Supercomputers in Biological Cells

Using the largest computer in Japan - one of the most powerful in the world - research led by an MSU scientist has achieved breakthroughs in understanding how proteins are affected by realistic biological environments. The work, published in the current issue of eLife, is a significant step forward in simulating biology in a computer. [16]

Researchers led by Carnegie Mellon University physicist Markus Deserno and University of Konstanz (Germany) chemist Christine Peter have developed a computer simulation that crushes viral capsids. By allowing researchers to see how the tough shells break apart, the simulation provides a computational window for looking at how viruses and proteins assemble. [15]

IBM scientists have developed a new lab-on-a-chip technology that can, for the first time, separate biological particles at the nanoscale and could enable physicians to detect diseases such as cancer before symptoms appear. [14]

Scientists work toward storing digital information in DNA. [13]

Leiden theoretical physicists have proven that DNA mechanics, in addition to genetic information in DNA, determines who we are. Helmut Schiessel and his group simulated many DNA sequences and found a correlation between mechanical cues and the way DNA is folded. They have published their results in PLoS One. [12]

We model the electron clouds of nucleic acids in DNA as a chain of coupled quantum harmonic oscillators with dipole-dipole interaction between nearest neighbours resulting in a van der Waals type bonding. [11]

Scientists have discovered a secret second code hiding within DNA which instructs cells on how genes are controlled. The amazing discovery is expected to open new doors to the diagnosis and treatment of diseases, according to a new study. [10]

There is also connection between statistical physics and evolutionary biology, since the arrow of time is working in the biological evolution also.

From the standpoint of physics, there is one essential difference between living things and inanimate clumps of carbon atoms: The former tend to be much better at capturing energy from their environment and dissipating that energy as heat. [8]

This paper contains the review of quantum entanglement investigations in living systems, and in the quantum mechanically modeled photoactive prebiotic kernel systems. [7]

The human body is a constant flux of thousands of chemical/biological interactions and processes connecting molecules, cells, organs, and fluids, throughout the brain, body, and nervous system. Up until recently it was thought that all these interactions operated in a linear sequence, passing on information much like a runner passing the baton to the next runner. However, the latest findings in quantum biology and biophysics have discovered that there is in fact a tremendous degree of coherence within all living systems.

The accelerating electrons explain not only the Maxwell Equations and the Special Relativity, but the Heisenberg Uncertainty Relation, the Wave-Particle Duality and the electron's spin also, building the Bridge between the Classical and Quantum Theories.

The Planck Distribution Law of the electromagnetic oscillators explains the electron/proton mass rate and the Weak and Strong Interactions by the diffraction patterns. The Weak Interaction changes the diffraction patterns by moving the electric charge from one side to the other side of the diffraction pattern, which violates the CP and Time reversal symmetry.

The diffraction patterns and the locality of the self-maintaining electromagnetic potential explains also the Quantum Entanglement, giving it as a natural part of the Relativistic Quantum Theory and making possible to understand the Quantum Biology.

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Author: George Rajna

Preface

Scientists have discovered a secret second code hiding within DNA which instructs cells on how genes are controlled. The amazing discovery is expected to open new doors to the diagnosis and treatment of diseases, according to a new study. Ever since the genetic code was deciphered over 40 years ago, scientists have believed that it only described how proteins are made. However, the revelation made by the research team led by John Stamatoyannopoulos of the University of Washington indicates that genomes use the genetic code to write two separate languages. [10]

Jeremy England, a 31-year-old assistant professor at the Massachusetts Institute of Technology, has derived a mathematical formula that he believes explains this capacity. The formula, based on established physics, indicates that when a group of atoms is driven by an external source of energy (like the sun or chemical fuel) and surrounded by a heat bath (like the ocean or atmosphere), it will often gradually restructure itself in order to dissipate increasingly more energy. This could mean that under certain conditions, matter inexorably acquires the key physical attribute associated with life. [8]

We define our modeled self-assembled supramolecular photoactive centers, composed of one or more sensitizer molecules, precursors of fatty acids and a number of water molecules, as a photoactive prebiotic kernel system. [7]

The human body is a constant flux of thousands of chemical/biological interactions and processes connecting molecules, cells, organs, and fluids, throughout the brain, body, and nervous system. Up until recently it was thought that all these interactions operated in a linear sequence, passing on information much like a runner passing the baton to the next runner. However, the latest findings in quantum biology and biophysics have discovered that there is in fact a tremendous degree of coherence within all living systems. [5]

Quantum entanglement is a physical phenomenon that occurs when pairs or groups of particles are generated or interact in ways such that the quantum state of each particle cannot be described independently – instead, a quantum state may be given for the system as a whole. [4]

I think that we have a simple bridge between the classical and quantum mechanics by understanding the Heisenberg Uncertainty Relations. It makes clear that the particles are not point like but have a dx and dp uncertainty.

Supercomputers capture the crush in biological cells

Using the largest computer in Japan - one of the most powerful in the world - research led by an MSU scientist has achieved breakthroughs in understanding how proteins are affected by realistic biological environments. The work, published in the current issue of eLife, is a significant step forward in simulating biology in a computer.

"Biological processes that make life happen and cause diseases largely take place inside cells, which can be studied with microscopes and other techniques, but not in enough detail," said Michael Feig, an MSU professor of biochemistry and molecular biology who led the research project. "Our research has revealed unprecedented details about what exactly takes place inside biological cells, and how proteins in particular behave in their natural environment."

