

The most concrete physical interpretation of the divisor code found in TGD framework is topological and based on TGD inspired vision about the role of dark matter in biology.

1. The generalized 8-D imbedding space has a book like structure with pages glued together along back which is 4-D surface of $H = M^4 \times CP_2$ [27, 54] . Particles at different pages are dark relative to each other since they cannot have local interactions (appear in the same vertex of Feynman diagram). The pages are partially characterized by the value of Planck constant which can be arbitrary large. This explains the macroscopic quantum coherence of living matter. Matter can leak between different pages meaning a phase transition changing Planck constant.
2. The notion of magnetic body with flux tubes carrying dark matter and connecting different bio-molecules central for the TGD inspired model of living matter [26] . Magnetic bodies of bio-molecules can be also connected by magnetic flux tubes, even those in different pages of the book. For instance, the phase transition reducing $\hbar$ reduces the distance between two bio-molecules connected in this manner and forces them near to each other. This explains the extreme selectivity of bio-catalysis and the miraculous ability of two bio-molecules to find each other in the dense soup of bio-molecules. In particular, DNA and its conjugate codons, mRNA codons, and tRNA would be connected by this kind of flux tubes. Also amino-acids would be connected to tRNA codons in this manner since tRNA molecules catch the amino-acids and bring them to the mRNA-amino-acid translation site. Genetic code could reduce to the selection rules for the flux tube connections connecting in general situation magnetic bodies belonging to different pages of the book.
3. The pages of book are almost copies of $M^4 \times CP_2$. This means that M^4 is replaced with n_a-fold singular covering and CP_2 with n_b-fold singular covering. The coverings have cyclic groups Z_{n_a} and Z_{n_b} act as discrete symmetries for the wave functions of particles in the covering. A given page is thus labeled by two pager numbers (n_a, n_b). Two pages contain common points and thus a direct tunneling of 3-surfaces between these pages is possible only if the number n_{a_1} of the sheets of covering divides n_{a_2} or vice versa. Same holds true for n_{b_1} and n_{b_2}. This rule is just the basic rule about how symmetries of system can change in phase transition. This number theoretic rule could be behind genetic code and the extreme selectivity of bio-catalysis.

4. Suppose that both bio-molecules correspond to ordinary matter with $n_a = n_b = 1$ but that the magnetic body of a given amino-acid corresponds to $(n_a(A), n_b(A))$ and DNA, RNA, and tRNA codon to $(r_a(DNA), r_b(DNA))$. Since the flux tube from tRNA codon to the amino-acid page is essential for the process in which amino-acid is attached to tRNA, only tRNA for with $r_a(tRNA)$ divides $n_a(A)$ can catch an amino-acid labeled by n_a. Same applies to r_b and n_b.
5. Without the presence of the integer n_b the code would fail since DNA codon labeled by r_a would code for all amino-acids for which n_a has r_a as a factor. n_b can indeed save the situation. Suppose that one has $r_b(tRNA) = n_b(A)$ if DNA codes for an amino-acid. Assume also that $n_b(a)$ is prime: $n_b(A) = p_b(A)$, and different for each amino-acid. This prime does not correspond to p-adic prime, which is expected to be very large in the length scales of atomic physics (electron corresponds to $M_{127} = 2^{127} - 1$). Note that the assumption that amino-acids are labeled by small primes was made in both TGD inspired number theoretical models of the genetic code.
6. The assumptions mean that tRNA and amino-acid can be connected by a magnetic flux tube only if one has

$$p_b(tRNA) = p_b(A)$$

and $r_a(tRNA)$ divides $n_a(A)$. If the pages numbers n_a vary in the range $[1, 21]$ the divisor code follows from the argument of the previous section. Taking the previous argument seriously, one should also understand why there is no amino-acid labeled by $n_a = 4$ and why corresponding DNAs correspond to prime characterizing $n_a = 4$, why the number of DNA codons labeled by the factors of $n_a = 8$ is two, and why the number of codons associated with $n_a = 16$ only one.

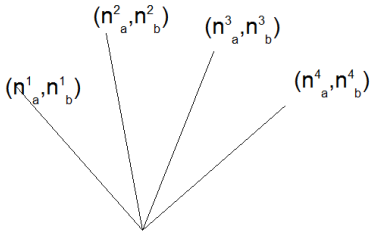

Figure 15.1: Illustration of the book-like structure of the generalized imbedding space.

Some further comments are in order.

1. The realization of the genetic code is not unique since the integers r_a and n_a could be replaced with Nn_a, where N is a product of primes larger than $p = 19$. It is also enough that the integers characterizing amino-acids are relative primes (have not common factors). The simplest assumption would be that the primes $p(A)$ satisfy $p(A) > 19$ so that $p(A)$ does not divide $n(A)$ for any A. If $p(A)$ is as small as possible the value spectrum of $p(A)$ is

$$\{23, 29, 31, 37, 41, 43, 47, 53, 59, 61, 67, 71, 73, 79, 83, 89, 97, 101, 103, 107, 109\} \ .$$

If one assumes that the two additional aminoacids coded in some cases by non-vertebrate genetic code correspond to primes also the primes $113, 127$ are included.

What is interesting is that Mersenne prime $M_7 = 2^7 - 1 = 127$ appears in the model of genetic code based on the notion of Combinatorial Hierarchy [33]. This model assumes that DNA codons correspond to 64 integers in the range $1, ..., 127$. This realization of the genetic code cannot however be consistent with the divisor code realized in the proposed manner since it would require that the integers $n(A)p(A)$ belong to the range $1, .., 127$. The prime factors of these integers can however belong to this range.

2. The model in principle allows an infinite number of analogous codes and an interesting question is whether the bio-catalysis involves this kind of codes. The quantum antenna model for remote replication

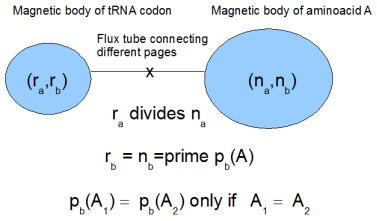

Figure 15.2: Illustration of the selection rules for magnetic flux tubes connecting magnetic bodies of tRNA and amino-acid.

discussed in [34] allows a dynamical interpretation for the flux tube realization of the genetic code as a divisor code in terms of quantum antenna hypothesis [50], and predicts that sequences of DNA codons serve as names for polar molecules quite generally so that genetic code would define a universal language in living matter. This leads to an identification of the basic mechanism responsible for the functioning and evolution of the immune system.

3. The quantum states of dark baryons realize vertebrate genetic code with very general assumptions group theoretically [1, 34, 77] , [1] . Since dark matter is involved in both cases, one might wonder whether these codes could be related somehow. A one-one correspondence between the quantum states of dark nucleons representing codon and the integers r_a, p_b is required in order to have this connection. The simplest possibility is that that energy minimization implies that given dark nucleon resides with high probability at flux tube labeled by unique value of r_a. Same applies to amino-acids.

The number theoretical model discussed in this chapter emerged before the topological explanation of the divisor code. Hence the model becomes somewhat obsolete. In particular, it involves un-necessarily strong assumptions. p-Adic thermodynamics might be used to understand the possible equivalence of the divisor code and the dark baryon code discussed in [77] but this problem will not be discussed here.

15.2.7 Is the fusion of geometric, thermodynamical, and divisor code approaches possible in the 5-adic case?

A very attractive general idea is that genetic code could be understood in two dual manners: as an assignment $n \to p(n)$ and as an assignment $p \to n(p)$.

1. Genetic code could be understood in terms of a 5-adic thermodynamics for the partitions of integers characterizing codons. Here $6 \leq n_{2)} = n_0 + n_1 5 \leq 24$, $n_k \neq 0$, labels the 2-codons formed by the first two letters of the codon. This approach would predict the assignment $n \to p(n)$ once the number theoretic thermodynamics is specified.

2. Genetic code could be understood as a geometric imbedding $p \to n(p)$ of amino-acid space labeled by 20 primes $31 \leq p < 124$ to DNA space such that one has $n(p) = p$ if possible. This cannot the case for 4 primes ($p = 53, 79, 101, 103$). Also the interpretation as an induction of number theoretical bundle structure over amino-acid base space from DNA space is possible. $n(p) = p$ constraint obviously poses strong constraints on the model but it turns out that it is possible to satisfy these constraints for other than exceptional primes.

3. Also the basic idea of the divisor code could be included to the model via the condition that the number of divisors of the integer $n_{2)}$ for one of the DNAs coding for a given amino-acid equals to the number of DNAs coding for the amino-acid. There would be thus *two* labelings of amino-acids so that the model would become highly predictive.

The natural starting point is the vertebrate mitochondrial code with full $A \leftrightarrow C$ and $G \leftrightarrow U$ symmetries and one could interpret the breaking of these symmetries in the case of eukaryote code in terms of the context sensitivity characterized by the number theoretic temperature T_5. The large number of constraints raises the hope that a rather unique code could result. It will be found that for the number theoretic Hamiltonian

depending only on the number partitions r of the integer $n_{2)}$ characterizing the first two letters of the 5-adic codon, only 4 solutions to the conditions can be found in the set of $N \sim 10^{30}$ candidates for $h(r)$.

15.3 5-adicity or 4-adicity?

It seems that 5-adic representation of $A - C$ and $T - G$ symmetries allows the unification of the geometric view about genetic code with the number theoretic thermodynamics view and the idea of the divisor code.

15.3.1 The problems of the 4-adic model of the divisor code

The 4-adic model for the divisor code has some problems.

1. 4-adic model is not consistent with the assumption that the set of DNAs coding for given amino-acid contains both the integer characterizing the degeneracy of the amino-acid as a number of its divisors and the codon labeled by the prime labeling the amino-acid. Hence the geometric realization must be given up unless one assumes that the primes associated with amino-acids associated with columns not containing primes are mapped to the integers in the columns by imbedding map. Even this option fails.
2. It is not easy to understand the emergence of singlets without assuming breaking of the number theoretical symmetries.
3. The proposed TGD inspired topological interpretation of the divisor code is not consistent with the presence of $n = 0$ codons. Also $n = 1$ codons are problematic.
4. There is no obvious connection with the maximization of the number theoretic negentropy assigning primes to amino-acids. 5-adic thermodynamics can do this and one could have dual descriptions. Geometric description in terms of imbedding of amino-acid space to DNA space (assigning DNAs to amino-acids) and thermodynamics description in terms of 5-adic thermodynamics assigning amino-acids to DNAs.

15.3.2 5-adic model works for thermodynamics based on partitions

5-adic variant of the model can overcome the problems of the 4-adic model.

Basic assumptions

1. Stopping codons do not correspond to formal amino-acids. The natural hypothesis is that the stopping codons do not possess negentropy maximizing prime in the range considered.
2. The question is whether conjugation $k \to 5-k$ for the last nucleotide corresponds 1) to DNA conjugation as in [11] or 2) to a symmetry of the last codon. The naive guess would be 1). The guess turns out to be wrong since it implies that 3 4-plets contain symmetry related primes so that the number of amino-acids would be reduced by 3 due to the $n \to n + 50$ symmetry of the last nucleotide. On the other hand, $k \to 5 - k$ as a representation of $A \leftrightarrow C$ and $G \leftrightarrow U$ symmetries takes odd integers to even integers so that there are no problems.
3. DNA codons correspond to 5-adic integers in the range [31,124] having no vanishing 5-digits. Amino-acids are labeled by the 20 primes in the same range. They are mapped to DNA triplets. For 16 primes this imbedding is just the identification $n(p) = p$. The 4 "outsider" primes $53, 79, 101, 103$, which have a vanishing 5-digit, have necessarily $n(p) \neq p$. The first guess is that the outsider primes $53, 79, 101, 103$ correspond to amino-acids that are somehow special. It turns out that a possible identification for the amino-acids is as Trp, Lys, Met, Gln but that Lys,Gln pair can be replaced by any pair in the set $\{Gln, Lys, Glu\}$. One could also argue that the amino-acids corresponding to 53 and $103 = 53 + 50$ should be related by some kind of symmetry. Trp and Met indeed have the comment feature that a codon coding for them can also act as stopping codon. On the other hand, also Lys, Gln, and Glu share the property of being polar amino-acids.

Further constraints

The observation that there are two 4-columns containing no primes when combined with some facts about the genetic code and its variants give strong constraints on the code.

