Quantum mechanical biology

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Abstract

This article focuses on the approach to biology in terms of quantum mechanics. Quantum biology is a hypothesis that allows experimental verification, and pretends to be a further refinement of the known gene-centric model. The state of the species is represented as the state vector in the Hilbert space, so that the evolution of this vector is described by means of quantum mechanics. Experimental verification of this hypothesis is based on the accuracy of quantum theory and the ability to quickly gather statistics when working with populations of bacteria. The positive result of such experiment would allow to apply to the living computational methods of quantum theory, which has not yet go beyond the particular "quantum effects".

1 Introduction

The main difficulty of biology is that we ourselves are its object. It seems that this loop will not allow biology to become a branch of physics even in perspective. Accumulated and continue to accumulate huge size data on "what happens in a living being", but there is no coherent theory to explain "why this is happening"(see, for example, computer models in [6]). The real explanation must give us the opportunity to build a plausible model of life as we build a model of the processes in inanimate nature, described by differential equations. Plausibility here we understand according to Turing: if we can not by external signs distinguish the model from a live prototype. Of course, it is not a simulation like android robots, but a model of life with reproduction and evolution, moreover, such a model, which would naturally fit into conventional physical models of nonliving environment of biological objects.

Attempts to build such a model are reduced, ultimately, to a good systematization of knowledge about "how things work", but their predictive power is small

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compared with models of relatively simple objects in physics. There is a huge gap between the description of the substance of the living cell on the physical or biochemical level and the desired holistic view of the living being; we do not know exactly what is a "living state" of the substance of the bacterial cell and why it is fundamentally different from inanimate. Mortality of living organisms compels us to appeal not only to individual animals, but to whole populations, species and entire biota, combining different species. We start from the genome centric point of view, according to which the main subject of biology are genes and genomes, whereas organisms are considered only as machines that serve to genes for its own replication ([4]).

Quantum physics gives us a unique mathematical apparatus that allows to transform biology into the branch of physics. This goal can not be achieved by other means, using only conventional concepts and methods of biology. For example, the quantum approach makes it easy to combine individual life with the life of the whole population and species. The concept of quantum biology gives hope to see how the evolutionary level is associated with biochemical processes in a single organism, in particular, with reliably established quantum effects, such as dephasing assisted transport in FMO complex in green sulphur bacteria, or avian magneto reception. Probabilistic nature of biological processes is consistent with the spirit of the quantum theory, which predicts only probabilities of events.

Quantum biology is yet a hypothesis, and all its advantages described below can become a reality only after the experimental verification of the main thesis. This requires clarification of a number of details that will be discussed further.

Central concept of quantum biology is the concept of life force of the genome, which is treated as a complex number - quantum amplitude. Its main feature: the linear character of the change with time, can be experimentally tested in biology. A necessary condition for such an experiment - a precise definition of the generalized genotype of species; its fulfillment is realistic and it seems to be quite achievable. Possibility of crucial experiment is related to rigid nature of the predictions of quantum theory. Such testing can be done on bacterial populations, and the populations of more highly beings; in the second case the difficulty is the correct definition of a generalized genome as units of biological process.

2 The amplitude as the life force of the genome

The basis of the scientific approach - the collection of statistics in experiments in biology meets fundamental difficulties. Experimental samples are - living beings, the number of which is limited, in contrast to inanimate objects. There are also ethical constraints in the case of higher beings to which we ourselves belong. It is necessary to keep the probability of key events $|i\rangle$ in the form of numbers p_i in the model, so that at any moment we might refer to these numbers and calculate the probability of the desired event theoretically.

The model must also include the rate of change of these probabilities, i.e. dynamics. Finally, we must be able to operate with many particles of the whole body, not just with individual atoms. Each outcome $|i\rangle$ must include the states of the set of atoms, molecules, and the state of photons. This requirement is called a scalability of the model.

Here we have no better choice but to use the language of quantum theory based on the concept of the amplitudes, i.e., numbers of the form $z = r\ exp(i\phi)$, where r is a real non-negative number, called module, and ϕ is a real number called amplitude. The amplitude is always connected with the probability by Born formula

$$p = r^2. \tag{1}$$

The amplitude may be a function of any basic (classical) state of any arbitrary complex ensemble of particles, or a function of any process that involves such ensembles, including not only matter, but also light (photons). For example, we can talk about the magnitude of such an event, that the ensemble, consisting of $n_1, n_2, \ldots, n_k$ atoms of certain chemical elements $e_1, e_2, \ldots, e_k$ occupies the determined spatial position $r_1, r_2, \ldots, r_n$, where $r_j = (x_j, y_j, z_j)$ are the coordinates of atom number $j = 1, 2, \ldots, n$; $n = \sum_i n_i$. It is possible to consider the amplitude of the transition of this ensemble from one of such positions to the other.

If the number n of real particles increases, the number of basis states of the system increases exponentially, so the application of quantum mechanics always requires a description of the states with the help of the semantics of the discipline, for example, in chemistry we will focus on the ortho- or para-hydrogen, or isomers of the enzyme molecule. Semantics of states is a way to deal with an insurmountable barrier of complexity that inevitably arises when we use the conventional coordinates of the particles. This is especially true for biology because a living cell is constantly " breathing " and moves. This precludes the use of standard physical precision instruments associated with precise coordinates, such as a scanning tunneling microscope for in vivo experiments.