The team set out to examine whether the crowding in biological cells alters the properties of biological molecules and their ability to carry out their function. Armed with access to the "K computer," a supercomputer housed at the RIKEN Advanced Institute for Computational Science in Kobe, Japan, the research team was able to conduct computer simulations that model the cellular interior of a bacterium, and show a detailed view of how the various molecular components interact in a very dense environment.

"Our computer simulations were not too far away from simulating an entire cell in full atomistic detail," Feig said. "These simulations exceeding 100 million atoms are the largest simulations of this kind and are several orders of magnitude larger than what is typical research work today."

The powerful computer simulation led to a discovery that some proteins may not be as stable in very dense environments, losing the structures necessary for biological function. The research also found that this cellular environment might bring proteins involved in related biological processes closer to each other, which would enhance the overall efficiency of the cell in converting food to energy.

"Proteins in cells are squeezed together like people in the Tokyo subway during rush hour, where the crush violates personal space. But for proteins this is sometimes more welcome than we thought," Feig said.

A third major finding is that smaller molecules, such as those providing food and carrying energy, appear to be distracted by the many opportunities to interact with the larger proteins, affecting their biological function.

"This is a breakthrough achievement in understanding how the molecules that biochemists normally study interact in real life conditions," said Thomas Sharkey, chair of the Department of Biochemistry and Molecular Biology at MSU. "It will provide critical insights that will be used by people working to cure cancer and other diseases that depend on the cellular processes that are now much better understood."

But this is just the beginning of detailed whole-cell simulations, according to Feig.

"Future studies will aim to reach longer time scales, and to move towards larger and more complex cells, especially human cells, to better relate to human diseases," Feig said.

Feig collaborated with Yuji Sugita, a computational biochemist at the RIKEN Institute, in the research.

"Professor Feig and his collaborators in Japan have linked molecular activity with cellular activity, and this will be crucial for the next wave of understanding biology," Sharkey said. [16]

Computer simulation breaks virus apart to learn how it comes together

Researchers led by Carnegie Mellon University physicist Markus Deserno and University of Konstanz (Germany) chemist Christine Peter have developed a computer simulation that crushes viral capsids. By allowing researchers to see how the tough shells break apart, the simulation provides a computational window for looking at how viruses and proteins assemble. The study is published in the October issue of The European Physical Journal Special Topics.

"The concept of breaking something to see how it's made isn't new. It's what's being done at particle accelerators and in materials science labs worldwide—not to mention by toddlers who break their toys to see what's inside," said Deserno, a professor in the department of physics and member of the department's Biological Physics Initiative. "With a simulation we can build the virus, crush it and see what happens at a very high level of resolution."

Viral capsids, the protein shells that encapsulate and transport the viral genome, are one of nature's strongest nanocontainers. The shells are made when copies of capsid proteins spontaneously come together and assemble into a round, geometric shell. Understanding how these proteins come together to form capsids may help researchers to make similar nanocontainers for a variety of uses, including targeted drug delivery. Additionally, the simulation could fill a void for virologists, allowing them to study the stages of viral assembly that they aren't able to see experimentally.

Studying the self-assembly of viral capsids is difficult. Most viruses are too small—about 30 to 50 nanometers—and the capsid proteins come together too rapidly for their assembly to be seen using traditional microscopy. As an alternative, Deserno and colleagues thought that a better way to learn about capsid assembly might be to see what happens when an already formed capsid breaks apart.

To do this, Deserno and colleagues created a coarse-grained model of the Cowpea Chlorotic Mottle Virus (CCMV) capsid. In the simulation, they applied forces to the capsid and viewed how it responded to those forces. Their model is based on the MARTINI force field, a commonly used coarse-grained model, with an added stabilizing network within the individual proteins that compensated for the model's shortcomings in stabilizing a protein's folding geometry.

The CCMV capsid is made up of 180 identical proteins. In assembly, the proteins first form pairs, called dimers, and those dimers then join together at interfaces.

While the proteins are the same, the interfaces can be different. At some locations on the capsid, five proteins meet; at others, six. In the simulation, the researchers found that when force was applied to the capsid, the capsid would start to fracture at the hexametric interfaces first, indicating that those protein-protein contacts were weaker than those at the pentametric interfaces. In contrast, the pentametric contacts never broke. Since stronger connections assemble first and weaker ones assemble later, the researchers can use this information to begin to recreate how the capsid formed.

In the simulation, the researchers also found a likely explanation for a strange structural feature found in the CCMV capsid. At the center of the hexametric association site, the tail-ends of the six proteins come together and form a beta barrel. Beta barrels are coiled secondary protein structures.

The researchers believe that they act to provide further late-stage stabilization to the weaker hexametric interfaces. [15]

IBM lab-on-a-chip breakthrough aims to help physicians detect cancer

IBM scientists have developed a new lab-on-a-chip technology that can, for the first time, separate biological particles at the nanoscale and could enable physicians to detect diseases such as cancer before symptoms appear.

As reported today in the journal Nature Nanotechnology, the IBM team's results show size-based separation of bioparticles down to 20 nanometers (nm) in diameter, a scale that gives access to important particles such as DNA, viruses and exosomes. Once separated, these particles can potentially be analyzed by physicians to reveal signs of disease even before patients experience any physical symptoms and when the outcome from treatment is most positive. Until now, the smallest bioparticle that could be separated by size with on-chip technologies was about 50 times or larger, for example, separation of circulating tumor cells from other biological components.