1. One of the prime-free columns must correspond to shared Ser-Arg column which transforms to Ser-Stop column for mitochondrial code. Otherwise one prime coding for an amino-acid would be lost.
2. In the case of the yeast mitochondria Thr is coded 8 times and Leu only twice. This forces the conclusion that second prime-free 4-column corresponds to Leu.

3. Since Leu must be coded by prime, Leu-Phe 4-column must correspond to the second 4-plet containing two primes. Hence the two 4-columns containing 2 primes give rise to three doublets. 6 additional doublets for eukaryote code and 9 additional doublets for mitochondrial code must be identified.
4. Thr 4-plet should contain n possessing 8 divisors. Only 3 4-columns contain $n = 8$ and correspond to 321, 131, and 231 columns.

Detailed identification of the code

Consider now a more detailed identification of the code.

1. Mitochondrial code is obtained as follows. 4 outsider primes which do not label DNAs directly are imbedded into 4-columns containing single prime. This gives 8 doublets altogether. Stopping codons in the 4-column containing Tyr and corresponding prime give one additional doublet so that a correct number of doublets result.
2. The breaking of the mitochondrial code to eukaryote code is easy to understand in the proposed framework. Trp and Met become singlets and Ile becomes triplet so that 9 doublets result.
3. Outsider primes would in this model correspond to Gln, Lys, Trp, Met. Gln and Lys could be replaced with any pair in the set {Gln,Lys,Glu} for the simple reason that corresponding amino-acid doublets cannot be distinguished from each other number theoretically. The identifications of the integers associated with amino-acids coded by 4 entire 4-column (Val, Ala, Pro, Gly) are unique apart from $4! = 24$ permutations of these amino-acids. It should be noticed that Lys,Gln,Glu belong to the group of 11 polar amino-acids and Met and Trp belong to the group of 8 hydrophobic amino-acids.
4. The multiplet containing Met is unique since there is only single codon ($n = 11^2 = 121$) for which the number of divisors is 3.
5. One can say that Ile and Met compete: either Ile^3-Met results when Ile wins. Ile^2-Met^2 results when Met wins. One can argue that Trp as outsider prime can also correspond to singlet or that Stop can "eat" any any prime and reduce the degeneracy. 5-adicity is broken for the first two nucleotides, which is not surprising.

These number theoretic constraints do not allow a unique identification of the code but pose considerable restrictions. The following table represents one example consistent with these conditions. Note that the table does not fix how the primes 53, 79, 101, and 103 are assigned to Trp, Lys, Met, and Gln. Trp and Met are indeed special since they can be replaced by stopping codon some variants of the code.

It will be found that under rather general conditions (roughly 10^{30} candidates for the Hamiltonian $h(r)$ characterizing the thermodynamics of partitions) there are only 4 choices of $h(r)$ reproducing the eukaryote code, vertebrate mitochondrial code as well as other variations of the code. If one requires that the polar amino-acids Lys and Gln (or any pair in the set {Gln,Lys,Glu}) correspond to the conjugation related primes 53 and 103 only single solution for $h(r)$ is found. The 5-adic thermodynamics based on spin-spin interaction fails as do also other simple models.

114	106	4	UG	214	107	2	GU	314	108		GC	414	109	2	GA
113	81		Trp	213	82	4	Val	313	83	2	Ala	413	84		Glu
112	56	4	Cys	212	57	4		312	58			412	59	2	Asp
111	31	2		211	32			311	33	4		411	34	4	
124	111	4	GG	224	112		UA	324	113	2	AC	424	114	6	CG
123	86	4	Gly	223	87	4	Stop	323	88	8	Thr	423	89	2	Arg
122	61	2		222	62	4	Tyr	322	63	4		422	64		
121	36			221	37	2		321	38	4		421	39	4	
134	116	6	CC	234	117	6	UC	334	118	4	AA	434	119	4	AG
133	91	4	Pro	233	92	6	Ser	333	93	4	Lys	433	94	4	Arg
132	66	8		232	67	2		332	68	6	Asn	432	69	4	Ser
131	41	2		231	42	8		331	43	2		431	44	6	
144	121	3	AU	244	122	4	UU	344	123	4	CA	444	124	6	CU
143	96		Met	243	97	2	Leu	343	98	6	Gln	443	99	6	Leu
142	71	2	Ile	242	72		Phe	342	73	2	His	442	74	4	
141	46	4		241	47	2		341	48			441	49	3	

Table 1. An example of a code obeying approximate 5-adic symmetry $k \leftrightarrow 5-k$ with respect to the last codon. Given are the integers associated with the codons of given 4-column in 5-adic and decimal notion, the number of divisors appearing if it belongs to the range of allowed values, and the 2-codon associated with the 4-column. Note that 5-adic symmetry for the first two nucleotides is broken.

15.4 5-adic thermodynamical model for the genetic code

The challenge is to guess the number theoretic Hamiltonian characterizing the thermodynamical model and the dependence of the 5-adic temperature T_5 on third nucleotide describing the splitting of 4-plets to doublets and further splitting of the doublets in the case of eukaryote code. There are two options concerning the choice of the Hamiltonian.

1. The Hamiltonian depends only on the number r of integers in the partition $n_{2)} = \sum n_k$ of $6 \leq n \leq 24$ of integer $n_{2)} = n_0 + n_1 5$ characterizing the first two nucleotides of the codon. Hamiltonian is tailored by evolution to reproduce the genetic code and its variants.
2. Hamiltonian is a direct analog of spin spin interaction $J \sum n_k n_l$ with n_k interpreted as spin associated with n_k Cooper pairs.

15.4.1 The simplest model for the 5-adic temperature

The simplest model for 5-adic temperature applies irrespective of the number theoretic Hamiltonian h and relies on the assumption inspired by the comparison of the mitochondrial and eukaryote code tables.

1. $T_5(n_3) = T_5$ hold true for common 4-plets, 4-plet parts of 6-plets, and 6-plets of the mitochondrial and eukaryote codes.
2. $T_5(n_3) = T_5(5-n_3)$ holds true for common 2-plets (A-C and T-G symmetries with respect to the third nucleotide) of eukaryote and mitochondrial code and for all 2-plets of mitochondrial code.
3. For eukaryote code this symmetry of 5-adic temperature would fail for Ile^3-Met, Cys^2-Stop-Trp and only for the second pair of values of n_3 corresponding to Met-Met$\rightarrow$ Ile-Met and Trp-Trp $\rightarrow$ Ttop-Trp $[n_3, 5-n_3) = (2,3)]$. Ser-Stop-Ser-Stop to Ser-Arg-Ser-Arg transition would in turn be induced by the change of 5-adic temperature. Stop would correspond to a 5-adic temperature for which no prime coding amino-acid divides the partition function.

The condition that the model reproduces correctly the $n \rightarrow p(n)$ correspondence to be discussed later in principle allows to fix number theoretic Hamilton and $T_5(n_3)$ to a high degree.

15.4.2 The simplest possible model for thermodynamics

Before dwelling into complex calculations it is useful to ask what could be the simplest model for the 5-adic thermodynamics.

1. Calculational simplicity would suggest that the partition function must be as small as possible and thus satisfy $Z(n) < 125$. This restriction also maximizes the probability that the prime divisors are in the range $31 \leq p \leq 113$ with stopping codons involving only divisors $p < 31$. This together with the 5-adicity at the level of partition function would suggest that the definition of $Z(n)$ should involve 5-adic cutoff in the form $Z(n) \to Z(n) \ mod \ 5^3$. The natural constraint on the values h of the number theoretical Hamiltonian would thus be $h \in \{0, 1, 2\} \in Z_3$. Modulo three arithmetics fits also nicely with the triplet structure of codons.

2. In this model the effect of changing 5-adic temperature form $T_5 = 1$ to $T_5 = 1/n$, $n = 1, 2$ would be expressed as $h(r) \to n \times h(r)$. Only two possible 5-adic temperatures would be possible and the symmetries of the vertebrate mitochondrial code would be predicted automatically. The symmetry breaking down to eukaryote code could be described in terms of 5-adic temperature if one allows formally infinite temperature for which one would have effectively $h(r) \to h(r) = 0$ so that partition function equivalent with $Z = 1$ would result and the codon in question would code for stopping sign. This is indeed the case for the codon coding originally Trp. For the breaking of Ile-Met doublet the splitting to triplet and singlet can be also understood as the dependence of T_5 on codon in symmetry breaking manner.

3. The simplest possible model would correspond to $Z(n) = p(n) = \sum p_k 5^k$ so that p_k would have interpretation as degeneracies of states modulo 5: this would imply that the doublets would correspond to primes related by exchange of p_1 and p_2, which does not make sense. Hence the integers p_k cannot directly correspond to the degeneracies of states with different energies and the partition function must be obtained via $Z \to Z \ mod \ 125$ prescription from a more complex partition function having values $Z > 125$. The three digits p_k for 5-adic code and Z_3 valuedness of $h(r)$ might relate naturally to 3-letter structure of codons.For $n = p(n)$ one would simply have $Z(n) = n = p(n)$. For the four exceptional amino-acid primes $p = 53, 79, 101, 103$ this would not hold true. The most general model would allow small integer $k \leq 4$ as an additional factor of $Z(n) \leq 124$.

Unfortunately, this simple model does not allow any obvious number theoretical realization. In particular, the models based thermodynamics of partitions and on spin-spin interaction fail with Z_3 valued $h(r)$ and Z_{125} valued $Z(n)$. The simplicity and explanatory power of the model encourage however to keep mind open for the existence of this kind of model.

15.4.3 Number theoretic Hamilton depending on the number of partitions of integer characterizing DNA

The number theoretic model for the genetic code discussed in [19] was based on the assumption that the number theoretic Hamiltonian depends only on the number of summands in the partition $n = \sum_k n_k$.

Generalizing to the recent context, the Hamiltonian $h(r)$ for the 5-adic thermodynamics should depend only on the number r of summands in the partition $n_{2)} = \sum_{k=1}^{r} n_k$. The deviations from the standard code would be explained in terms of the variation 5-adic temperature which has values $T = 1/n$, n positive integer, implying Boltzmann weights $5^{h(r)/T_5}$. The fact that same codon does not always code same amino-acid [29] , [95] , could be understood in terms of temporal variation of 5-adic temperature. A possible interpretation is in terms of a breaking of conformal invariance characterized completely the number r of subsets in the partition.

A further assumption motivated by 5-adicity is the replacement $X \equiv h(r)/T_5$ in Boltzmann weight with $X \ mod \ N$, where N characterizes the highest power of 5 appearing in partition function. $N = 3$ would be the minimal option but it turns that only $N = 25$ works. It will be assumed that evolution has gradually tailored $h(r)$ so that the observed genetic code maximizes for a given DNA the p-adic information measure defined by the prime $p(DNA)$ coding the corresponding amino-acid in practice this means that partition function is divisible by a power of $p(DNA)$.

The interpretation in terms of the number of sub-condensates of Cooper pairs containing n_k spin 1 Cooper pairs is an alternative interpretation and would look attractive physically but in this case the Hamilton depending on the number r of partitions only does no look natural. The number theoretic Hamiltonian would depend on the number r of bound states only if the interaction energy $E(n_k, n_l)$ between two sub-condensates with n_k and n_l Cooper pairs is a constant integer $E(n_k, n_l) = E$, so that the interaction energy between sub-condensates would behave as $r(r-1)E \ mod \ N$. This could give rise to a rather random looking behavior of $h(r)$ as a function of r. The modulo arithmetic constraint would restrict considerably the number of choices of $h(r)$. This model does not reproduce realistic genetic code.

Formula for the partition function

The formula for the partition function is given as

$$\begin{aligned} Z &= \sum_r d(n,r)5^{H(r)} \ , \\ H(r) &= \frac{h(r)}{T_5} \ mod \ 25 \ . \end{aligned} \tag{15.4.1}$$

$T_5 = 1/n$ varies in the range $n \in [1, 24]$.

The partition numbers appearing in are conveniently calculated by using the recurrence relation [5]

$$d(n,r) = P(n,r) = P(n-1,r-1) + P(n-r,r) \ , \ P(n,1) = 1 \ . \tag{15.4.2}$$

The structure of the calculation

The flow of calculation proceeds along the rows of the code table as given in Table 1 coding for the constraints coming from the assumption that the number of divisors for of the integers labeling DNAs is same as the degeneracy of corresponding amino-acid and from the consistency with the geometric model of the code.