It is impossible to give a mathematically precise definition of a living creature. We consider only living beings, consisting of cells which can multiply in the inanimate environment forming populations, which are composed of independent individuals. Independence we understand as the ability for one or a few creatures to restore the population after removing any other individuals. Natural integral characteristic of living - its DNA codes, which we take as the basic states of any species. Such a code can be further supplemented by hidden variables, such as bits encoding one or the other isomer, the spin states of atoms or photons of electromagnetic field associated with the cell. In what follows, genome is understood in this extended sense.

Only genome may play a role of the argument g of the wave function Ψ. But what will be the quantum probability $p(g) = |\Psi(g)|^2$? In physics it is - the probability of finding the particle at the point g. In chemical physics it is - the probability for a molecule to obtain some configuration of isomer. We always treat the probability

$p(g)$ as the fraction of such uniform objects for which the classical state g takes place. In biology the probability $p(g)$ must be the fraction of such creatures, which genome is g. Of course, to make any biological conclusions we must average the density on genomes $p(g)$ over a large number of generations; this will exclude the random fluctuations caused by abrupt changes that could distort the overall picture.

The set of all known genomes is available for direct manipulation; it allows to apply the methods of quantum physics. Biology, in its gene-centric form, is thus within the scope of efficient classical algorithms that implement the principle of quantum interference of amplitudes. This is an area in which quantum mechanics is able to reliably predict the outcome of a statistical experiment. (Outside of this area is, for example, the project of Feynman scalable quantum computer.) The amplitude is a complex number, which is obtained by summing the contributions from all paths leading to that state (see a short explanation of quantum mechanics in [2]). Exponential barrier of complexity mentioned above can be overcome only if it is assumed that the number of states is accessible for direct manipulation.

Biologically this means the following. We treat the amplitude as numerical expression of the "life force" of the genome. The state of life, with all its biochemical details, is simply the elementary box of very complex division of all possible classical states of matter, such that the falling into such a box ensures the "living state" for a given peace of initially inanimate matter. And this cell is so huge that its size can compensate the monstrous number of possible combinations of molecules that make up the creature. The life arises when the configuration of a matter appears in this box, and the probability of such event is large. In the world with genomes the realization of random combinations of molecules is impossible; only that combinations takes place, which leads to some of such a boxes.

If quantum biology is true, live becomes a class of amazing physics objects, for which the principle of interference in irregular systems allows an accurate computations.

Let we have a set $G = \{g_1, g_2, \ldots, g_N\}$ of classical states of some object S, which we want to treat as quantum. In our case S is the genome of some species, $G = \{g_1, g_2, \ldots, g_N\}$ are all possible varieties of this genome on some population. Quantization procedure consists in the transition from G to the space $\mathcal{L}(G)$ of formal linear combinations of the form $\Psi = \sum\limits_j \lambda_j g_j$ with elements from G and complex numbers λ_j. Quantization procedure can be briefly written as follows:

$$G \longrightarrow \mathcal{L}(G).$$

This procedure is the essence of quantum mechanics. Elements of $\mathcal{L}(G)$ are called "psi-functions" and are denoted by the letter Ψ. They behave as a vector: we can add and multiply them by numbers, as well as to find the scalar product according to the standard rules of algebra: $\psi'\psi'' = \sum_j \bar{\lambda}'_j \lambda''_j$, where the bar is a complex conjugation. Linear operations on vectors correspond to some imaginary operations on populations in biology. It can be assumed that the addition of state vectors reflects

the mechanical merger of the two populations into one. For a correct summation of psi-functions, we must make sure that possible genomes of these two populations would coincide. In practice, this requirement is difficult to achieve, since the genomes of different populations differ from each other. Note that the sum of arbitrary state vectors are typically difficult to implement in the well-studied quantum mechanics as well.

Nevertheless, the experiment to test the linearity of biological evolution can be arranged if to operate with different populations of the same species, for example a certain type of bacteria. Population here should be interpreted as a certain quantum state (wave function) of the species.

In fact, the very Hilbert space of quantum states $\mathcal{H}$ has a virtual character. In the ideal case we have only one state vector Ψ but not the whole space. The issue is that we do not know exactly the vector Ψ. In quantum mechanics of one-two particles there is the procedure of quantum tomography, which allows to restore the vector Ψ provided we have a lot of its copies; in biology this way is closed. We are not able to have even two identical populations. We can only partially determine the type of the state vector of the population, in order then to theoretically predict its evolution. All other state vectors are imaginary. But quantum approach requires that we not only pointed out how the state vector Ψ changes with time: $\Psi(t)$, but how all other vectors Ψ' change, if they represent the populations. We will see that this change of state vectors must be very tightly coordinated with each other - this follows from the fact that the evolution operator $U_t : \ \Psi(0) \longrightarrow \Psi(t)$, must be unitary, that is it must preserve the length of all vectors.

If the vector $\Psi = (a_1, a_2, \ldots, a_N)$ is normalized to unity, then $|a_j|^2$ is the probability for the system in the state Ψ, to get into the state g_j after measurement (Born rule). The measurement is the inverse process to quantization. It has the character of a random variable with values of g_j and the probability distribution $p_j = |a_j|^2$. Biologist may assume that p_j is proportional to the number of carriers of the genome g_j in the population. Then, the measurement result will be a simple life of a particular individual in a given population.