IBM is collaborating with a team from the Icahn School of Medicine at Mount Sinai to continue development of this lab-on-a-chip technology and plans to test it on prostate cancer, the most common cancer in men in the U.S.

In the era of precision medicine, exosomes are increasingly being viewed as useful biomarkers for the diagnosis and prognosis of malignant tumors. Exosomes are released in easily accessible bodily fluids such as blood, saliva or urine. They represent a precious biomedical tool as they can be used in the context of less invasive liquid biopsies to reveal the origin and nature of a cancer.

The IBM team targeted exosomes with their device as existing technologies face challenges for separating and purifying exosomes in liquid biopsies. Exosomes range in size from 20-140nm and contain information about the health of the originating cell that they are shed from. A determination of the size, surface proteins and nucleic acid cargo carried by exosomes can give essential information about the presence and state of developing cancer and other diseases.

IBM's results show they could separate and detect particles as small as 20 nm from smaller particles, that exosomes of size 100 nm and larger could be separated from smaller exosomes, and that separation can take place in spite of diffusion, a hallmark of particle dynamics at these small scales. With Mt. Sinai, the team plans to confirm their device is able to pick up exosomes with cancerspecific biomarkers from patient liquid biopsies.

"The ability to sort and enrich biomarkers at the nanoscale in chip-based technologies opens the door to understanding diseases such as cancer as well as viruses like the flu or Zika," said Gustavo Stolovitzky, Program Director of Translational Systems Biology and Nanobiotechnology at IBM Research. "Our lab-on-a-chip device could offer a simple, noninvasive and affordable option to potentially detect and monitor a disease even at its earliest stages, long before physical symptoms manifest. This extra amount of time allows physicians to make more informed decisions and when the prognosis for treatment options is most positive."

With the ability to sort bioparticles at the nanoscale, Mt. Sinai hopes that IBM's technology can provide a new method to eavesdrop on the messages carried by exosomes for cell-to-cell

communications. This can elucidate important questions about the biology of diseases as well as pave the way to noninvasive and eventually affordable point-of-care diagnostic tools. Monitoring this intercellular conversation more regularly could allow medical experts to track an individual's state of health or progression of a disease.

"When we are ahead of the disease we usually can address it well; but if the disease is ahead of us, the journey is usually much more difficult. One of the important developments that we are attempting in this collaboration is to have the basic grounds to identify exosome signatures that can be there very early on before symptoms appear or before a disease becomes worse," said Dr. Carlos Cordon-Cardo, Professor and Chairman for the Mount Sinai Health System Department of Pathology. "By bringing together Mount Sinai's domain expertise in cancer and pathology with IBM's systems biology experience and its latest nanoscale separation technology, the hope is to look for specific, sensitive biomarkers in exosomes that represent a new frontier to offering clues that might hold the answer to whether a person has cancer or how to treat it."

Sorting bioparticles at the nanoscale

Lab-on-a-chip technologies have become an incredibly helpful diagnostic tool for physicians as they can be significantly faster, portable, easy to use and require less sample volume to help detect diseases. The goal is to shrink down to a single silicon chip all of the processes necessary to analyze a disease that would normally be carried out in a full-scale biochemistry lab.

Using a technology called nanoscale deterministic lateral displacement, or nano-DLD, IBM scientists Dr. Joshua Smith and Dr. Benjamin Wunsch led development of a lab-on-a-chip technology that allows a liquid sample to be passed, in continuous flow, through a silicon chip containing an asymmetric pillar array. This array allows the system to sort a microscopic waterfall of nanoparticles, separating particles by size down to tens of nanometers resolution. IBM has already scaled down the chip size to 2cm by 2cm, while continuing development to increase the device density to improve functionality and throughput.

Much like how a road through a small tunnel only allows smaller cars to pass while forcing bigger trucks to detour around, nano-DLD uses a set of pillars to deflect larger particles while allowing smaller particles to flow through the gaps of the pillar array unabated, effectively separating this particle "traffic" by size while not disrupting flow. Interestingly, IBM scientists noticed that nano-DLD arrays can also split a mixture of many different particle sizes into a spread of streams, much like a prism splits white light into different colors. The continuous flow nature of this technology circumvents stop-and-go batch processing typical of conventional separation techniques.

Leveraging IBM's vast semiconductor expertise with its growing capabilities in experimental biology, IBM scientists used manufacturable silicon processes to produce the nano-DLD arrays for their labon-a-chip device. As part of its on-going strategy, IBM researchers are working to increase the diversity of bioparticles that can be separated with their device, and improving the precision and specificity for real-world clinical applications. [14]

Scientists work toward storing digital information in DNA

Her computer, Karin Strauss says, contains her "digital attic"—a place where she stores that published math paper she wrote in high school, and computer science schoolwork from college.

She'd like to preserve the stuff "as long as I live, at least," says Strauss, 37. But computers must be replaced every few years, and each time she must copy the information over, "which is a little bit of a headache."

It would be much better, she says, if she could store it in DNA—the stuff our genes are made of.

Strauss, who works at Microsoft Research in Redmond, Washington, is working to make that sci-fi fantasy a reality.

She and other scientists are not focused in finding ways to stow high school projects or snapshots or other things an average person might accumulate, at least for now. Rather, they aim to help companies and institutions archive huge amounts of data for decades or centuries, at a time when the world is generating digital data faster than it can store it.

To understand her quest, it helps to know how companies, governments and other institutions store data now: For long-term storage it's typically disks or a specialized kind of tape, wound up in cartridges about three inches on a side and less than an inch thick. A single cartridge containing about half a mile of tape can hold the equivalent of about 46 million books of 200 pages apiece, and three times that much if the data lends itself to being compressed.