1. It is assumed $0 \leq h(r) \leq h_{max} = 2$ for $r > 1$. $h(1) = 0$ can be assumed without a loss of generality if one assumes that $r = 1$ (trivial partition) corresponds to the most probable minimum energy partition in the sense of 5-adic thermodynamics. This implies that 3^{23} candidates for $h(r)$ must be scanned. All possible $4! = 24$ assignments of Trp, Lys, Met, Gln with the primes $p = 53, 101, 79, 103$ which do not label codons are considered.
2. At the first step those guesses for $h(r)$, $r \leq 6$, for which the DNA-Cys correspondence with $p(Cys) = 31$ is reproduced and stored.
3. At the next step calculation branches to four separate calculations corresponding to the four possible values of $p(Trp) \in \{53, 101, 79, 103\}$. 5-adic temperature T_5 is varied and it is found whether the $p(Trp)$ can be reproduced for some value of $T_5 \in \{1, 2, ..., 24\}$. If this is not possible, the candidate for $h(r)$, $r \leq 6$ is rejected. After this the calculation proceeds for given $p(Trp)$ assignment through next values of $h(r)$ to $r = 18$ where one checks whether $p(Asn) = 43$ can be reproduced. In the transitions to new row corresponding to $r = 10, 11$ and $r = 15, 16$ two values of of $0 \leq h(r) \leq 2$ appear and bring in additional degrees of freedom. In $Glu - Asp$ column at the end of the first row T_5 is varied to see whether also $p(Asp) = 59$ can be reproduced.
4. After this the calculation for given value of $p(Trp)$ branches to 6 alternatives corresponding to different assignments of remaining exceptional primes to Lys, Met, Gln. Since Arg-Ser four-column does not give any conditions the values of $h(r)$ for $r = 19, 20, 21$ appear as free parameters. This part of calculation is especially critical since the first 4-columns of the last row of the table contain only doublets. The last 4-column (Leu) corresponding to $r = 24$ does not pose any conditions on $h(24)$ unless one requires that also $n = 49$ gives partition function for $p(Leu) = 97$ is the maximizing prime.

Results

The difficulties involved with the numerical computation were considerable since only University MATLAB was available and for the extensive computations involved its functioning turned out to be somewhat unreliable and reasons for this could not be identified. 22 solutions to the conditions expressed in Table 2 has been found from the set of about 10^{30} candidates, and have been checked separately to satisfy all the conditions.

(1,1) tlmg	(1,2) tglm	(1,3) tmgl	(1,4) tlgm	(1,5) tgml	(1,6) tmlg
(2,1) ltmg	(2,2) gtlm	(2,3) mtgl	(2,4) ltgm	(2,5) gtml	(2,6) mtlg
(3,1) lmtg	(3,2) mgtl	(3,3) gltm	(3,4) lgtm	(3,5) gmtl	(3,6) mltg
(4,1) lmgt	(4,2) glmt	(4,3) mglt	(4,4) lgmt	(4,5) gmlt	(4,6) mlgt

Table 2. There are 24 different solution types depending on which permutation $xyzu$ of (Trp,Lys,Met,Gln) corresponds to the exceptional primes $(53, 79, 101, 103)$. For instance, lmtg means $(Lys, Met, Trp, Gln) \to (53, 79, 101, 103)$, and tglm means $(Trp, Gln, Lys, Met) \to (53, 79, 101, 103)$. It is convenient to label the 24 possibilities by pairs of integers (m, n). $m = 1, 2, 3, 4$ according to whether Trp,Lys,Met or Gln corresponds to

$p = 53$. The second integer $n = 1, ..., 6$ specifies which of the six permutations of remaining three amino-acids corresponds to $(79, 101, 103)$ in a manner expressed by the table. For instance, for $(m, n) = (1, 1) \leftrightarrow (tlmg)$ codes for $(Trp, Lys, Gln, Met) \to (53, 79, 101, 103)$.

The 11 number theoretic Hamiltonians $h(r)$ for $r = 1, 2, ..., 23$ are given in the table below with conventions expressed in the Table 2.

m	1	1	1	1	2	3	3	3	3	3	4
n	2	2	5	5	2	1	1	1	2	6	2
r	h_1	h_2	h_3	h_4	h_5	h_6	h_7	h_8	h_9	h_{10}	h_{11}
1	0	0	0	0	0	0	0	0	0	0	0
2	1	1	4	5	3	2	0	0	0	0	0
3	3	3	24	23	11	0	10	10	13	13	13
4	19	19	12	24	2	14	16	16	4	4	4
5	3	3	13	15	9	18	21	21	12	12	12
6	0	0	19	6	5	2	9	9	12	12	12
7	1	1	12	4	14	5	16	16	9	9	9
8	15	15	16	0	10	18	20	20	7	7	7
9	17	17	7	15	9	2	14	14	12	12	12
10	3	3	17	10	15	12	14	14	16	16	16
11	17	17	9	22	3	1	24	24	5	5	5
12	8	8	14	12	18	3	4	4	11	11	11
13	4	4	24	3	17	12	5	5	19	19	19
14	16	16	5	11	19	6	4	4	18	18	18
15	13	13	9	19	3	16	1	1	7	7	7
16	11	11	20	11	20	7	2	2	7	7	7
17	23	23	14	5	17	22	14	14	21	21	21
18	7	7	13	3	4	1	5	5	6	6	6
19	14	16	1	11	8	6	11	14	9	4	4
20	16	14	1	22	22	1	6	12	7	17	23
21	6	19	17	11	19	12	13	15	13	23	22
22	14	0	6	22	2	7	19	5	15	21	16
23	13	12	6	17	7	2	7	12	12	4	15

Table 3. The table represents the 11 solutions found for the Hamiltonian of partition thermodynamics consistent with the code table represented in Table 1. The integer pair (m,n) given in the first two rows codes for the correspondence between amino-acids (Trp,Lys,Met,Gln) and exceptional primes $(53, 79, 101, 103)$ according via the correspondence given in Table 2.

One can consider additional symmetry assumptions reducing the number of solutions.

1. One might argue that the "unstable" amino-acids Trp and Met naturally correspond to the conjugation related primes 53 and 103. The are only 2 solutions (h_1 and h_2 in Table 3) corresponding to the assignment $(Trp, Met) \to (53, 103)$ or vice versa (the integer pairs (m,n) corresponding to txym and mxyt in Table 2 are (1,2),(1,4),(4,3),(4,6)). These two solutions differ only for last 5 values of r.
2. One might also argue that the polar amino-acids Lys and Gln (or any pair in the set $\{Lys, Gln, Glu\}$) correspond to the conjugation related primes 53 and 103 (the integer pairs (m,n) corresponding to lxyg and gxyl in Table 2). There are 3 solutions (h_6, h_7 and h_8 in Table 3) corresponding to the assignment $(Lys, Gln) \to (53, 103) orviceversa$ (the integer pairs (m,n) corresponding to txym and mxyt in Table 2 are (2,1),(2,4),(3,1),(3,4)).

That not too many solutions exist to the conditions together with the fact that the model is consistent with the basic ideas of geometric code and of divisor code and results from 5-adic thermodynamics, raises the hope that something more than a mere complex parametrization of the genetic code might be in question. For $r = 2$ $h(r)$ only the values $h(r) \leq 5$ have been scanned (the reasons were the strange problems that made the continuation of calculations very difficult) so that a portion $6/25 = 24$ per cent of all possible candidates for $h(r)$ are scanned. The number of solutions found is 11. If the solutions are distributed evenly, the estimate for the total number solutions is about 45.

The 5-adic temperature is $T_5 = 1$ for all lower doublets in the code table (the two smallest values of $n(DNA)$ in a given 4-column). The values of 5-adic temperature for the upper vertebrate mitochondrial doublets are given by the table below for some cases. For eukaryote code symmetry breaking means only a

change of 5-adic temperature for the symmetry breaking codon so that it codes for either Stop as in case of Trp-Cys doublet or for Ile instead of Met. Also the context dependence observed for some variants of the genetic code [95] can be understood in terms of a temporary change of the 5-adic temperature. Note however that the amino-acid coded temporarily does not belong to the group of standard amino-acids.

For the stopping codon $1/T_5 = 2$ is the minimum temperature implying that no prime $31 \leq p \leq 113$ divides the partition function.

m	n	$\beta(1)$	$\beta(4)$	$\beta(11)$	$\beta(13)$	$\beta(14)$	$\beta(15)$
1	2	19	11	6	5	24	21
1	2	19	11	6	5	23	7
1	5	21	5	15	6	4	7
1	5	15	13	10	23	21	13
2	2	10	16	23	15	16	21
3	1	6	17	16	17	3	19
3	1	10	2	23	17	20	11
3	1	10	2	23	4	4	12
3	2	5	6	5	18	18	7
3	6	5	6	5	8	23	16
4	2	11	6	5	24	23	18

Table 4. Inverse 5-adic temperatures $\beta = 1/t_5$ for doublets of the vertebrate mitochondrial code. The notational conventions and the ordering of solutions are same as in the previous table.

15.4.4 Number theoretical Hamiltonian identified as spin-spin interaction

The hypothesis that Hamiltonian depends on the number r of summands in the partition is of course only a very simple working hypothesis allowing a relatively easy numerical search of the Hamiltonian (in the original model one had $n \leq 63$ so that rather large numbers of partitions had to be considered). If one takes seriously the idea about sub-condensates of spin 1 Cooper pairs, one could argue that the interaction energy between blocks of Cooper pairs is spin-spin interaction proportional to the product of net spins of electrons and is therefore of form $E(n_k, n_l) = Jn_kn_l$, $k \neq l$. A number theoretical analog of rather spin glass variant of Ising model would be in question.

In this case one would have $h = J\sum_{k,l} n_kn_l = \sum_k n_k(n - n_k) = n^2 - \sum_k n_k^2$ and thermodynamically equivalent with $h = J\sum_k n_k^2$. This Hamiltonian or rather, its modulo N variant ($N = 3$ in the minimal case), would distinguish between partitions with the same value of r. In the recent model one has $6 \leq n_{2)} \leq 24$ so that the numbers of partitions are quite reasonable.

What makes this Hamiltonian so attractive would be its clear physical interpretation and involve a minimal amount of ad hoc elements.

The simplest working option is that third nucleotide affects only the 5-adic temperature so that one would have

$$h(n_1, ..., n_r) = \frac{J}{T_5} \times \sum_{pairs} n_kn_l \quad ,$$

where one has $T_5 = 1, 2$. This interpretation conforms with the idea about living matter as spin glass like structure for which interaction strengths for spin-spin interactions are variable parameters. This would also conform with the general vision about TGD Universe as a four-dimensional spin glass like structure [3] .

Calculation of the partition function for a model based on spin-spin interaction

The task is to calculate the partition function $Z(T(n_3)) = \sum_P 5^{h(n_2,P)/T_5}$. To achieve this one can generalize the recursion formulas for the numbers $d(n, r)$ of partitions of n to sum of r terms.

1. One can arrange the integers in the partition so that one has always $n_k \leq n_{k+1}$ and start the recursive calculation from $h_r(1, ...1, n - r + 1) = (n - r + 1)(r - 1)$.
2. This gives rise to general recursion formula given by

$$\begin{aligned} h_r(n_1, ..., n_{r-1}, n - r + 1 - k_1) &= J(n - r + 1 - k_1)(r - 1 + k_1) \\ &+ h_{r-1}(n_1, ..., n_{r-1}) \quad . \end{aligned} \tag{15.4.3}$$

Using this recursion formula one can express the formula for Hamiltonian as

$$\begin{aligned}&\tfrac{1}{J}h_r(k_r+1,k_{r-1}+1-k_r,...,k_2+1-k_3,k_1+1-k_2,n-r+1-k_1)\\&=(n-r+1-k_1)(r-1+k_1)+(k_1-r+2-k_2)1)(r-2+k_2)\\&+...+(k_{s-1}-r+s-k_s)1)(r-s+k_s)+...+(k_{r-1}-k_r)k_r\end{aligned} \tag{15.4.4}$$

In this formula $h \to h \mod 25$ operation is not written explicitly.