Squared molule of the wave function $|\Psi(g)|^2$ is the number of individuals with the genome g. What does it mean for one single individual that has this genome? The more "clones" it has, the higher is its viability[1]. So, psi-function, which is used to reflect the state of the entire population, also characterizes one, separately taken individual. But it is an abstract individual, which characterizes the entire population as a whole. If we want to apply this method to the study of a particular individual, conclusions will be valid only in so far that this individual is a typical representative of the population. Abstract living creature - a typical representative of the species is similar to a typical electron. A single electron wave function describes, in fact, whole

[1]Of course, this is only valid at a given time. To make some biological findings, we have averaged the number of individuals over the adequate period of time. Otherwise, it may happen that a mutation that leads, for example, the conversion of grasshoppers in the locust, is a step towards increasing the viability, although after a long time, this mutation is fatal.

ensemble of electrons, which can be prepared sequentially in one and the same state. The statistical nature of the wave function implies precisely the ensemble approach, rather than a description of a specific individual particle.

Let the object of our study S is a complex system consisting of two disjoint parts $S = S_1 \cup S_2$, so that the set of classical states of S_1 and S_2 is $G_1 = \{g_1^1, g_2,^1, \ldots, g_l^1\}$, and $G_2 = \{g_1^2, g_2,^2, \ldots, g_s^2\}$ correspondingly. Then G is the Cartesian product $G = G_1 \times G_2$, consisting of all pairs (g^1, g^2), such that $g^1 \in G_1,\ g^2 \in G_2$.

For example, S_1 and S_2 may be separate parts of the same genome. The result of quantization of G, $\mathcal{L}(G)$ is then called the tensor product of quantum spaces of states for subsystems $G_1 \quad G_2$: $\mathcal{L}(G) = \mathcal{L}(G_1) \bigotimes \mathcal{L}(G_2)$. Hence $N = ls$. We see that the dimension of space of states for growing number of particles will grow as exponential. Hence, there is no hope of getting something useful in biology, while remaining within the Hilbert spaces, rigidly associated with specific particles that make up a living organism. Quantum mechanics gives the general method of predicting the behavior of complex systems.

What is the "evolution" in quantum physics? If genomes of living creatures change merely as a result of systematic "training" (in the spirit of Lamarck) we would call the evolution the simple dependence of the genome from the time: $g(t) \in G$. This is the classical description of the evolution. One would think that in quantum terms the "evolution" means the time dependence of the psi-vector: $\Psi = \Psi(t)$. This is not quite true. Quantum mechanics treats the evolution as the operator, which acts on all possible quantum states Ψ simultaneously! This operator must be, at first, linear, and at second it must preserve the length of each vector. The first requirement is not subject to any justification, except for precedent. In physics it worked, and should work in biology. If we do not require linearity, we'll get a decoration rather than a working tool. The second requirement follows from the Born rule. The evolution operator has the following form:

$$\Psi(t) = exp(-iHt)\Psi(0). \tag{2}$$

Here H is Hermitian operator in $\mathcal{L}(G)$, called Hamiltonian. The formula (2) is equivalent to Shoedinger equation (it describes the general solution of that equation), in physics it is used for computation of the evolution of "pure states" that are vectors in Hilbert space. In biology, " evolution " of the population must also be described by this equation, if only we can provide the necessary conditions, namely precisely define the set of classical states G. Populations S, for which the exact definition of G is possible, we call pure. Purity is a function of our knowledge of the mechanisms of biology. If we knew everything we would ensure that any population is pure, choosing appropriate G, and by choosing appropriate H, we could predict its future. Of course, this is impossible, since we ourselves belong to the human population, and full knowledge would lead to a logical paradox.

We can hardly hope to accurately determine the G for even the simplest population. The actual population will not be pure. This means that (the genome of) S is divided into two parts S_1 and S_2, and we know only one of them, for example, S_1,

the second part S_2 is hidden from us. We introduce a virtual ensemble consisting of fictional particles, which set of classical states is G, and the corresponding Hilbert space of quantum states $\mathcal{H}$, and we call this virtual ensemble the quantum kernel of a living being or of the population of living beings. Quantum kernel must have the following two properties: firstly, its evolution must be unitary, and secondly, the kernel must be compact enough to fit in the memory of our computers.

We will clarify the concept of the genome. At first, we will consider it as fully functional. This means that the genome contains all the genes necessary for the multiplication of individuals. Any species corresponds to the set of genomes $\bar{G} = \{G_1, G_2, \ldots, G_N\}$, which contains the constant part G_{common}, common for all genomes, whereas the rest part of genomes can vary in some limits, for example, in the framework of some set $\bar{G}_{var}$.

At second, every state of a particular species should include spatial location of individuals on the Earth's surface and inside it, that is the spatial coordinate x. Thus, under the genome we should understand the genome, equipped with spatial coordinate: (g, x), without mentioning it every time specifically.

We define the notion of life force of the genome g as the amplitude

$$\Psi(g) \tag{3}$$

of the state Ψ of the species, which this genome belongs to. Thus, the life force is a complex-valued function on the genomes.