A tape cartridge can store data for about 30 years under ideal conditions, says Matt Starr, chief technology officer of Spectra Logic, which sells data-storage devices. But a more practical limit is 10 to 15 years, he says.

It's not that the data will disappear from the tape. A bigger problem is familiar to anybody who has come across an old eight-track tape or floppy disk and realized he no longer has a machine to play it. Technology moves on, and data can't be retrieved if the means to read it is no longer available, Starr says.

So for that and other reasons, long-term archiving requires repeatedly copying the data to new technologies.

Into this world comes the notion of DNA storage. DNA is by its essence an information-storing molecule; the genes we pass from generation to generation transmit the blueprints for creating the human body. That information is stored in strings of what's often called the four-letter DNA code. That really refers to sequences of four building blocks—abbreviated as A, C, T and G—found in the DNA molecule. Specific sequences give the body directions for creating particular proteins.

Digital devices, on the other hand, store information in a two-letter code that produces strings of ones and zeroes. A capital "A," for example, is 01000001.

Converting digital information to DNA involves translating between the two codes. In one lab, for example, a capital A can become ATATG. The idea is once that transformation is made, strings of DNA can be custom-made to carry the new code, and hence the information that code contains.

One selling point is durability. Scientists can recover and read DNA sequences from fossils of Neanderthals and even older life forms. So as a storage medium, "it could last thousands and thousands of years," says Luis Ceze of the University of Washington, who works with Microsoft on DNA data storage.

Advocates also stress that DNA crams information into very little space. Almost every cell of your body carries about six feet of it; that adds up to billions of miles in a single person. In terms of information storage, that compactness could mean storing all the publicly accessible data on the internet in a space the size of a shoebox, Ceze says.

In fact, all the digital information in the world might be stored in a load of whitish, powdery DNA that fits in space the size of a large van, says Nick Goldman of the European Bioinformatics Institute in Hinxton, England.

What's more, advocates say, DNA storage would avoid the problem of having to repeatedly copy stored information into new formats as the technology for reading it becomes outmoded.

"There's always going to be someone in the business of making a DNA reader because of the health care applications," Goldman says. "It's always something we're going to want to do quickly and inexpensively."

Getting the information into DNA takes some doing. Once scientists have converted the digital code into the 4-letter DNA code, they have to custom-make DNA.

For some recent research Strauss and Ceze worked on, that involved creating about 10 million short strings of DNA.

Twist Bioscience of San Francisco used a machine to create the strings letter by letter, like snapping together Lego pieces to build a tower. The machine can build up to 1.6 million strings at a time.

Each string carried just a fragment of information from a digital file, plus a chemical tag to indicate what file the information came from.

To read a file, scientists use the tags to assemble the relevant strings. A standard lab machine can then reveal the sequence of DNA letters in each string.

Nobody is talking about replacing hard drives in consumer computers with DNA. For one thing, it takes too long to read the stored information. That's never going to be accomplished in seconds, says Ewan Birney, who works on DNA storage with Goldman at the bioinformatics institute.

But for valuable material like corporate records in long-term storage, "if it's worth it, you'll wait," says Goldman, who with Birney is talking to investors about setting up a company to offer DNA storage.

Sri Kosuri of the University of California Los Angeles, who has worked on DNA information storage but now largely moved on to other pursuits, says one challenge for making the technology practical is making it much cheaper.

Scientists custom-build fairly short strings DNA now for research, but scaling up enough to handle information storage in bulk would require a "mind-boggling" leap in output, Kosuri says. With current technology, that would be hugely expensive, he says.

George Church, a prominent Harvard genetics expert, agrees that cost is a big issue. But "I'm pretty optimistic it can be brought down" dramatically in a decade or less, says Church, who is in the process of starting a company to offer DNA storage methods.

For all the interest in the topic, it's worth noting that so far the amount of information that researchers have stored in DNA is relatively tiny.

Earlier this month, Microsoft announced that a team including Strauss and Ceze had stored a record 200 megabytes. The information included 100 books—one, fittingly, was "Great Expectations"— along with a brief video and many documents. But it was still less than 5 percent the capacity of an ordinary DVD.

Yet it's about nine times the mark reported just last month by Church, who says the announcement shows "how fast the field is moving."

Meanwhile, people involved with archiving digital data say their field views DNA as a possibility for the future, but not a cure-all.

"It's a very interesting and promising approach to the storage problem, but the storage problem is really only a very small part of digital preservation," says Cal Lee, a professor at the University of North Carolina's School of Information and Library Science.

It's true that society will probably always have devices to read DNA, so that gets around the problem of obsolete readers, he says. But that's not enough.

"If you just read the ones and zeroes, you don't know how to interpret it," Lee says.

For example, is that string a picture, text, a sound clip or a video? Do you still have the software to make sense of it?

What's more, the people in charge of keeping digital information want to check on it periodically to make sure it's still intact, and "I don't know how viable that is with DNA," says Euan Cochrane, digital preservation manager at the Yale University Library. It may mean fewer such check-ups, he says.

Cochrane, who describes his job as keeping information accessible "10 years to forever," says DNA looks interesting if its cost can be reduced and scientists find ways to more quickly store and recover information.

Starr says his data-storage device company hasn't taken a detailed look at DNA technology because it's too far in the future.