The expression for the partition function can be written as

$$\begin{aligned}Z(n) &= \sum_r Z(n,r)\\ Z(n,r) &= \sum_{k_1,...,k_r} 5^{h_r(k_r+1,k_{r-1}+1-k_r,...,k_2+1-k_3,k_1+1-k_2,n-r+1-k_1)} .\end{aligned} \tag{15.4.5}$$

The lower and up upper bounds for k_s in the summation can be deduced as follows. An upper bound for k_1 obtained from the condition $rk_1 = n$ and gives $k_1 \leq k_{max} = [n/r]$ where $[x]$ denotes the integer $n \leq x$ nearest to x. The corresponding upper bound for k_s reads as $k_s \leq [k_{s-1}/r - s + 1]$. A lower bound for k_s comes from the requirement $n_s \geq 1$ and gives $k_s \leq k_{s-1}$.

To avoid problems caused by the fact that the numbers for various loops are dynamical, one can use recursion to calculate $Z(n,r)$ such that the module in question calculates $h(...)$ by calling itself repeatedly. What simplifies the calculation dramatically is that it is not necessary to store the data about the values of Hamiltonian since partition function is all that is needed.

1. At s^{th} level the module first adds to the Hamiltonian of a given branch the contribution from that level and after that adds the contributions from from $(s+1)^{th}$ level.
2. The calculation branches which means a a loop over the values of k_{s+1}. This means that module calls itself at each step of the loop to calculate the contributions of the next level to the Hamiltonian at a given branch.
3. The module adds also to Z the contribution from $(s+1)^{th}$ level is added. The addition is trivial until the r^{th} level is reached and all contributions to the Hamilton are known.
4. At the last level of tree the situation looks like follows. At given branch of the tree at $(r-1)^{th}$ level the module adds in loop-wise manner to Z the contributions from r^{th} level for that branch. After the return to $(r-2)^{th}$ branch next branch at $(r-1)^{th}$ level is selected and same process is repeated. Etc...
5. In order to avoid overflow problems it is safest to express the terms of the partition function in pinary series with respect to the p-adic prime $31 \leq p \leq 113$ considered and perform the addition of contributions to Z in terms of the pinary series.

Structure of the calculation

The general structure of the calculation is following.

1. Perform a loop over n labeling the 2-codons and find for each of them the prime p for which negentropy $S_p(n)$ is minimum and look whether for a suitable choice of T_5 the resulting assignment $n \to p(n)$ is consistent with the geometric model of the code and with the basic idea of the divisor code.
2. For a given n perform a loop over allowed values of p to see whether anyone of them appears as a divisor of the partition function and which of them maximizes the number theoretic negentropy. Unless this occurs the codon in question is identified as a stopping codon. The proposed geometric model of course fixes the integers n associated with the stopping codon.
3. For given n and p perform a loop over the values of r and sum their contributions to the partition function $Z(n,r)$ by applying the recursive procedure described in the previous subsection. In order to avoid overflow problems (possibly appearing in the case of MATLAB), the calculation must be performed for each value of p separately using pinary expansions for $Z(n,r)$. If Hamiltonian belongs to Z_3, overflow problems are of course avoided automatically.
4. An alternative manner to view the calculation is to take the proposal for the $n \to p(n)$ correspondence represented as a table at the end of previous section as an input and by a suitable selection of $0 \leq J(n_2)) \leq 2$ try to reproduce it. Note that the correspondence between primes 53,79,101,103 and amino-acids Trp, Met, Gln,Lys if not fixed by the model represented in the table.

5. The most practical manner to perform the calculation is to take $J = 1$ and allow T_5 to run from 1 to 2 for every value of n and look whether the resulting spectrum of primes is consistent with the proposed $n \to n(p)$ correspondence or possible modification of it. At the roughest level the calculation serves as a test for 5-adicity that is whether the integer $n = n_0 + n_1 5$ corresponds to prime of form $n + 25$ or $n + 75$.

Results

The proposed spin-spin interaction model allowing varying value of T_5 cannot reproduce the model summarized by Table 1. The roughest test for the model is whether 5-adic description of A-C and T-G symmetries works. For mod 25 thermodynamics with $n = n_0 + n_1 5$ determining the thermodynamics the fails to be consistent with the predictions of the simplest model.

15.5 A possible physical interpretation of various codes in TGD framework

The inspiration for attempts to interpret physically the origin of various codes in TGD framework (summaries of quantum TGD, TGD inspired theory of consciousness, and TGD inspired view about quantum biology are given in articles [5, 4, 3]) springs from the following ideas.

1. At fundamental level quantum TGD reduces to almost topological quantum field theory at light-like 3-surfaces of $H = M^4 \times CP_2$ having also interpretation as random lightlike orbits of 2-dimensional partons, which can have arbitrarily large sizes. Quantum TGD involves fusion of real physics and its p-adic variants relying crucially to the assumption that S-matrix involves only data at intersections of real 2-surfaces and their p-adic counterparts obeying same algebraic equations consisting of rational points and and algebraic points in the algebraic extension of p-adic numbers characterization physical states in question. These intersections consist of discrete points giving rise to cognitive representations which should naturally relate to the genetic code.
2. TGD based view about dark matter as a hierarchy of quantum coherent phases labeled by symmetry groups $G_a \times G_b \subset SU(2) \times SU(2) \subset SL(2,C) \times SU(3)$, where $SL(2,C)$ is Lorentz group and $SU(3)$ corresponds to the gauge group of color interactions. These phases are characterized by arbitrarily large values of Planck constants and are assumed to be responsible for the quantum control in living matter.
3. The generalization of the notion of imbedding space $H = M^4 \times CP_2$ based on the geometric realization of the dark matter hierarchy and involving a hierarchy of discrete sub-groups $G_a \times G_b$.

The basic idea is that the maximal cyclic subgroup Z_n of G_a could correspond to the group Z_n assigned with amino-acid and corresponding codons in the proposed group theoretic interpretation of the divisor code. n would give the order of the maximal cyclic subgroup $Z_n \subset G_a$ acting as symmetry group of wave functions of free electron pairs and (r, s), $rs = n$ could define a decomposition of $Z_n = Z_r \times Z_s$ with Z_r leaving invariant the electronic wave function.

15.5.1 Generalization of imbedding space and interpretation of discrete bundle like structures

One should understand how the discrete number theoretical structures associated with various realizations of the genetic code emerge from TGD based physics. TGD suggests a very general geometric realization of the geometric codes in terms of points in the intersection of p-adic and real space-time sheets (actually a 2-D "partonic" surfaces having arbitrarily large size) consisting of algebraic points and of the TGD based generalization of imbedding space obtained by gluing together infinite number of copies of the imbedding space having singular bundle structure $H = M^4 \times CP_2 \to H/G_a \times G_b$, where one has $G_a \times G_b \subset SU(2) \times SU(2) \subset SL(2,C) \times SU(3)$.

G_a would manifest itself directly as discrete rotational symmetries of biomolecules basically due the presence of dark matter having G_a as exact group of rotational symmetries. Hence only G_a would be interesting in the recent case. In fact, the maximal cyclic subgroup Z_n for arbitrary G_a is in a special physical role and it might be possible to identify the group characterizing amino-acid and DNA as this group.

The bundle structure $H \to H/G_a \times G_b$ has singular points corresponding to the points of H for which $G_a \times G_b$ or its subgroup acts as an isotropy group leaving the point invariant. Quite generally, the singular points, in particular those for which G_a acts as isotropies, are involved with the phase transitions changing Planck constant and interpreted as a leakage of 3-surfaces between sectors of H labeled by different groups $G_a \times G_b$.

The interpretation of G_r characterizing DNA as an isotropy of singular point of bundle structure does not seem however natural. Rather, the wave functions of (say) free electron pairs (possibly Cooper pairs) defined in the set of points defined by the orbit of $Z_n \subset G_a$ could be invariant under some subgroup of $Z_r \subset Z_n$ for DNA labeled by (r,s), $r \times s = n$. Thus codons coding for an amino-acid having Z_n as a symmetry group would be characterized by wave functions for free electron pairs transforming under representations of Z_n and remaining invariant under $Z_r \subset Z_n$ and thus reducing to representations of $Z_s = Z_n/Z_r$. Note that $r = 1$ corresponds to all irreps of Z_n and $r = n$ to singlets under Z_n.

15.5.2 A possible interpretation for the divisor code

Consider now a model for what might happen in the coding of amino-acid by DNA.

1. Suppose that the maximal cyclic subgroup $Z_n \subset G_a$ acts as symmetries of "dark" space-time sheets and wave functions of "dark" free electron pairs for the amino-acid and corresponding DNAs so that the 2-surfaces in question are n-fold coverings of CP_2 points by M^4 points (corresponding to positions of say 5 molecules in a cyclic molecule) and corresponding codons. Free electron pairs could correspond to the dark matter in question.
2. Suppose that DNA characterized by n and its particular divisor r has electronic wave functions invariant under Z_r and thus forming irreducible representations of $Z_s = Z_n/Z_r$, $n = r \times s$. The electronic wave functions assignable to the amino-acid would in general transform according to some irreducible representations of $Z_n = \prod_i Z_{p_i}$, $n = \prod_i p_i$, where same prime p_i can appear several times. This assumption would explain why the product decompositions (r,s) and (s,r) are not equivalent.

15.5.3 About the geometric interpretation for the thermodynamics of partitions of $n_{2)}$

Suppose that the maximization of the information content for the thermodynamics for the partitions of the integer $n_2 = n \ mod \ 5^2$ belonging to the range $[6,24]$ and labeling 2-codons provides a dual manner to understand the genetic code. $n \to n \ mod \ 25$ would have an interpretation in terms of reduction to a subset of the finite finite field $G(5,2)$ and would be natural in 5-adic context.

One could try to interpret the modulo arithmetics in terms of the generalized notion of imbedding space.

1. One could label the points of M^4 covering of CP_2 by integers $0 \leq m \leq n$. The sheets points m and $m+k25$ should be equivalent from the point of view of mitochondrial genetic code so that Z_{25} equivalence classes would give rise to $n_{2)}$ points.
2. A more concrete interpretation would be that first nucleotide along gives rise to n_0-fold covering, second nucleotide adds $5n_1$ sheets so that $n_{2)} = n_0 + 5n_1$-fold covering results, and third nucleotide adds $n_3 5^2$ sheets so that to $n = n_{2)} + n_3 \times 5^2$-fold covering results. The sheets contributed by the third nucleotide would not participate in the partition thermodynamics and the third nucleotide would only determine the 5-adic temperature $T_5 = 1/n$.

15.5.4 About the physical interpretation for the thermodynamics of partitions of $n_{2)}$

The 5-adic thermodynamics relies on the partitions of $n_2 = n \ mod \ 5^2$. n_2 could have interpretation both as a net conformal weight or spin associated with spin one electronic Cooper pairs.

1. Modulo 5^2 property could be due to the invariance of electronic wave functions under Z_{25} acting as rotations. There would be 25-periodicity of physics in the covering, the analog of a lattice structure in angle degree of freedom with sub-lattices forming dynamical units. Also quantum group with quantum phase $q = exp(i\pi/25)$ implies the analog of lattice structure in angle degrees of freedom.
2. Each equivalence class analogous to a sub-lattice with points having distance of 25 units would effectively carry one unit conformal weight or one unit of spin (L_0 and iL_0 act as infinitesimal scaling and rotation respectively). At the concrete physical level the following alternative interpretations suggest themselves.

The interpretation in terms of conformal symmetry

The partitions of the integer $n_{2)} = n_0 + n_1 5$, $n_i \neq 0$ could have interpretation as partitions of the set of equivalence classes to a union of subsets with the number n_k of elements in the subset giving the total conformal weight created by L_{n_k} rather than L_1^k. These partitions could be interpreted as partitions of a molecular Z_{25} equivalence classes of building blocks of the molecular structure with Z_n rotational symmetry to subsets of basic building blocks and Virasoro generators L_{n_k} would act on various building blocks. A

formation of bound states each binding single particle states associated with n_k sheets and created by L_1 suggests itself. The reduction of Virasoro algebra defined in Z to a Virasoro algebra defined in the finite field $G(5,2)$ or in the ring Z_{25} is natural in this framework.