Complex amplitude has the form $\Psi(g) = r(g)\ exp(i\phi(g))$. We treat $r(g)$ as the square root of the share of this genome in the population, or the density of population on this genome. The phase $\phi(g)$ of the state of species has the biological sense as well. Accordingly to quantum mechanics, the gradient of this phase $\nabla_{genome}\phi(g)$ is the aspiration of the genome to change in the framework of the set of admissible genomes $\bar{G}_{var}$. The aspiration to change is the real vector, every of which coordinates corresponds some variative part g'_{var} of the genome from the set $\bar{G}_{var}$ and shows the degree of aspiration of the initial genome g to this variative part. We emphasize that the aspiration to change is not an absolute characteristic of the genome, it depends on the state of species as a whole. The most important role is played here by the life force of genomes closer to g; the role of others will be far less.

Quantum mechanics puts stringent requirements on the states. They should form a Hilbert space, that is a linear space with the scalar product. It means that if Ψ_1 and Ψ_2 are two states of the same species, then their sum $\Psi_1 + \Psi_2$ as well as the result of multiplication by a constant $\lambda\Psi_1$ must be possible states of this species as well. The multiplication by a constant corresponds to the proportional growth of the population; hence the constant λ is determined by the normalization to the full probability 1.

Summation of states is more interesting. Practically it is convenient to consider the state of species as some population. Then the summation of states will correspond to the simultaneous deployment of two populations of the same species in the same physical space. Under laboratory conditions, for the populations of bacteria

by the coordinate x we can understand the relative coordinate inside the retort, because the absolute coordinate is at the disposal of the experimenter and can be made insignificant. Thus, the mechanical merger of two populations can serve as a good approximation to the sum of states. For the more highly organized species the coordinate will have more complex meaning.

The population density typically changes much faster along coordinates than on genomes. When taking gradient on genomes we then must average the population density over large time segments, on which the fluctuation of density caused by the fast movements of creatures in space will vanish. However, in some cases these movements may be slower than the change of genomes. For example, in the case very slow migration of the population when genomes can change significantly. Under mechanical merger of populations the time frame for averaging should be chosen long enough to smooth the density fluctuations that inevitably arise here. Dependence of the generalized genome of the spatial coordinates allows include in the consideration factors of an environment (see [12]).

3 Operator of evolution

We consider the evolution of the state of the species, which is not subject to gross interference from outside, but is only under the influence of relatively slowly varying external influences. This evolution is described in quantum physics by the unitary evolution operator U_t, which, acting on an arbitrary initial state $|\Psi(0)\rangle$, gives the final state obtained at the instant t : $|\Psi(t)\rangle$: $|\Psi(t)\rangle = U_t|\Psi(0)\rangle$. It is important that the evolution operator acts not only to one state, but to all possible initial states simultaneously. It gives the possibility to check the concept of quantum biology on experiment.

Let we be given two states of the form $|\Psi_1\rangle$ and $|\Psi_2\rangle$, which we treat as two different populations of the same species. The linearity of the evolutionary operator U_t means the following. If given the opportunity to separate two populations to evolve during the time t, and then merge them into one, the result will be the same as if we first merged them into one, and then gave this combined populations evolve over the same period t. In other words, the linearity is the commutativity of the diagram shown in the Figure 1.

Linearity is the nontrivial property of evolution, which can be checked in experiment. Its meaning is that the population does not react to the presence of other populations of the same species. This property, at first glance, contradicts common sense. Two populations are two different states of the same species. They differ according to the distribution of the life force on genomes, they have different state vectors $\Psi(g)$, different genome densities $|\Psi(g)|^2$ and different aspirations of genomes to change $\nabla\phi(g)$. We merge them in space so that they "interact " at an individual level. What will this lead to? Since the merger their evolution will be joint, and we will not be able to distinguish between these populations, if only they will not

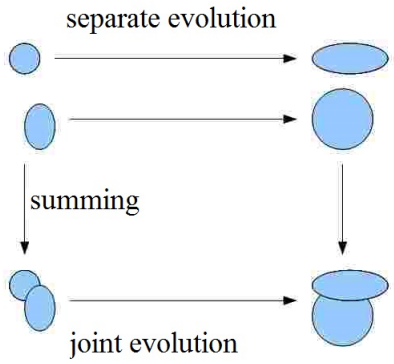

Figure 1: Linearity of evolution 1.

be able " to break up " in space after the intensive interference, such as bees do it, forming a new swarm. It is important that after the natural separation the fact of the previous " cohabitation " will not play any role. The population does not remember the past merging with other populations of the same species.

" Interaction" between individuals of the same species, which originally belonged to different populations can be quite dramatic, and be accompanied by the death of individual representatives of both populations during intraspecific competition. The difference in the aspirations of the genomes of two populations tend to cause large fluctuations in the populations of genomes (constructive and destructive interference of the wave functions). But as soon as again populations disperse in space and direct contact between their representatives stop the memory of conflicts of cohabitation will completely disappear (see. Figure 2).