There are "always things out on the horizon that could store data for a very long time," he says. But the challenge of turning those ideas into a practical product "really trims the field down pretty quickly." [13]

Second layer of information in DNA confirmed

Leiden theoretical physicists have proven that DNA mechanics, in addition to genetic information in DNA, determines who we are. Helmut Schiessel and his group simulated many DNA sequences and

found a correlation between mechanical cues and the way DNA is folded. They have published their results in PLoS One.

When James Watson and Francis Crick identified the structure of DNA molecules in 1953, they revealed that DNA information determines who we are. The sequence of the letters G, A, T and C in the famous double helix determines what proteins are made ny our cells. If you have brown eyes, for example, this is because a series of letters in your DNA encodes for proteins that build brown eyes. Each cell contains the exact same letter sequence, and yet every organ behaves differently. How is this possible?

Mechanical cues

Since the mid 1980s, it has been hypothesized that there is a second layer of information on top of the genetic code consisting of DNA mechanical properties.

Each of our cells contains two meters of DNA molecules, and these molecules need to be wrapped up tightly to fit inside a single cell. The way in which DNA is folded determines how the letters are read out, and therefore which proteins are actually made. In each organ, only relevant parts of the genetic information are read. The theory suggests that mechanical cues within the DNA structures determine how preferentially DNA folds.

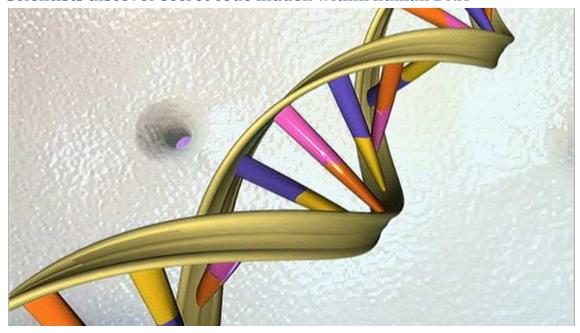
Simulation

For the first time, Leiden physicist Helmut Schiessel and his research group provide strong evidence that this second layer of information indeed exists. With their computer code, they have simulated the folding of DNA strands with randomly assigned mechanical cues. It turns out that these cues indeed determine how the DNA molecule is folded into so-called nucleosomes. Schiessel found correlations between the mechanics and the actual folding structure in the genome of two organisms—baker's yeast and fission yeast. This finding reveals evolutionary changes in DNA—mutations—that have two very different effects: The letter sequence encoding for a specific protein can change, or the mechanics of the DNA structure can change, resulting in different packaging and levels of DNA accessibility, and therefore differing frequency of production of that protein. [12]

Quantum entanglement between the electron clouds of nucleic acids in DNA

We model the electron clouds of nucleic acids in DNA as a chain of coupled quantum harmonic oscillators with dipole-dipole interaction between nearest neighbours resulting in a van der Waals type bonding. Crucial parameters in our model are the distances between the acids and the coupling between them, which we estimate from numerical simulations . We show that for realistic parameters nearest neighbour entanglement is present even at room temperature. We quantify the amount of entanglement in terms of negativity and single base von Neumann entropy. We find that the strength of the single base von Neumann entropy depends on the neighbouring sites, thus questioning the notion of treating single bases as logically independent units. We derive an analytical expression for the binding energy of the coupled chain in terms of entanglement and show the connection between entanglement and correlation energy, a quantity commonly used in quantum chemistry. [11]

Scientists discover secret code hidden within human DNA



This undated handout illustration shows the DNA double helix (AFP Photo)This undated handout illustration shows the DNA double helix (AFP Photo)

Scientists have discovered a secret second code hiding within DNA which instructs cells on how genes are controlled. The amazing discovery is expected to open new doors to the diagnosis and treatment of diseases, according to a new study.

Ever since the genetic code was deciphered over 40 years ago, scientists have believed that it only described how proteins are made. However, the revelation made by the research team led by John Stamatoyannopoulos of the University of Washington indicates that genomes use the genetic code to write two separate languages.

"For over 40 years we have assumed that DNA changes affecting the genetic code solely impact how proteins are made," said Stamatoyannopoulos, according to the press release. "Now we know that this basic assumption about reading the human genome missed half of the picture."

Scientists discovered that the second language instructs the cells on how genes are controlled, according to findings published in Science magazine on Friday. The study is part of the Encyclopedia of DNA Elements Project, also known as ENCODE.

DNA (Deoxyribonucleic acid) is a nucleic acid that is the main constituent of the chromosomes of all organisms, except some viruses. DNA is self-replicating, plays a central role in protein synthesis, and is responsible for the transmission of hereditary characteristics from parents to offspring.

The second language remained hidden for so long because one language is written on top of the other, scientists said.

Scientists already knew that the genetic code uses a 64-letter alphabet called codons. The research team discovered that some of the codons can have two meanings – one related to proteins, the other to gene control. Those codons were given the name 'duons.'

And it's those duons that are expected to change the way physicians interpret human genomes, and give clues for the treatments of diseases.

"The fact that the genetic code can simultaneously write two kinds of information means that many DNA changes that appear to alter protein sequences may actually cause disease by disrupting gene control programs or even both mechanisms simultaneously," said Stamatoyannopoulos.