Interpretation in terms of irreducible representations of symmetric group and braids

Partitions label the conjugacy classes of symmetric group S_n consisting of the permutations of n objects. The summand n_k corresponds to a cyclic permutation of n_k objects. Partitions label also the irreducible representations of S_n. S_n can be defined by generators e_m representing permutation of m^{th} and $(m+1)^{th}$ object satisfying the conditions

$$\begin{aligned} e_m e_m &= e_n e_m \ \text{ for } \ |m-n|>1, \\ e_n e_{n+1} e_n &= e_n e_{n+1} e_n e_{n+1} \ \text{ for } \ n=1,...,n-2 \ , \\ e_n^2 &= 1 \ . \end{aligned} \tag{15.5.1}$$

By dropping the condition $e_n^2 = 1$ one obtains the defining relations of the braid group B_n of braid consisting of n strands. The irreducible representations of B_n are projective representations of S_n and give as a special case the representations of S_n.

1. Could the dynamics for partitions of n correspond to the dynamics for irreducible representations of S_n?

S_n brings in mind braids and topological quantum computation and the suggestion of [81] that DNA and/or RNA might act as a topological quantum computer. The so called number theoretical braids, which provide representations for Galois groups permuting roots of an n^{th} order irreducible polynomial are subgroups of S_n (and equal to S_n in the generic case), are in a central role in the formulation of quantum TGD [17] , [3] .

This interpretation would assign to a given codon a braid with n strands, whose states would correspond to irreducible representations of S_n [6] . The thermodynamics would be for the irreducible representations of S_n with the number n of braids varying in the range $[6,24]$. Braid would be a 5-adic thermodynamical system such that all $d(n,r)$ irreducible representations with a given value of r would have the same value of the 5-adic Hamiltonian $h(r)$ (definitely not the most general dynamics now). The reason for the absence of n-braids for which n has zeros in its 5-adic expansion could relate to the fact that the quantum phase $q = exp(i\pi/m)$ defines a universal topological quantum computer for $m \geq 5$. $m = 5$ is suggested strongly in case of DNA since it manifests itself in the geometry of DNA (twisting angle for single nucleotide and the presence of 5-cycles).

2. More general dynamics?

The alternative interpretation forces to reconsider the definition of 5-adic thermodynamics. Let us denote by (n,r,i) the irrep of S_n corresponding to a particular partition of n with r summands. It would seem natural to interpret the dimension $D_{n,r,i}$ of the irrep as the additional degeneracy factor replacing $d(n,r)$ so that the number $d(n,r)$ of partitions with r summands (subsets) would be replaced by the degeneracy factor

$$D(n,r) = \sum_i D_{n,r,i} \ ,$$

and $D_{n,r,i}$ is the dimension of the irrep in question. The irreps $d(n,r,i)$ are in one-one-correspondence with Yang tableaus consisting of n boxes in r rows and $D(n,r,i)$ can be calculated using standard formulas [7] .

One might hope that this modification could allow to simplify the dynamics. The best one might dream of would be that $h(r)$ could be taken to be Z_3 valued: $0 \leq h(r) \leq 2$. One could also check whether the definition of the partition sum using modulo 125 arithmetics as $Z = \sum_r D(n,r)5^{h(r)} \ \ mod \ \ 125$ gives sensible results. Only two possible temperatures $1/T_5 = 1,2$ besides $1/T_5 = 0$ corresponding to stopping codon are possible so that doublets pose very strong conditions on the model. The transformation $Z = Z_0 + Z_1 5 + Z_2 5^2 \rightarrow Z_0 + Z_2 5 + Z_1 5^2$ corresponds to the temperature scaling by 2. Hence it is not surprising that the simplest model does not work. In any case, the modification of earlier computational model to this case involves only the replacement of $d(n,r)$ with $D(n,r)$.

The dynamics could be however much more flexible. The 5-adic thermodynamics for irreducible representations of S_n instead of partitions allows the replacement of $h(r)$ with $h(n,r,i)$, say $h(n,r,d(n,r,i))$, where $d(n,r,i)$ is the dimension of the representation in question. The dynamics for a given n would be independent of the dynamics for other values of n unless one assumes that $h(n,r,d(n,r,i))$ is some simple function, say $h = d(n,r,i) \ \ mod \ \ 3$. In the most general case the number of parameters $h(n,r,i)$ would be the number of irreps given by the number $d(n) = \sum_r d(n,r)$ of partitions. For $n = 6$ one has $d(6) = 11$ partitions and $n = 24$ would give $d(24) = 3^2 \times 5^2 \times 7 = 1575$ partitions. Even for $h(n,r,i) \in Z_3$ this would increase the number of

parameters dramatically and might allow to reproduce the genetic code in consistency with the constraints from the divisor code.

3. What could be the physical interpretation?

One can ask how this picture could relate to the picture provided by the divisor code in which representations of cyclic group Z_n reduced to some of its subgroup with integer $31 \leq n \leq 124$ being one of the integers associated with a given amino-acid. Is there place in TGD Universe for these two discrete symmetries? This might be the case if one takes seriously both the hierarchy of Planck constants involving the generalization of the imbedding space concept and the notion of number theoretic braid.

1. The permutation group $S_{n_{2)}}$, $n_{2)} \in [6, 24]$ for braid strands associated with the first two letters of the codon $n > n_{2)}$ would act on the number theoretical braids with $n_{2)}$ strands. The increase of n_2 could have interpretation as an increase of complexity in the sense that the number of braid strands increases.
2. The cyclic group Z_n, $n \in [31, ..., 124]$, possibly associated with electron pairs, could correspond to the G_a covering of $M^4_\pm$ defined by the hierarchy of Planck constants associated with the hierarchy of fiber bundle structures $H_\pm = M^4_\pm \times CP_2 \to H_\pm/G_a \times G_b$, $G_a \times G_b \subset SU(2) \times SU(2) \subset SL(2,C) \times SU(3)$. Cyclic group Z_n would be identified as the maximal cyclic group of G_a. Note however that topological quantum computer considerations would suggest that G_a has Z_5 as maximal cyclic subgroup so that Z_n cannot correspond to the number of sheets in the cyclic covering essential for topological quantum computation. A more natural interpretation would be as a cyclic group of symmetries for the magnetic flux quanta action as rotations permuting the flux tubes of the topologically quantized dipole type magnetic field. What remains a mystery is why $n_1 = n \mod 5$, $n_2 = n - n_1 \mod 5^2$,... cannot vanish. Could the irreducible representation of $S_{n_{2)}}$ corresponding to the partition $n_{2)} = \sum_k n_k 5^k$ defined by 5-adic expansion and having $r = 2$ summands have a special role? Ir could the sub-group $\prod_k S_{n_k 5^k}$ of S_n have a special role?

The interpretation in terms of decomposition to many-particle states consisting of free electron pairs or Cooper pairs

The fact that iL_0 corresponds to rotations allows to consider also the interpretation of the partitions in terms of decompositions of the state to a product of angular momentum eigen states with values of $J_z = n_k$. Basic building blocks could have spin $S_z = 1$ so that codon would be characterized by its total spin $S_z = n_2 = n \mod 5^2$ possible associated with dark Cooper pairs with spin quantum number $S_z = 1$. The blocks of the partition would be coherent sub-Bose-Einstein condensates of dark Cooper pairs and the number theoretic Hamiltonian would characterize the change of energy like quantity as this kind of state is formed.

This interpretation conforms with the general TGD based view about living matter. High T_c superconductivity indeed plays a key role in TGD based model of living matter [12, 13] and there is experimental evidence that DNA can have anomalously high conductivity [141] . TGD based model [13] relies on the hypothesis that free electron pairs associated with the 5- and/or 6-rings of sugars in the backbone of DNA correspond to dark matter with Planck constant $\hbar = n\hbar_0$, $n = 5$ and/or $n = 6$. Also the observation that the twist angle of single nucleotide in double helix is $\pi/5$ is suggestive of 5-adicity. Note that $n = 5$ defines the minimum value of n making possible universal topological quantum computation and in [81] it is proposed that DNA and/or RNA could act as topological quantum computer.

15.5.5 A possible interpretation for the p-adic prime labeling amino-acid and DNAs coding it

The notion of field body or magnetic body is central for the TGD inspired model of living matter [23] , [3] . This notion is justified by so called topological quantization of classical fields making it possible to assign to a given physical system a field body which is typically much larger than the physical body. For instance, in case of brain the magnetic body is of astrophysical size (EEG wavelengths are of order Earth size). Dark magnetic body containing Bose Einstein condensates of ions with large value of Planck constant would be the fundamental bio-controller utilizing biological body as a sensory receptor and motor instrument [23] .

A possible interpretation for the p-adic prime labeling amino-acid and DNAs coding for it could be as a characterizer of the effective p-adic topology associated with their magnetic bodies and the genuine p-adic topology for their p-adic counterparts obeying same algebraic equations. This is possible since for large values of Planck constant possibly associated with the magnetic body the small p-adic primes could correspond to size scales of order EEG wave lengths. Notice however that the p-adic primes characterizing elementary particles are much larger. For instance, electron is characterized by Mersenne prime $M_{127} = 2^{127} - 1$.

The preferred values of n_a and n_b are given by $n_i = 2^k \prod F_i$, where F_i are distinct Fermat primes (only four of them corresponding to $F = 3, 5, 17, 257, 2^{16}+1$ are known). The 2-adic hierarchy $n_a = 2^k$ could provide a deeper justification for the p-adic length scales hypothesis.

The 2-adic sub-hierarchy $n_a = 2^{k11}$, $k = 0, 1, 2...$ is especially interesting. For $n_b = 1$ $k = 11$ would correspond to the time scale $T_{121} = T(127)/64$, $T_{127}(2) = .1$ s, which defines the fundamental 10 Hz biorhythm. $T_{121} \simeq 1.6$ ms corresponds to a typical time scale for nerve pulse activity. For this option primary *resp.* secondary p-adic length scales associated with an amino-acid labeled by prime p would be $T_p = \sqrt{p}T_{121}$ *resp.* $T_p = pT_{121}$ and could define a small-p p-adic hierarchy of time scales of neuronal activity.

Obviously, the maximal cyclic subgroup of G_a containing 2^{121} elements and acting naturally as symmetries of magnetic and electric flux tube structures accompanying DNA and amino-acids cannot correspond to the group Z_n, $n \leq 124$ associated with DNA and amino-acid molecules.

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15.6 Appendix: 4-adic realization of $n \to n+32$ symmetry, divisor code, and labeling of amino-acids by primes are not mutually consistent

For the four-adic realization of the divisor code geometrically 18 amino-acids would correspond to primes $p < 63$ whereas the integers $n = 0$ and $n = 1$ would correspond to special amino-acids. $n \to n+32$ symmetry means that 4-columns of the code table contain either even or odd integers depending on whether the row is odd or even. Hence the 4-columns containing even integers cannot contain the prime coding for the amino-acid so that the geometric realization in which DNAs coding amino-acid contain both prime labeling for the amino-acid and the integer characterizing the degeneracy of the amino-acid as the number of its divisors is not possible.

One could weaken the condition by requiring that $n(p) = p$ holds true only when one of the coding codons is labeled by a prime. This however leads to a further difficulty since the primes $(5, 5+32 = 27)$ and $(11, 11+32 = 43)$ belong to same 4-column and should code for same amino-acid. Hence the assumption that amino-acids correspond to $n = 0, 1$ and 18 primes $p < 63$ does not look natural. One could however consider a less ambitious realization of the divisor code by giving up this requirement altogether and requiring only that one of the DNAs is labeled by an integer for which the number of divisors equals to the degeneracy of the corresponding codon.

For eukaryote code Met would naturally correspond to $n = 1$. For mitochondrial code the multiplets containg $n = 0$ and $n = 1$ DNA would contain also second DNA. The problem is that the number of its divisors should be $n = 2$ for the mitochondrial code for both Met and Ile and one end ups with a contradiction unless one somehow loosens the rules. One could say that the prime $n = 17$ determines the degeneracy of Ile for mitochondrial code so that Met takes the rest.

The multiplet coding for a particular amino-acid would contain DNA labeled by the prime coding for amino-acid and an integer with a number of divisors equal to the degeneracy of the codon. For odd rows of the code table 4-columns contain only even primes so that primes are contained in 4-columns in even rows of the table.