Mass mortality of individuals of one of the populations in contact with other populations of the same species is clearly observed in the experiments. The illusion of contradiction with linearity of the evolution is explained as follows. The first possible reason: superficial determining the causes of death, which lie in the adaptation to changing environmental conditions (in the quantum representation this is the interference picture of the dynamics). Direct and apparent murder of individuals gives the same effect for the wave function of the population, but being emotionally charged, masks the true, the interference mechanism of evolution. The second reason: incorrect definition of the population, when the carrier of genome is considered as extremely autonomous living being, and not a small community (clan - see below), which is necessary to support the existence of the genome within a few generations, sufficient for its expression. This error leads to an incorrect definition of the wave function itself.

For the separation of populations after merger we can use along with the aspi-

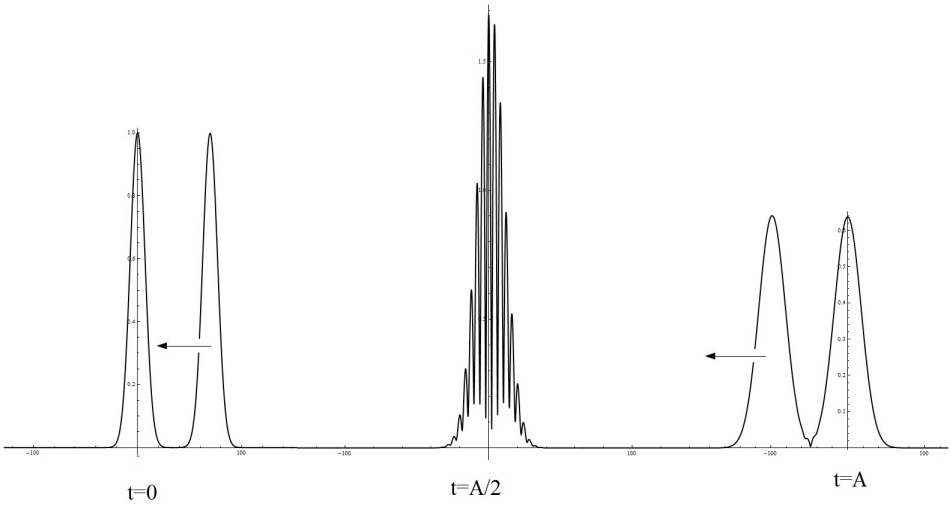

Figure 2: Linearity of evolution 2. The superposition of two wave functions: both Gaussian evolve independently of each other, it becomes clear after their divergence. The complex nature of the total wave function at the "meeting" is the result of interference; physical interaction is absent.

ration to change the coordinates (recall that our genome contains coordinates) and also the aspiration to change the nucleotide part of the genome. It is only necessary at the beginning to create a population in which the aspiration to change varies greatly. In this case, the separation of populations after co-evolution occurs naturally. It concerns bacteria, but also more highly organized forms, such as migratory birds or fish.

"Interaction" at an individual level has not in fact the sense that this term has in physics. Biological "interaction" of individuals is only the interference effect originating from the quantum dynamics, which describes the evolution of the species. True interaction, which physical roots must be sought - is the interaction of genes. This true interaction goes at the level of a single individual of the species, but not a specific; this is an abstract individual, which characterizes the species as a whole. This true interaction is represented as a very subtle process at the level of a single organism. It should be described as the evolution of the state vector in the functional space of the genome of this species. This is what opens the door to quantum "effects", which are studied in physics, and which are not at all exotic, but constitute the essence of biological evolution.

This situation is unusual for the biologist. Of course, some individuals interact closely in a competitive relationship, exchanging matter and photons of electromagnetic field. But these physical interactions can be represented in the form of the

potential between the parts of the body, if we add to this intra-organismic process also interference of the wave function of the population. The wave function of the species can be thought of as a state of the individual organism, typical for the species. In quantum mechanics, there are various bases and conversion operators that convert local interactions in non-local, and vice versa, for example, a canonical transformation or transform of Jordan-Wigner. Such transforms radically simplify the picture of the evolution after the transition to the new coordinates in the Hilbert space of states. The linearity of the evolution can not be inferred from the arsenal of physics, because we will not be able to overcome the barrier of complexity of biological objects. It makes sense to discuss the use of mathematical apparatus at the level of biological objects only if we take the general concept of quantum biology, consisting in linear evolution. The concept of quantum biology can only be verified by experiment.

4 Functional space of a single gene and the state of species

Any genome κ consists of the different genes:

$$\kappa = \kappa_1 \kappa_2 \dots \kappa_k. \tag{4}$$

Every part κ_j of the genome has its own functionality. We assume that these functionalities can be added with each other and can be multiplied by numbers so that they form complex Euclidean space $\mathcal{H}_j$, like genomes. The passage from the set of genes $\{\kappa_j\}$ to the whole genome κ corresponds to the quantum operation called tensor product.Tensor product of functional spaces of separate genes is Hilbert space of states of the corresponding species: $\mathcal{H} = \otimes_j \mathcal{H}_j$.