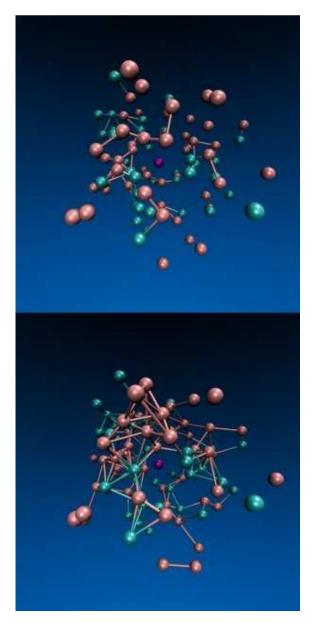
Speaking about the discovery, Stamatoyannopoulos said that the "new findings highlight that DNA is an incredibly powerful information storage device, which nature has fully exploited in unexpected ways." [10]

This Physicist Has a Groundbreaking Idea about Why Life Exists

"You start with a random clump of atoms, and if you shine light on it for long enough, it should not be so surprising that you get a plant," England said.

England's theory is meant to underlie, rather than replace, Darwin's theory of evolution by natural selection, which provides a powerful description of life at the level of genes and populations. "I am certainly not saying that Darwinian ideas are wrong," he explained. "On the contrary, I am just saying that from the perspective of the physics, you might call Darwinian evolution a special case of a more general phenomenon."

At the heart of England's idea is the second law of thermodynamics, also known as the law of increasing entropy or the "arrow of time." Hot things cool down, gas diffuses through air, eggs scramble but never spontaneously unscramble; in short, energy tends to disperse or spread out as time progresses. Entropy is a measure of this tendency, quantifying how dispersed the energy is among the particles in a system, and how diffuse those particles are throughout space. It increases as a simple matter of probability: There are more ways for energy to be spread out than for it to be concentrated.



A computer simulation by Jeremy England and colleagues shows a system of particles confined inside a viscous fluid in which the turquoise particles are driven by an oscillating force. Over time (from top to bottom), the force triggers the formation of more bonds among the particles.

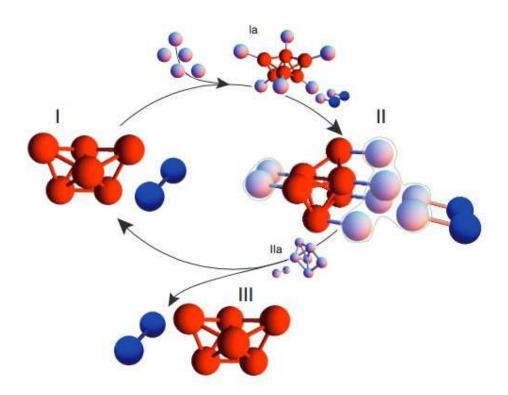
Thus, as particles in a system move around and interact, they will, through sheer chance, tend to adopt configurations in which the energy is spread out. Eventually, the system arrives at a state of maximum entropy called "thermodynamic equilibrium," in which energy is uniformly distributed. A cup of coffee and the room it sits in become the same temperature, for example.

Although entropy must increase over time in an isolated or "closed" system, an "open" system can keep its entropy low — that is, divide energy unevenly among its atoms — by greatly increasing the entropy of its surroundings. In his influential 1944 monograph "What Is Life?" the eminent quantum physicist Erwin Schrödinger argued that this is what living things must do. A plant, for example, absorbs extremely energetic sunlight, uses it to build sugars, and ejects infrared light, a much less

concentrated form of energy. The overall entropy of the universe increases during photosynthesis as the sunlight dissipates, even as the plant prevents itself from decaying by maintaining an orderly internal structure.

Self-replication (or reproduction, in biological terms), the process that drives the evolution of life on Earth, is one such mechanism by which a system might dissipate an increasing amount of energy over time.

As England put it, "A great way of dissipating more is to make more copies of yourself."



Self-Replicating Sphere Clusters: According to new research at Harvard, coating the surfaces of microspheres can cause them to spontaneously assemble into a chosen structure, such as a polytetrahedron (red), which then triggers nearby spheres into forming an identical structure.

Scientists have already observed self-replication in nonliving systems. According to new research led by Philip Marcus of the University of California, Berkeley, and reported in Physical Review Letters in August, vortices in turbulent fluids spontaneously replicate themselves by drawing energy from shear in the surrounding fluid. And in a paper in Proceedings of the National Academy of Sciences, Michael Brenner, a professor of applied mathematics and physics at Harvard, and his collaborators present theoretical models and simulations of microstructures that self-replicate. These clusters of specially coated microspheres dissipate energy by roping nearby spheres into forming identical clusters. "This connects very much to what Jeremy is saying," Brenner said. [8]

Photoactive Prebiotic Systems

We propose that life first emerged in the form of such minimal photoactive prebiotic kernel systems and later in the process of evolution these photoactive prebiotic kernel systems would have produced fatty acids and covered themselves with fatty acid envelopes to become the minimal cells of the Fatty Acid World. Specifically, we model self-assembling of photoactive prebiotic systems with observed quantum entanglement phenomena. We address the idea that quantum entanglement was important in the first stages of origins of life and evolution of the biospheres because simultaneously excite two prebiotic kernels in the system by appearance of two additional quantum entangled excited states, leading to faster growth and self-replication of minimal living cells. The quantum mechanically modeled possibility of synthesizing artificial self-reproducing quantum entangled prebiotic kernel systems and minimal cells also impacts the possibility of the most probable path of emergence of photocells on the Earth or elsewhere. We also examine the quantum entangled logic gates discovered in the modeled systems composed of two prebiotic kernels. Such logic gates may have application in the destruction of cancer cells or becoming building blocks of new forms of artificial cells including magnetically active ones.