The code below is the best variant found hitherto. One of the integers in 4-column is consistent with the the degeneracy of amino-acid according to divisor code and for each amino-acid one of DNAs corresponds to the integers consistent with the degeneracy. For Trp in case of eukaryote code stop breaks the symmetry. 7 codes only for a singlet (Trp).

```
    UCC Ser       AGC Ser       CCC Pro      CUC Leu
    UCA Ser       AGA Stop      CCA Pro      CUA Leu
(16)UCU Ser    20 AGU Ser       CCU Pro      CUU Leu
 0  UCG Ser    (4)AGG Stop    8 CCG Pro   12 CUG Leu


(49)AUC Ile    53 CAC His    57 GUC Val   61 UUC  Leu
(33)AUA Ile   (37)CAA Gln   (41)GUA Val  (45)UUA  Phe
 17 AUU Ile       CAU His       GUU Val   29 UUU  Leu
 1  AUG Met    5  CAG Gln    (9)GUG Val   13 UUG  Phe


    CGC Arg      GCC Ala       ACC Thr      GGC Gly
 34 GGA Arg      GCA Ala       ACA Thr      GGA Gly
 18 GGU Arg      GCU Ala       ACU Thr      GGU Gly
```

2	GGG	Arg	6	GCG	Ala	10	ACG	Thr	14	GGG	Gly
	GAC	Asp		UGC	Cys	59	AAC	Asn	63	UAC	Tyr
	GAA	Glu	39	UGA	Trp	(43)	AAA	Lys	(47)	UAA	Stop
19	GAU	Asp	23	UGU	Cys		AAU	Asn	(31)	UAU	Tyr
3	GAG	Glu	7	UGG	Trp	11	AAG	Lys	(15)	UAG	Stop

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Chapter 1

Appendix

A-1 Basic properties of CP_2

A-1.1 CP_2 as a manifold

CP_2, the complex projective space of two complex dimensions, is obtained by identifying the points of complex 3-space C^3 under the projective equivalence

$$(z^1, z^2, z^3) \equiv \lambda(z^1, z^2, z^3) \quad . \tag{A-1.1}$$

Here λ is any non-zero complex number. Note that CP_2 can be also regarded as the coset space $SU(3)/U(2)$. The pair z^i/z^j for fixed j and $z^i \neq 0$ defines a complex coordinate chart for CP_2. As j runs from 1 to 3 one obtains an atlas of three oordinate charts covering CP_2, the charts being holomorphically related to each other (e.g. CP_2 is a complex manifold). The points $z^3 \neq 0$ form a subset of CP_2 homeomorphic to R^4 and the points with $z^3 = 0$ a set homeomorphic to S^2. Therefore CP_2 is obtained by "adding the 2-sphere at infinity to R^4".

Besides the standard complex coordinates $\xi^i = z^i/z^3$, $i = 1, 2$ the coordinates of Eguchi and Freund [33] will be used and their relation to the complex coordinates is given by

$$\begin{aligned} \xi^1 &= z + it \quad , \\ \xi^2 &= x + iy \quad . \end{aligned} \tag{A-1.2}$$

These are related to the "spherical coordinates" via the equations

$$\begin{aligned} \xi^1 &= rexp(i\frac{(\Psi + \Phi)}{2})cos(\frac{\Theta}{2}) \quad , \\ \xi^2 &= rexp(i\frac{(\Psi - \Phi)}{2})sin(\frac{\Theta}{2}) \quad . \end{aligned} \tag{A-1.3}$$

The ranges of the variables r, Θ, Φ, Ψ are $[0, \infty], [0, \pi], [0, 4\pi], [0, 2\pi]$ respectively.

Considered as a real four-manifold CP_2 is compact and simply connected, with Euler number Euler number 3, Pontryagin number 3 and second $b = 1$.

A-1.2 Metric and Kähler structure of CP_2

In order to obtain a natural metric for CP_2, observe that CP_2 can be thought of as a set of the orbits of the isometries $z^i \to exp(i\alpha)z^i$ on the sphere S^5: $\sum z^i \bar{z}^i = R^2$. The metric of CP_2 is obtained by projecting the metric of S^5 orthogonally to the orbits of the isometries. Therefore the distance between the points of CP_2 is that between the representative orbits on S^5.

The line element has the following form in the complex coordinates

$$ds^2 = g_{a\bar{b}} d\xi^a d\bar{\xi}^b \quad , \tag{A-1.4}$$

where the Hermitian, in fact Kähler metric $g_{a\bar{b}}$ is defined by

$$g_{a\bar{b}} = R^2 \partial_a \partial_{\bar{b}} K \ , \tag{A-1.5}$$

where the function K, Kähler function, is defined as

$$\begin{aligned} K &= log(F) \ , \\ F &= 1 + r^2 \ . \end{aligned} \tag{A-1.6}$$

The Kähler function for S^2 has the same form. It gives the S^2 metric $dzd\bar{z}/(1+r^2)^2$ related to its standard form in spherical coordinates by the coordinate transformation $(r, \phi) = (tan(\theta/2), \phi)$.

The representation of the CP_2 metric is deducible from S^5 metric is obtained by putting the angle coordinate of a geodesic sphere constant in it and is given

$$\frac{ds^2}{R^2} = \frac{(dr^2 + r^2\sigma_3^2)}{F^2} + \frac{r^2(\sigma_1^2 + \sigma_2^2)}{F} \ , \tag{A-1.7}$$

where the quantities σ_i are defined as

$$\begin{aligned} r^2\sigma_1 &= Im(\xi^1 d\xi^2 - \xi^2 d\xi^1) \ , \\ r^2\sigma_2 &= -Re(\xi^1 d\xi^2 - \xi^2 d\xi^1) \ , \\ r^2\sigma_3 &= -Im(\xi^1 d\bar{\xi}^1 + \xi^2 d\bar{\xi}^2) \ . \end{aligned} \tag{A-1.8}$$

R denotes the radius of the geodesic circle of CP_2. The vierbein forms, which satisfy the defining relation

$$s_{kl} = R^2 \sum_A e_k^A e_l^A \ , \tag{A-1.9}$$

are given by

$$\begin{aligned} e^0 &= \tfrac{dr}{F} \ , \quad e^1 = \tfrac{r\sigma_1}{\sqrt{F}} \ , \\ e^2 &= \tfrac{r\sigma_2}{\sqrt{F}} \ , \quad e^3 = \tfrac{r\sigma_3}{F} \ . \end{aligned} \tag{A-1.10}$$

The explicit representations of vierbein vectors are given by

$$\begin{aligned} e^0 &= \tfrac{dr}{F} \ , & e^1 &= \tfrac{r(sin\Theta cos\Psi d\Phi + sin\Psi d\Theta)}{2\sqrt{F}} \ , \\ e^2 &= \tfrac{r(sin\Theta sin\Psi d\Phi - cos\Psi d\Theta)}{2\sqrt{F}} \ , & e^3 &= \tfrac{r(d\Psi + cos\Theta d\Phi)}{2F} \ . \end{aligned} \tag{A-1.11}$$

The explicit representation of the line element is given by the expression

$$ds^2/R^2 = \frac{dr^2}{F^2} + \frac{r^2}{4F^2}(d\Psi + cos\Theta d\Phi)^2 + \frac{r^2}{4F}(d\Theta^2 + sin^2\Theta d\Phi^2) \ . \tag{A-1.12}$$

The vierbein connection satisfying the defining relation

$$de^A = -V_B^A \wedge e^B \ , \tag{A-1.13}$$

is given by

$$\begin{aligned} V_{01} &= -\tfrac{e^1}{r} \ , & V_{23} &= \tfrac{e^1}{r} \ , \\ V_{02} &= -\tfrac{e^2}{r} \ , & V_{31} &= \tfrac{e^2}{r} \ , \\ V_{03} &= (r - \tfrac{1}{r})e^3 \ , & V_{12} &= (2r + \tfrac{1}{r})e^3 \ . \end{aligned} \tag{A-1.14}$$

The representation of the covariantly constant curvature tensor is given by

$$\begin{aligned} R_{01} &= e^0\wedge e^1 - e^2\wedge e^3 \ , \quad & R_{23} &= e^0\wedge e^1 - e^2\wedge e^3 \ , \\ R_{02} &= e^0\wedge e^2 - e^3\wedge e^1 \ , \quad & R_{31} &= -e^0\wedge e^2 + e^3\wedge e^1 \ , \\ R_{03} &= 4e^0\wedge e^3 + 2e^1\wedge e^2 \ , \quad & R_{12} &= 2e^0\wedge e^3 + 4e^1\wedge e^2 \ . \end{aligned} \tag{A-1.15}$$

Metric defines a real, covariantly constant, and therefore closed 2-form J

$$J = -ig_{a\bar{b}}d\xi^a d\bar{\xi}^b \ , \tag{A-1.16}$$

the so called Kähler form. Kähler form J defines in CP_2 a symplectic structure because it satisfies the condition

$$J^k_{\ r}J^{rl} = -s^{kl} \ . \tag{A-1.17}$$

The form J is integer valued and by its covariant constancy satisfies free Maxwell equations. Hence it can be regarded as a curvature form of a $U(1)$ gauge potential B carrying a magnetic charge of unit $1/2g$ (g denotes the gauge coupling). Locally one has therefore

$$J = dB \ , \tag{A-1.18}$$

where B is the so called Kähler potential, which is not defined globally since J describes homological magnetic monopole.

It should be noticed that the magnetic flux of J through a 2-surface in CP_2 is proportional to its homology equivalence class, which is integer valued. The explicit representations of J and B are given by

$$\begin{aligned} B &= 2re^3 \ , \\ J &= 2(e^0\wedge e^3 + e^1\wedge e^2) = \frac{r}{F^2}dr\wedge(d\Psi + cos\Theta d\Phi) + \frac{r^2}{2F}sin\Theta d\Theta d\Phi \ . \end{aligned} \tag{A-1.19}$$

The vierbein curvature form and Kähler form are covariantly constant and have in the complex coordinates only components of type (1,1).

Useful coordinates for CP_2 are the so called canonical coordinates in which Kähler potential and Kähler form have very simple expressions

$$\begin{aligned} B &= \sum_{k=1,2} P_k dQ_k \ , \\ J &= \sum_{k=1,2} dP_k\wedge dQ_k \ . \end{aligned} \tag{A-1.20}$$

The relationship of the canonical coordinates to the "spherical" coordinates is given by the equations

$$\begin{aligned} P_1 &= -\frac{1}{1+r^2} \ , \\ P_2 &= \frac{r^2 cos\Theta}{2(1+r^2)} \ , \\ Q_1 &= \Psi \ , \\ Q_2 &= \Phi \ . \end{aligned} \tag{A-1.21}$$

A-1.3 Spinors in CP_2

CP_2 doesn't allow spinor structure in the conventional sense [28] . However, the coupling of the spinors to a half odd multiple of the Kähler potential leads to a respectable spinor structure. Because the delicacies associated with the spinor structure of CP_2 play a fundamental role in TGD, the arguments of Hawking are repeated here.

To see how the space can fail to have an ordinary spinor structure consider the parallel transport of the vierbein in a simply connected space M. The parallel propagation around a closed curve with a base point x leads to a rotated vierbein at x: $e^A = R^A_B e^B$ and one can associate to each closed path an element of $SO(4)$.

Consider now a one-parameter family of closed curves $\gamma(v) : v \in (0,1)$ with the same base point x and $\gamma(0)$ and $\gamma(1)$ trivial paths. Clearly these paths define a sphere S^2 in M and the element $R^A_B(v)$ defines a closed path in $SO(4)$. When the sphere S^2 is contractible to a point e.g., homologically trivial, the path in $SO(4)$ is also contractible to a point and therefore represents a trivial element of the homotopy group $\Pi_1(SO(4)) = Z_2$.

For a homologically nontrivial 2-surface S^2 the associated path in $SO(4)$ can be homotopically nontrivial and therefore corresponds to a nonclosed path in the covering group Spin(4) (leading from the matrix 1 to -1 in the matrix representation). Assume this is the case.

Assume now that the space allows spinor structure. Then one can parallel propagate also spinors and by the above construction associate a closed path of Spin(4) to the surface S^2. Now, however this path corresponds to a lift of the corresponding $SO(4)$ path and cannot be closed. Thus one ends up with a contradiction.

From the preceding argument it is clear that one could compensate the non-allowed -1- factor associated with the parallel transport of the spinor around the sphere S^2 by coupling it to a gauge potential in such a way that in the parallel transport the gauge potential introduces a compensating -1-factor. For a $U(1)$ gauge potential this factor is given by the exponential $exp(i2\Phi)$, where Φ is the magnetic flux through the surface. This factor has the value -1 provided the $U(1)$ potential carries half odd multiple of Dirac charge $1/2g$. In case of CP_2 the required gauge potential is half odd multiple of the Kähler potential B defined previously. In the case of $M^4 \times CP_2$ one can in addition couple the spinor components with different chiralities independently to an odd multiple of $B/2$.