We can introduce trial values: the scalar product of individual variants of single genes that characterize their functional proximity. Let we be given two genes κ_j and κ'_j, responsible for a narrow range of functions corresponding to the number j, as vectors in the functional space $\mathcal{H}_j$, which is in charge of this functions. Scalar product $\langle \kappa_j | \kappa'_j \rangle$ of these vectors is the measure of their similarity. If we pass to the level of the whole genomes $\kappa = \kappa_1 \kappa_2 \dots \kappa_k,\ \kappa' = \kappa'_1 \kappa'_2 \dots \kappa'_k$ (the sign of tensor product is omitted) then the similarity of these genomes will be $\langle \kappa | \kappa' \rangle = \prod_{j=1}^{k} \langle \kappa_j | \kappa'_j \rangle$.Thus, even if some of these genes in the genome are not very different from each other genomes are almost orthogonal, i.e. their difference is nearly maximal.

A state of species usually has not the form of tensor product $\Psi_1 \otimes \Psi_2$ of states of genes contained in the genome of this species. It means that the state is usually entangled. Entangled state does not contain any state of the separate gene, it is common for all genes. The simplest example is EPR state of the form $\frac{1}{\sqrt{2}}(|0\rangle \otimes |0\rangle + |1\rangle \otimes |1\rangle)$. Here two qubits means two genes in the genome.

According to quantum concept, any interaction is only the interaction between individual genes or groups of genes. This interaction has the form of a real function $V(g_1, g_2, \ldots, g_l)$ on separate genes. Interaction of individual beings belonging to the same species, is reduced only to the interaction of individual genes. This means that the biological interaction with the physical root goes within the single body.

For determining the potential of interaction V it is necessary a) to define correctly the geometry of functional space $\mathcal{H}$, and b) transform the functions of genes to the relations in this space. For example, if there are two genes that are mutually inhibit the activity of each, we could ascribe to them the opposite vectors: $g, -g$ in some subspace $\mathcal{H}_j^0$ of the whole space $\mathcal{H}_j$. But if the function of the second gene is wider than the suppression of the first, we can assign to the second gene the vector in a larger space $\mathcal{H}_j^1$, so that only the projection of this vector onto $\mathcal{H}_j^0$ will be opposite to g. If the gene functions can be described in geometrical terms as in the case of genes regulating the synthesis of enzymes, we can rewrite their function in terms of the scalar product of vectors in $\mathcal{H}_j$ of low dimensionality. For these genes, this work seems really doable.

One can try to make a potential V, sequentially adding to it separate potentials of different groups of genes that provide some of the functions of the cell, such as ATP synthesis or transport of neurotransmitters. Then the state of living bacterial cell can be treated as a vector in the ground state space $\mathcal{H}$, accordingly to [8].

There are different types of genes that are not directly related to the potential energy of V; their function can not be reduced to the synthesis of individual proteins with functions uniquely dependent on their geometry. To create functional spaces for such genes we have to use the limited model of quantum dynamics (see. below). In any case, functional spaces of genes must allow to represent quantum dynamics by sufficiently simple Hamiltonians.

5 Quantum kernel

Functional space of the genome $\mathcal{H}$ can be very large. There is some evidence that it may include all the matter of living cells, so that not only gene effects but also the state of the cytoplasm, mitochondria, and cytoskeleton etc. up to the states of the photon field. Such a general model is needed to reflect the key property of the life: its stability (see [9], [10]).

At the same time, experience in the development of quantum theory shows that in all important for application cases it is possible to emulate the quantum dynamics of such complex systems in a small virtual ensemble whose Hamiltonian is quite simple. This possibility should be found for quantum biology as well. Such a small ensemble of virtual particles we call quantum kernel of the organism. Since we have agreed that we consider not a specific organism, but the virtual creature that is typical for this population, it is necessary to consider the quantum kernel as the compact model of the whole population. The situation is completely analogous to

quantum mechanics. There is no wave function $\Psi(x)$ of the single elecnron. The wave function implies that there is some classical device produces many uniformly prepared electrons in turn. We measure them, gather the statistics and then only can assert that this device prepared electrons with the wave function Ψ.

The picture of the evolution in terms of quantum kernel looks as follows. All physical interactions goes only inside the kernel. The interactions between living creatures is the result of interference in course of the quantum dynamics of the kernel. Each individual organism is the result of virtual measurement of the state of quantum kernel, if we treat the kernel as the model of the whole population. This view point is consistent with the existing theoretical models in biology associated with quantum physics.For example, self-consciousness interpreted by R. Penrose and S.Hameroffom ([7], [5]) as the "orchestrated act" of the measurement of the electrons in the microtubules of nerve cells. Conformity: "individual life - measurement of the wave function" is the most convenient interpretation of the concept of self-consciousness from the view point of physics, if such an interpretation is possible at all. Self consciousness is not our subject, but this correspondence is remarkable for the way to the life from the physics of atoms, which we are engaged.

One of the most convenient models for quantum kernel is Jaynes-Cummings-Hubbard model with phonon bath ([3]). This model includes a number of nodes, each of which is an atom or molecule, so that nodes can be in the ground or excited state, and share photons, which serve as the source of excitation. Nodes are experiencing dephasing effects from the environment (collision with the surrounding molecules or interaction with their own vibrational and rotational degrees of freedom). This model describes the dynamics of the density matrix of the atoms and the photon field, if the wavelength of the photons is not very small, the energy gap between the ground and excited states and phonon energy are small compared with the excitation energy.