Significance Statement

Our investigated self-assembly of molecules towards supramolecular bioorganic and minimal cellular systems depends on the quantum mechanics laws which induce hydrogen and Van der Waals bindings (Tamulis A, Grigalavicius, M, Orig Life Evol Biosph 41:51-71, 2011).

In the work presented here, quantum entanglement takes the form of a quantum superposition of the active components in synthesized self-assembling and self-replicating living systems. When a quantum calculation of an entangled system is made that causes one photoactive biomolecule of such a pair to take on a definite value (e.g., electron density transfer or electron spin density transfer), the other member of this entangled pair will be found to have taken the appropriately correlated value (e.g., electron density transfer or electron spin density transfer). In our simulations, the separation distance of supramolecular bio systems changes took place during geometry optimization procedures, which mimic real-world intermolecular interaction processes.

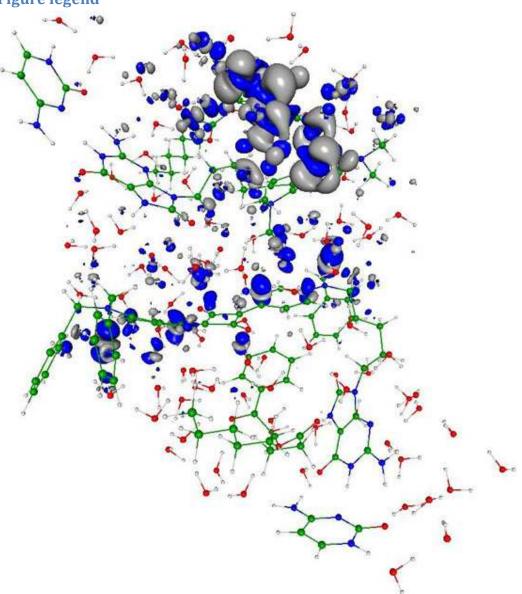
Our discovered phenomenon of the quantum entanglement in the prebiotic systems enhance the photosynthesis in the proposed systems because simultaneously excite two prebiotic kernels in the system by appearance of two additional quantum entangled excited states (Tamulis A, Grigalavicius M, Baltrusaitis J, Orig Life Evol Biosph 43:49-66, 2013; Tamulis A, Grigalavicius M, Krisciukaitis S (2014), J Comput Theor Nanos, 11, 1597-1608, 2014; Tamulis A, Grigalavicius M, 8:117-140, 2014.). We can propose that quantum entanglement enhanced the emergence of photosynthetic prebiotic kernels and accelerated the evolution of photosynthetic life because of additional absorbed light energy, leading to faster growth and self-replication of minimal living cells.

We can state that: Livings are self-assembled and self-replicating wet and warm stochastically moving supramolecular systems where quantum entanglement can be continuously generated and destroyed by non-equilibrium effects in an environment where no static entanglement exists; quantum entanglement involve the biomolecule inside one living or between other neighboring livings.

This warm quantum coherence is basic for the explanation of DNA stability and for the understanding of brain magnetic orientation during migration in more than 50 species of birds, fishes and insects. Exists experimental evidence for quantum-coherent is used for more efficient light-harvesting in plant photosynthesis. Quantum entanglement exists in supramolecules determining the sense of smell and in the brain neurons microtubules due to quantum vibrations.

In the work presented here, we started to design and quantum mechanical investigations of the molecular logical devices which are useful for construction of nano medicine biorobots against the molecular diseases such a cancer tumors, and against the new kinds of synthesized microorganisms and nano guns.





You can see in the enclosed figure the quantum entanglement phenomenon in the closely self-assembled two synthesized protocell system due to the photo excited electron charge transfer from one protocell to another that leads to closer self-assembly and exchange of energy and information.

Visualization of the electron charge tunneling associated with the 6th (467.3 nm) excited state. The transition is mainly from squarine molecule of the first protocell situated in the bottom of this bi cellular system to precursor of fatty acid (pFA) molecule of the second subsystem (in the top) and little from the 1,4-bis(N,N-dimethylamino)naphthalene molecule (in the top-right) to the same pFA molecule of the second subsystem (in the top). The electron cloud hole is indicated by the dark blue color while the transferred electron cloud location is designated by the gray color.

As a result, these nonlinear quantum interactions compressed the overall molecular system resulting in a smaller gap between the HOMO and LUMO electron energy levels which allows enhanced tunneling of photo excited electrons from the sensitizer squarine and (1,4-bis(N,N-dimethylamino)naphthalene) to the pFA molecule resulting in its cleavage. The new fatty acid joins the existing minimal cell thus increasing it in size. After reaching some critical size, the minimal cell should divide (i.e. self-replicate) into two separate smaller minimal cells. [7]

Quantum Biology

Researchers have long suspected that something unusual is afoot in photosynthesis. Particles of light called photons, streaming down from the Sun; arrive randomly at the chlorophyll molecules and other light-absorbing 'antenna' pigments that cluster inside the cells of every leaf, and within every photosynthetic bacterium. But once the photons' energy is deposited, it doesn't stay random. Somehow, it gets channeled into a steady flow towards the cell's photosynthetic reaction centre, which can then use it at maximum efficiency to convert carbon dioxide into sugars. Quantum coherence in photosynthesis seems to be beneficial to the organisms using it. But did their ability to exploit quantum effects evolve through natural selection? Or is quantum coherence just an accidental side effect of the way certain molecules are structured? [6]

Quantum Consciousness

Extensive scientific investigation has found that a form of quantum coherence operates within living biological systems through what is known as biological excitations and biophoton emission. What this means is that metabolic energy is stored as a form of electromechanical and electromagnetic excitations. These coherent excitations are considered responsible for generating and maintaining long-range order via the transformation of energy and very weak electromagnetic signals. After nearly twenty years of experimental research, Fritz-Albert Popp put forward the hypothesis that biophotons are emitted from a coherent electrodynamics field within the living system.