A-1.4 Geodesic sub-manifolds of CP_2

Geodesic sub-manifolds are defined as sub-manifolds having common geodesic lines with the imbedding space. As a consequence the second fundamental form of the geodesic manifold vanishes, which means that the tangent vectors h^k_α (understood as vectors of H) are covariantly constant quantities with respect to the covariant derivative taking into account that the tangent vectors are vectors both with respect to H and X^4.

In [18] a general characterization of the geodesic sub-manifolds for an arbitrary symmetric space G/H is given. Geodesic sub-manifolds are in 1-1-correspondence with the so called Lie triple systems of the Lie-algebra g of the group G. The Lie triple system t is defined as a subspace of g characterized by the closedness property with respect to double commutation

$$[X,[Y,Z]] \in t \quad \text{for} \quad X,Y,Z \in t \quad . \tag{A-1.22}$$

$SU(3)$ allows, besides geodesic lines, two nonequivalent (not isometry related) geodesic spheres. This is understood by observing that $SU(3)$ allows two nonequivalent $SU(2)$ algebras corresponding to subgroups $SO(3)$ (orthogonal 3×3 matrices) and the usual isospin group $SU(2)$. By taking any subset of two generators from these algebras, one obtains a Lie triple system and by exponentiating this system, one obtains a 2-dimensional geodesic sub-manifold of CP_2.

Standard representatives for the geodesic spheres of CP_2 are given by the equations

$$S^2_I \quad : \quad \xi^1 = \bar{\xi}^2 \quad \text{or equivalently} \quad (\Theta = \pi/2, \Psi = 0) \quad ,$$

$$S^2_{II} \quad : \quad \xi^1 = \xi^2 \quad \text{or equivalently} \quad (\Theta = \pi/2, \Phi = 0) \quad .$$

The non-equivalence of these sub-manifolds is clear from the fact that isometries act as holomorphic transformations in CP_2. The vanishing of the second fundamental form is also easy to verify. The first geodesic manifold is homologically trivial: in fact, the induced Kähler form vanishes identically for S^2_I. S^2_{II} is homologically nontrivial and the flux of the Kähler form gives its homology equivalence class.

A-2 CP_2 geometry and standard model symmetries

A-2.1 Identification of the electro-weak couplings

The delicacies of the spinor structure of CP_2 make it a unique candidate for space S. First, the coupling of the spinors to the $U(1)$ gauge potential defined by the Kähler structure provides the missing $U(1)$ factor in

the gauge group. Secondly, it is possible to couple different H-chiralities independently to a half odd multiple of the Kähler potential. Thus the hopes of obtaining a correct spectrum for the electromagnetic charge are considerable. In the following it will be demonstrated that the couplings of the induced spinor connection are indeed those of the GWS model [15] and in particular that the right handed neutrinos decouple completely from the electro-weak interactions.

To begin with, recall that the space H allows to define three different chiralities for spinors. Spinors with fixed H-chirality $e = \pm 1$, CP_2-chirality l, r and M^4-chirality L, R are defined by the condition

$$\begin{aligned} \Gamma\Psi &= e\Psi \ , \\ e &= \pm 1 \ , \end{aligned} \tag{A-2.1}$$

where Γ denotes the matrix $\Gamma_9 = \gamma_5 \times \gamma_5$, $1 \times \gamma_5$ and $\gamma_5 \times 1$ respectively. Clearly, for a fixed H-chirality CP_2- and M^4-chiralities are correlated.

The spinors with H-chirality $e = \pm 1$ can be identified as quark and lepton like spinors respectively. The separate conservation of baryon and lepton numbers can be understood as a consequence of generalized chiral invariance if this identification is accepted. For the spinors with a definite H-chirality one can identify the vielbein group of CP_2 as the electro-weak group: $SO(4) = SU(2)_L \times SU(2)_R$.

The covariant derivatives are defined by the spinorial connection

$$A = V + \frac{B}{2}(n_+ 1_+ + n_- 1_-) \ . \tag{A-2.2}$$

Here V and B denote the projections of the vielbein and Kähler gauge potentials respectively and $1_{+(-)}$ projects to the spinor H-chirality $+(-)$. The integers $n_\pm$ are odd from the requirement of a respectable spinor structure.

The explicit representation of the vielbein connection V and of B are given by the equations

$$\begin{aligned} V_{01} &= -\tfrac{e^1}{r_2} \ , & V_{23} &= \tfrac{e^1}{r_2} \ , \\ V_{02} &= -\tfrac{e^2}{r} \ , & V_{31} &= \tfrac{e^2}{r} \ , \\ V_{03} &= (r - \tfrac{1}{r})e^3 \ , & V_{12} &= (2r + \tfrac{1}{r})e^3 \ , \end{aligned} \tag{A-2.3}$$

and

$$B = 2re^3 \ , \tag{A-2.4}$$

respectively. The explicit representation of the vielbein is not needed here.

Let us first show that the charged part of the spinor connection couples purely left handedly. Identifying Σ_3^0 and Σ_2^1 as the diagonal (neutral) Lie-algebra generators of $SO(4)$, one finds that the charged part of the spinor connection is given by

$$A_{ch} = 2V_{23}I_L^1 + 2V_{13}I_L^2 \ , \tag{A-2.5}$$

where one have defined

$$\begin{aligned} I_L^1 &= \frac{(\Sigma_{01} - \Sigma_{23})}{2} \ , \\ I_L^2 &= \frac{(\Sigma_{02} - \Sigma_{13})}{2} \ . \end{aligned} \tag{A-2.6}$$

A_{ch} is clearly left handed so that one can perform the identification

$$W^\pm = \frac{2(e^1 \pm ie^2)}{r} \ , \tag{A-2.7}$$

where $W^\pm$ denotes the charged intermediate vector boson.

Consider next the identification of the neutral gauge bosons γ and Z^0 as appropriate linear combinations of the two functionally independent quantities

$$\begin{aligned} X &= re^3 \ , \\ Y &= \frac{e^3}{r} \ , \end{aligned} \tag{A-2.8}$$

appearing in the neutral part of the spinor connection. We show first that the mere requirement that photon couples vectorially implies the basic coupling structure of the GWS model leaving only the value of Weinberg angle undetermined.

To begin with let us define

$$\begin{aligned} \bar{\gamma} &= aX + bY \ , \\ \bar{Z}^0 &= cX + dY \ , \end{aligned} \tag{A-2.9}$$

where the normalization condition

$$ad - bc = 1 \ ,$$

is satisfied. The physical fields γ and Z^0 are related to $\bar{\gamma}$ and $\bar{Z}^0$ by simple normalization factors.

Expressing the neutral part of the spinor connection in term of these fields one obtains

$$\begin{aligned} A_{nc} &= [(c+d)2\Sigma_{03} + (2d-c)2\Sigma_{12} + d(n_+1_+ + n_-1_-)]\bar{\gamma} \\ &+ [(a-b)2\Sigma_{03} + (a-2b)2\Sigma_{12} - b(n_+1_+ + n_-1_-)]\bar{Z}^0 \ . \end{aligned} \tag{A-2.10}$$

Identifying Σ_{12} and $\Sigma_{03} = 1 \times \gamma_5 \Sigma_{12}$ as vectorial and axial Lie-algebra generators, respectively, the requirement that γ couples vectorially leads to the condition

$$c = -d \ . \tag{A-2.11}$$

Using this result plus previous equations, one obtains for the neutral part of the connection the expression

$$A_{nc} = \gamma Q_{em} + Z^0(I_L^3 - sin^2\theta_W Q_{em}) \ . \tag{A-2.12}$$

Here the electromagnetic charge Q_{em} and the weak isospin are defined by

$$\begin{aligned} Q_{em} &= \Sigma^{12} + \frac{(n_+1_+ + n_-1_-)}{6} \ , \\ I_L^3 &= \frac{(\Sigma^{12} - \Sigma^{03})}{2} \ . \end{aligned} \tag{A-2.13}$$

The fields γ and Z^0 are defined via the relations

$$\begin{aligned} \gamma &= 6d\bar{\gamma} = \frac{6}{(a+b)}(aX + bY) \ , \\ Z^0 &= 4(a+b)\bar{Z}^0 = 4(X - Y) \ . \end{aligned} \tag{A-2.14}$$

The value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{3b}{2(a+b)} \ , \tag{A-2.15}$$

and is not fixed completely. Observe that right handed neutrinos decouple completely from the electro-weak interactions.

The determination of the value of Weinberg angle is a dynamical problem. The angle is completely fixed once the YM action is fixed by requiring that action contains no cross term of type γZ^0. Pure symmetry non-broken electro-weak YM action leads to a definite value for the Weinberg angle. One can however add a symmetry breaking term proportional to Kähler action and this changes the value of the Weinberg angle.

To evaluate the value of the Weinberg angle one can express the neutral part F_{nc} of the induced gauge field as

$$F_{nc} = 2R_{03}\Sigma^{03} + 2R_{12}\Sigma^{12} + J(n_+1_+ + n_-1_-) \ , \tag{A-2.16}$$

where one has

$$\begin{aligned} R_{03} &= 2(2e^0 \wedge e^3 + e^1 \wedge e^2) \ , \\ R_{12} &= 2(e^0 \wedge e^3 + 2e^1 \wedge e^2) \ , \\ J &= 2(e^0 \wedge e^3 + e^1 \wedge e^2) \ , \end{aligned} \tag{A-2.17}$$

in terms of the fields γ and Z^0 (photon and Z- boson)

$$F_{nc} = \gamma Q_{em} + Z^0(I_L^3 - sin^2\theta_W Q_{em}) \ . \tag{A-2.18}$$

Evaluating the expressions above one obtains for γ and Z^0 the expressions

$$\begin{aligned} \gamma &= 3J - sin^2\theta_W R_{03} \ , \\ Z^0 &= 2R_{03} \ . \end{aligned} \tag{A-2.19}$$

For the Kähler field one obtains

$$J = \frac{1}{3}(\gamma + sin^2\theta_W Z^0) \ . \tag{A-2.20}$$

Expressing the neutral part of the symmetry broken YM action

$$\begin{aligned} L_{ew} &= L_{sym} + fJ^{\alpha\beta}J_{\alpha\beta} \ , \\ L_{sym} &= \frac{1}{4g^2}Tr(F^{\alpha\beta}F_{\alpha\beta}) \ , \end{aligned} \tag{A-2.21}$$

where the trace is taken in spinor representation, in terms of γ and Z^0 one obtains for the coefficient X of the γZ^0 cross term (this coefficient must vanish) the expression

$$\begin{aligned} X &= -\frac{K}{2g^2} + \frac{fp}{18} \ , \\ K &= Tr\left[Q_{em}(I_L^3 - sin^2\theta_W Q_{em})\right] \ , \end{aligned} \tag{A-2.22}$$

In the general case the value of the coefficient K is given by

$$K = \sum_i \left[-\frac{(18 + 2n_i^2)sin^2\theta_W}{9} \right] \ , \tag{A-2.23}$$

where the sum is over the spinor chiralities, which appear as elementary fermions and n_i is the integer describing the coupling of the spinor field to the Kähler potential. The cross term vanishes provided the value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{9\sum_i 1}{(fg^2 + 2\sum_i(18 + n_i^2))} \ . \tag{A-2.24}$$

In the scenario where both leptons and quarks are elementary fermions the value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{9}{(\frac{fg^2}{2} + 28)} \ . \tag{A-2.25}$$

The bare value of the Weinberg angle is 9/28 in this scenario, which is quite close to the typical value 9/24 of GUTs [29] .

A-2.2 Discrete symmetries

The treatment of discrete symmetries C, P, and T is based on the following requirements:
a) Symmetries must be realized as purely geometric transformations.
b) Transformation properties of the field variables should be essentially the same as in the conventional quantum field theories [6] .

The action of the reflection P on spinors of is given by

$$\Psi \rightarrow P\Psi = \gamma^0 \otimes \gamma^0 \Psi \ . \tag{A-2.26}$$

in the representation of the gamma matrices for which γ^0 is diagonal. It should be noticed that W and Z^0 bosons break parity symmetry as they should since their charge matrices do not commute with the matrix of P.