This model can roughly describe the positive influence of thermal phonons to the conductivity of excitons along the chain of Bacteriochlorophyll molecules in Fenna-Matthews-Olson (FMO) complex in green sulphur bacteria. FMO- complex function is converting sunlight into chemical energy, where exciton transport plays a key role. The fact that this fundamental life process is described by a very compact quantum model, speaks in favor of quantum biology.

6 Generalization on biota

Representation of a species as a functional Hilbert space of the genome can be generalized to the biota, consisting of several species. To do this, we must take for the basis vectors all possible combinations of genes that enable the existence of biota in the inanimate environment. Each such combination of genes may be called meta genome. Meta-genome consists of genomes of various inter-dependent creatures, for example, it should include the genomes of plants that produce oxygen, the genomes

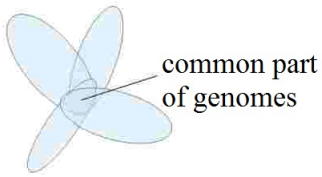

Figure 3: Extended genome of biota

of bacteria involved in the recycling of dead bodies and in the metabolism of higher animals, etc. Here we assume that we can somehow separate biota from the non-living environment. Hilbert space of biota $\mathcal{H}_{bio}$ consists of all linear combinations of meta-genes. Function spaces of various species will be included in $\mathcal{H}_{bio}$ almost as the tensor factors, only they have some common to all living beings part (see. Figure 3).

We do not discuss here the transformation of species, so that the history of species is conserved. The concept of functional space of biota may be interesting in terms of the expansion of the species genome, namely, the additional functional elements of the genome should be added as a tensor factors to the existing parts of the genome. If the environment surrounding some species, does not remember its evolution, then the evolution of this species is random process of Markovian type. In this case the evolution can be represented in the Lindblad form (see, for example, [11]). Even if in the beginning the state was pure, in the course of evolution the state becomes mixed. Operations with mixed states are economical in terms of computer models and accurately reflect the physics of simple processes.

But mixed states have little sense in evolitionary biology, because they are controlled by a random factor. Here we expressly exclude the possibility for ourselves to find out the deep mechanisms of biology. Get lost one of the main advantages of pure states - the decrease in entropy during expansion of the system. How to "raise" the evolution of mixed states to the evolution of the pure? If we can expand the system, and the environment has no memory (i.e., interaction with the environment is a Markov random process), it is possible. However, this method leads to an expansion of the dimension of the Hilbert space in any attempt to take into account the influence of environment. This increase in dimension will take place and when the influence of environment occurs in a purely unitary scheme of evolution. Since quantum kernel should be limited, such a path does not suit us.

We can save the limited size of the quantum kernel, if not expand the dimension of the state space, but change the semantics of the basis states. Memes (see the book ([4]) is a natural remedy for this. Memes - units of heredity that do not belong to the genome in the narrow sense (DNA). For example, the concepts of human language are memes. Feature of memetics is that we do not expand the space, and endow basis states in the old space with new meaning.

The description of evolution should not contain explicit random factor, as randomness has already been included in the psi-function. Using the tools of the density matrix - Lindblad superoperators is suitable only for clarification of some quantum effects, such as dephasing assisted transport in FMO- complex ([1]). We should

treat the biological evolution as unitary dynamics of the quantum kernel.

We must consider all living creatures as equal, despite the fact that it does not agree with biological classification. The possibility of an autonomous existence of a cteature means that its internal quantum state is a representation of the wave function of the biota, and not only of itself. Immiscibility of species does not contradict this. Simply each type has a specific set of possible genomes, and these sets for different species do not overlap. Quantum evolution will not mix species precisely because they do not share genomes.

Introduction of memes makes sense only is we identify them with the real physical objects and include memes in quantum kernel. In JCH model by memes we mean the states of electromagnetic field, e.g. photonic states. Here we should distinguish photonic states permitting quasi classical description and states of purely quantum form. The states of the first type can contain the large number of photon so that we can represent the field strength by classical wave. The purely quantum states contains the small number of photons. (There are coherent states, which have the medium character, though it is convenient to represent quantumly.) We can treat a quantum state Ψ of the field as an oracle, which for each classical state of the field x gives the complex amplitude $\Psi(x)$, with which this state is present in Ψ. Since every classical state of the field is the function of the form $A(r)$, where r is the ordinary coordinate, the wave function of the field Ψ is something immense. Fields can be included in physical models in two ways. The first is applicable for fields with many photons and the state is almost classical, with strength of the form $cos(\phi(x-ct))$ where the phase ϕ is exactly determiced just because there is a lot of photons and even their number is not determined. The second way is applicable when there are only a few photons and the state has the form of finite sum $\lambda_0|0\rangle + \lambda_1|1\rangle + ...$ (coherent states factually belong to this type because for them the states with many photons have negligible amplitudes). There is no simple terms for the description of intermediate states of the field. Memes probably belongs to these intermediate states of the field. The representation of memes in JCH model can be ensured by the appropriate semantics of photon states, where the realistic picture of dynamics of complex quantum states of the field can be found with only few photons in quantum kernel.

Coding states of the atoms in the states of the field is peculiar "memory of ashes". This technique makes it possible to simulate with a single quantum kernel series of successive generations, each of which consists of a mortal individuals. This is necessary to ensure the full reversibility of the dynamics that results from its unitary character. For living it means the conservation of the idendity of individual in time.

The main condition for the application of quantum mechanics to biological evolution is the independence of the carriers of genomes. This ensures that all physical interactions will be contained within the living creatures and visible "biological" interaction between individuals will be reduced to interference. In the idealized model, which we have considered so far, the creatures were autonomous, while in practice

it is not so. Only for bacterial populations we can assume autonomous, but also partially. For higher beings there is no autonomy. Sexual reproduction is already requires two beings of different sexes. For species with sexual reproduction under genome we should mean the genome of a germ cell in which meiosis has already occurred.

The notion of creature should be expanded to include all individuals required for its autonomous existence (e.g., bacteria needed for digestion). This "creature" can be called a clan. The size of the clan depends on the time during which we are going to consider the evolutionary process. In the extreme case, when the time increases indefinitely, the clan is such a part of the biota, which, if isolated (by elimination of all other animals) can survive by filling their offspring all oikoumene. For shorter periods of time and narrow set of species the size of the clan is determined by the possibility of replication of these species during this time frame without participation of the rest part of biota.

7 Conclusions

Quantum biology treats the living state in the form of the wave function on genomes, possibly extended by incorporating additional elements such as the electromagnetic field or spin states. For higher animals, including humans, the genome should include memes - objects that are not reducible to the nucleotide bases. Memes supposedly can be represented through the states of the electromagnetic field that have the property of inheritance.

The squared module of the wave function is the number of carriers of the genome, and the phase has the property that its gradient is the aspiration of the genome to change. All physical interactions that are responsible for life, should, ideally, take place within a single living creature, while relationships between individuals are completely described by the interference of the wave functions at their unitary evolution. The principle of linearity that underlies quantum biology can be checked in the proposed experiment, when merged together two different populations of the same species. Condition resulting from co-evolution within a certain time δt, must coincide with what happens as a result of the merger at the final of two independently developing populations.

The principle of linearity makes the independence of living beings the most fundamental property of the biological evolution. Independence has such a high priority that determines even the concept of a living being as such, and the line that separates the living from the nonliving environment.

Confirmation of the principle of linearity means the possibility of modeling the evolution using a virtual ensemble: the quantum kernel of creatures. Quantum kernel must be small enough to make possible to operate with it directly, without resorting to a complex computations. At the same time, the state of quantum kernel will be the quantum state of population of the independent individuals.

Quantum representation involves a high degree of autonomy of living beings; in order to achieve that it may be appropriate to combine some set of individuals of different species in the clan, which will be considered as a separate unit of the living. Competition for the best fitness (Darwinian) goes between clans and subject only to the laws of quantum interference of amplitudes. All physical interactions that are essential for the process of life, go within a single clan. These interactions can be interpreted as the interaction between different genes within one (ideal) organism representing the entire species (or the whole biota).

Catastrophic events in the interaction of living species associated with mass deaths of individuals, follow from renormalization of the wave function of biota in non-adiabatic evolution, accompanied by rapid changes in the environment. For the community of highly developed creatures such catastrophes are related to incorrect definition of clans. Conditions for the most progressive development are provided in the case of such a definition of clans, which makes evolution as close to the unitary as possible. This implies the complete independence of clans and removal of all obstacles to the development of their competitive, in particular, the elimination of factors of monopolization.

References

[1] F.Caruzo et al., "Highly efficient energy excitation transfer in light-harvesting complexes: The fundamental role of noise-assisted transport", Journal of Chemical Physics 131, p. 105106 (2009).

[2] R.Feynman, QED: The strange theory of light and matter, Princeton University Press, 1985.

[3] S.Huelga, M.Plenio, "Vibration, Quanta and Biology", Contemp. Phys. 54, 181 - 207 (2013).

[4] R.Dawkins, The Selfish Gene. New York City: Oxford University Press, 1976. ISBN 0-19-286092-5.

[5] Hameroff, S. "The "conscious pilot"dendritic synchrony moves through the brain to mediate consciousness". Journal of Biological Physics, 2009, 36 (1): 7193. doi:10.1007/s10867-009-9148-x

[6] J.Karr et al, A whole cell computational model predicts phenotype from genotype, Cell, 150, 389-401, July 20, 2012.

[7] S. Hameroff, R. Penrose, "Consciousness in the universe: A review of the Orch OR theory". Physics of Life Reviews (Elsevier), 2014, 11 (1): 3978. doi:10.1016/j.plrev.2013.08.002

[8] V.V.Ogryzko, "On two quantum approaches to adaptive mutations in bacteria", NeuroQuantology, 7(4), (2009).

[9] V.V.Ogryzko, "Erwin Schroedinger, Francis Crick and epigenetic stability", Biol Direct. 2008 Apr 17;3(1):15

[10] V.V.Ogryzko, Y.I.Ozhigov, Biologically inspired path to quantum computer, Proceedings of SPIE, vol. 9440, 2014.

[11] Plenio, M., et al., "Dephasing assisted transport: Quantum networks and biomolecules", New J. Phys. 10, 113019 (2008).

[12] S.E.Shnoll, Kosmofysiska faktorer i slumpmassiga processer, Stockholm: Svenska fysikarkivat, 2009 (Rus.). 388 . ISBN 978-91-85917-06-8