The guess that a complex conjugation in CP_2 is associated with T transformation of the physicist turns out to be correct. One can verify by a direct calculation that pure Dirac action is invariant under T realized according to

$$\begin{aligned} m^k &\rightarrow T(M^k) \ , \\ \xi^k &\rightarrow \bar{\xi}^k \ , \\ \Psi &\rightarrow \gamma^1\gamma^3 \otimes 1\Psi \ . \end{aligned} \tag{A-2.27}$$

The operation bearing closest resemblance to the ordinary charge conjugation corresponds geometrically to complex conjugation in CP_2:

$$\begin{aligned} \xi^k &\rightarrow \bar{\xi}^k \ , \\ \Psi &\rightarrow \Psi^\dagger \gamma^2\gamma^0 \otimes 1 \ . \end{aligned} \tag{A-2.28}$$

As one might have expected symmetries CP and T are exact symmetries of the pure Dirac action.

A-3 Basic facts about induced gauge fields

Since the classical gauge fields are closely related in TGD framework, it is not possible to have space-time sheets carrying only single kind of gauge field. For instance, em fields are accompanied by Z^0 fields for extremals of Kähler action. Weak forces is however absent unless the space-time sheets contains topologically condensed exotic weakly charged particles responding to this force. Same applies to classical color forces. The fact that these long range fields are present forces to assume that there exists a hierarchy of scaled up variants of standard model physics identifiable in terms of dark matter.

Classical em fields are always accompanied by Z^0 field and some components of color gauge field. For extremals having homologically non-trivial sphere as a CP_2 projection em and Z^0 fields are the only non-vanishing electroweak gauge fields. For homologically trivial sphere only W fields are non-vanishing. Color rotations does not affect the situation.

For vacuum extremals all electro-weak gauge fields are in general non-vanishing although the net gauge field has U(1) holonomy by 2-dimensionality of the CP_2 projection. Color gauge field has $U(1)$ holonomy for all space-time surfaces and quantum classical correspondence suggest a weak form of color confinement meaning that physical states correspond to color neutral members of color multiplets.

A-3.1 Induced gauge fields for space-times for which CP_2 projection is a geodesic sphere

If one requires that space-time surface is an extremal of Kähler action and has a 2-dimensional CP_2 projection, only vacuum extremals and space-time surfaces for which CP_2 projection is a geodesic sphere, are allowed. Homologically non-trivial geodesic sphere correspond to vanishing W fields and homologically non-trivial sphere to non-vanishing W fields but vanishing γ and Z^0. This can be verified by explicit examples.

$r = \infty$ surface gives rise to a homologically non-trivial geodesic sphere for which e_0 and e_3 vanish imply the vanishing of W field. For space-time sheets for which CP_2 projection is $r = \infty$ homologically non-trivial geodesic sphere of CP_2 one has

$$\gamma = (\frac{3}{4} - \frac{sin^2(\theta_W)}{2})Z^0 \simeq \frac{5Z^0}{8} \ .$$

The induced W fields vanish in this case and they vanish also for all geodesic sphere obtained by $SU(3)$ rotation.

$Im(\xi^1) = Im(\xi^2) = 0$ corresponds to homologically trivial geodesic sphere. A more general representative is obtained by using for the phase angles of standard complex CP_2 coordinates constant values. In this case e^1 and e^3 vanish so that the induced em, Z^0, and Kähler fields vanish but induced W fields are non-vanishing. This holds also for surfaces obtained by color rotation. Hence one can say that for non-vacuum extremals with 2-D CP_2 projection color rotations and weak symmetries commute.

A-3.2 Space-time surfaces with vanishing em, Z^0, or Kähler fields

In the following the induced gauge fields are studied for general space-time surface without assuming the extremal property. In fact, extremal property reduces the study to the study of vacuum extremals and surfaces having geodesic sphere as a CP_2 projection and in this sense the following arguments are somewhat obsolete in their generality.

Space-times with vanishing em, Z^0, or Kähler fields

The following considerations apply to a more general situation in which the homologically trivial geodesic sphere and extremal property are not assumed. It must be emphasized that this case is possible in TGD framework only for a vanishing Kähler field.

Using spherical coordinates (r, Θ, Ψ, Φ) for CP_2, the expression of Kähler form reads as

$$\begin{aligned} J &= \frac{r}{F^2} dr \wedge (d\Psi + cos(\Theta) d\Phi) + \frac{r^2}{2F} sin(\Theta) d\Theta \wedge d\Phi \ , \\ F &= 1 + r^2 \ . \end{aligned} \tag{A-3.1}$$

The general expression of electromagnetic field reads as

$$\begin{aligned} F_{em} &= (3+2p) \frac{r}{F^2} dr \wedge (d\Psi + cos(\Theta) d\Phi) + (3+p) \frac{r^2}{2F} sin(\Theta) d\Theta \wedge d\Phi \ , \\ p &= sin^2(\Theta_W) \ , \end{aligned} \tag{A-3.2}$$

where Θ_W denotes Weinberg angle.

a) The vanishing of the electromagnetic fields is guaranteed, when the conditions

$$\begin{aligned} \Psi &= k\Phi \ , \\ (3+2p) \frac{1}{r^2 F} (d(r^2)/d\Theta)(k + cos(\Theta)) &+ (3+p) sin(\Theta) = 0 \ , \end{aligned} \tag{A-3.3}$$

hold true. The conditions imply that CP_2 projection of the electromagnetically neutral space-time is 2-dimensional. Solving the differential equation one obtains

$$\begin{aligned} r &= \sqrt{\frac{X}{1-X}} \ , \\ X &= D \left[| \frac{(k+u}{C} | \right]^{\epsilon} \ , \\ u &\equiv cos(\Theta) \ , \ C = k + cos(\Theta_0) \ , \ D = \frac{r_0^2}{1+r_0^2} \ , \ \epsilon = \frac{3+p}{3+2p} \ , \end{aligned} \tag{A-3.4}$$

where C and D are integration constants. $0 \leq X \leq 1$ is required by the reality of r. $r = 0$ would correspond to $X = 0$ giving $u = -k$ achieved only for $|k| \leq 1$ and $r = \infty$ to $X = 1$ giving $|u + k| = [(1 + r_0^2)/r_0^2)]^{(3+2p)/(3+p)}$ achieved only for

$$sign(u+k) \times [\frac{1+r_0^2}{r_0^2}]^{\frac{3+2p}{3+p}} \leq k+1 \ ,$$

where $sign(x)$ denotes the sign of x.

The expressions for Kähler form and Z^0 field are given by

$$\begin{aligned} J &= -\frac{p}{3+2p} X du \wedge d\Phi \ , \\ Z^0 &= -\frac{6}{p} J \ . \end{aligned} \tag{A-3.5}$$

The components of the electromagnetic field generated by varying vacuum parameters are proportional to the components of the Kähler field: in particular, the magnetic field is parallel to the Kähler magnetic field. The generation of a long range Z^0 vacuum field is a purely TGD based feature not encountered in the standard gauge theories.

b) The vanishing of Z^0 fields is achieved by the replacement of the parameter ϵ with $\epsilon = 1/2$ as becomes clear by considering the condition stating that Z^0 field vanishes identically. Also the relationship $F_{em} = 3J = -\frac{3}{4}\frac{r^2}{F} du \wedge d\Phi$ is useful.

c) The vanishing Kähler field corresponds to $\epsilon = 1, p = 0$ in the formula for em neutral space-times. In this case classical em and Z^0 fields are proportional to each other:

$$\begin{aligned} Z^0 &= 2e^0 \wedge e^3 = \frac{r}{F^2}(k+u)\frac{\partial r}{\partial u} du \wedge d\Phi = (k+u) du \wedge d\Phi \ , \\ r &= \sqrt{\frac{X}{1-X}} \ , \quad X = D|k+u| \ , \\ \gamma &= -\frac{p}{2} Z^0 \ . \end{aligned} \tag{A-3.6}$$

For a vanishing value of Weinberg angle ($p = 0$) em field vanishes and only Z^0 field remains as a long range gauge field. Vacuum extremals for which long range Z^0 field vanishes but em field is non-vanishing are not possible.

The effective form of CP_2 metric for surfaces with 2-dimensional CP_2 projection

The effective form of the CP_2 metric for a space-time having vanishing em,Z^0, or Kähler field is of practical value in the case of vacuum extremals and is given by

$$\begin{aligned} ds^2_{eff} &= (s_{rr}(\frac{dr}{d\Theta})^2 + s_{\Theta\Theta}) d\Theta^2 + (s_{\Phi\Phi} + 2k s_{\Phi\Psi}) d\Phi^2 = \frac{R^2}{4}[s^{eff}_{\Theta\Theta} d\Theta^2 + s^{eff}_{\Phi\Phi} d\Phi^2] \ , \\ s^{eff}_{\Theta\Theta} &= X \times \left[\frac{\epsilon^2(1-u^2)}{(k+u)^2} \times \frac{1}{1-X} + 1 - X \right] \ , \\ s^{eff}_{\Phi\Phi} &= X \times \left[(1-X)(k+u)^2 + 1 - u^2 \right] \ , \end{aligned} \tag{A-3.7}$$

and is useful in the construction of vacuum imbedding of, say Schwartchild metric.

Topological quantum numbers

Space-times for which either em, Z^0, or Kähler field vanishes decompose into regions characterized by six vacuum parameters: two of these quantum numbers (ω_1 and ω_2) are frequency type parameters, two (k_1 and k_2) are wave vector like quantum numbers, two of the quantum numbers (n_1 and n_2) are integers. The parameters ω_i and n_i will be referred as electric and magnetic quantum numbers. The existence of these quantum numbers is not a feature of these solutions alone but represents a much more general phenomenon differentiating in a clear cut manner between TGD and Maxwell's electrodynamics.

The simplest manner to avoid surface Kähler charges and discontinuities or infinities in the derivatives of CP_2 coordinates on the common boundary of two neighboring regions with different vacuum quantum numbers is topological field quantization, 3-space decomposes into disjoint topological field quanta, 3-surfaces having outer boundaries with possibly macroscopic size.

Under rather general conditions the coordinates Ψ and Φ can be written in the form

$$\begin{aligned} \Psi &= \omega_2 m^0 + k_2 m^3 + n_2 \phi + \text{Fourier expansion} \ , \\ \Phi &= \omega_1 m^0 + k_1 m^3 + n_1 \phi + \text{Fourier expansion} \ . \end{aligned} \tag{A-3.8}$$

m^0,m^3 and ϕ denote the coordinate variables of the cylindrical M^4 coordinates) so that one has $k = \omega_2/\omega_1 = n_2/n_1 = k_2/k_1$. The regions of the space-time surface with given values of the vacuum parameters ω_i,k_i and

n_i and m and C are bounded by the surfaces at which space-time surface becomes ill-defined, say by $r > 0$ or $r < \infty$ surfaces.

The space-time surface decomposes into regions characterized by different values of the vacuum parameters r_0 and Θ_0. At $r = \infty$ surfaces n_2,ω_2 and m can change since all values of Ψ correspond to the same point of CP_2: at $r = 0$ surfaces also n_1 and ω_1 can change since all values of Φ correspond to same point of CP_2, too. If $r = 0$ or $r = \infty$ is not in the allowed range space-time surface develops a boundary.

This implies what might be called topological quantization since in general it is not possible to find a smooth global imbedding for, say a constant magnetic field. Although global imbedding exists it decomposes into regions with different values of the vacuum parameters and the coordinate u in general possesses discontinuous derivative at $r = 0$ and $r = \infty$ surfaces. A possible manner to avoid edges of space-time is to allow field quantization so that 3-space (and field) decomposes into disjoint quanta, which can be regarded as structurally stable units a 3-space (and of the gauge field). This doesn't exclude partial join along boundaries for neighboring field quanta provided some additional conditions guaranteing the absence of edges are satisfied.

For instance, the vanishing of the electromagnetic fields implies that the condition

$$\Omega \equiv \frac{\omega_2}{n_2} - \frac{\omega_1}{n_1} = 0 \ , \tag{A-3.9}$$

is satisfied. In particular, the ratio ω_2/ω_1 is rational number for the electromagnetically neutral regions of space-time surface. The change of the parameter n_1 and n_2 (ω_1 and ω_2) in general generates magnetic field and therefore these integers will be referred to as magnetic (electric) quantum numbers.

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