What this means is that each living cell is giving off, or resonating, a biophoton field of coherent energy. If each cell is emitting this field, then the whole living system is, in effect, a resonating field-a ubiquitous nonlocal field. And since biophotons are the entities through which the living system communicates, there is near-instantaneous intercommunication throughout. And this, claims Popp, is the basis for coherent biological organization -- referred to as quantum coherence. This discovery

led Popp to state that the capacity for evolution rests not on aggressive struggle and rivalry but on the capacity for communication and cooperation. In this sense the built-in capacity for species evolution is not based on the individual but rather living systems that are interlinked within a coherent whole: Living systems are thus neither the subjects alone, nor objects isolated, but both subjects and objects in a mutually communicating universe of meaning. . . . Just as the cells in an organism take on different tasks for the whole, different populations enfold information not only for themselves, but for all other organisms, expanding the consciousness of the whole, while at the same time becoming more and more aware of this collective consciousness.

Biophysicist Mae-Wan Ho describes how the living organism, including the human body, is coordinated throughout and is "coherent beyond our wildest dreams." It appears that every part of our body is "in communication with every other part through a dynamic, tunable, responsive, liquid crystalline medium that pervades the whole body, from organs and tissues to the interior of every cell."

What this tells us is that the medium of our bodies is a form of liquid crystal, an ideal transmitter of communication, resonance, and coherence. These relatively new developments in biophysics have discovered that all biological organisms are constituted of a liquid crystalline medium. Further, DNA is a liquid-crystal, lattice-type structure (which some refer to as a liquid crystal gel), whereby body cells are involved in a holographic instantaneous communication via the emitting of biophotons (a source based on light). This implies that all living biological organisms continuously emit radiations of light that form a field of coherence and communication. Moreover, biophysics has discovered that living organisms are permeated by quantum wave forms. [5]

Information – Entropy Theory of Physics

Viewing the confined gas where the statistical entropy not needs the information addition is not the only physical system. There are for example quantum mechanical systems where the information is a very important qualification. The perturbation theory needs higher order calculations in QED or QCD giving more information on the system as in the chess games happens, where the entropy is not enough to describe the state of the matter. The variation calculation of chess is the same as the perturbation calculation of physics to gain information, where the numbers of particles are small for statistical entropy to describe the system. The role of the Feynman graphs are the same as the chess variations of a given position that is the depth of the variations tree, the Information is the same as the order of the Feynman graphs giving the Information of the micro system. [9]

Information - Entropy Theory of Life

There is also connection between statistical physics and evolutionary biology, since the arrow of time is working in the biological evolution also.

The Fluctuation Theorem says that there is a probability that entropy will flow in a direction opposite to that dictated by the Second Law of Thermodynamics. In this case the Information is growing that

is the matter formulas are emerging from the chaos. So the Weak Interaction has two directions, samples for one direction is the Neutron decay, and Hydrogen fusion is the opposite direction. The living biological systems have also entropy lowering and information growing direction by building more complicated or entangled molecules, governed by the quantum mechanics and the general weak interaction. On the other hand there is the arrow of time; the entropy growing is lowering the information by dissipating these entangled or otherwise connected biomolecules, aging the living systems.

Creating quantum technology

Another area of potential application is in quantum computing. The long-standing goal of the physicists and engineers working in this area is to manipulate data encoded in quantum bits (qubits) of information, such as the spin-up and spin-down states of an electron or of an atomic nucleus. Qubits can exist in both states at once, thus permitting the simultaneous exploration of all possible answers to the computation that they encode. In principle, this would give quantum computers the power to find the best solution far more quickly than today's computers can — but only if the qubits can maintain their coherence, without the noise of the surrounding environment, such as the jostling of neighboring atoms, destroying the synchrony of the waves. [6]

Quantum Entanglement

Measurements of physical properties such as position, momentum, spin, polarization, etc. performed on entangled particles are found to be appropriately correlated. For example, if a pair of particles is generated in such a way that their total spin is known to be zero, and one particle is found to have clockwise spin on a certain axis, then the spin of the other particle, measured on the same axis, will be found to be counterclockwise. Because of the nature of quantum measurement, however, this behavior gives rise to effects that can appear paradoxical: any measurement of a property of a particle can be seen as acting on that particle (e.g. by collapsing a number of superimposed states); and in the case of entangled particles, such action must be on the entangled system as a whole. It thus appears that one particle of an entangled pair "knows" what measurement has been performed on the other, and with what outcome, even though there is no known means for such information to be communicated between the particles, which at the time of measurement may be separated by arbitrarily large distances. [4]

The Bridge

The accelerating electrons explain not only the Maxwell Equations and the Special Relativity, but the Heisenberg Uncertainty Relation, the wave particle duality and the electron's spin also, building the bridge between the Classical and Quantum Theories. [1]

Accelerating charges

The moving charges are self maintain the electromagnetic field locally, causing their movement and this is the result of their acceleration under the force of this field. In the classical physics the charges will distributed along the electric current so that the electric potential lowering along the current, by

linearly increasing the way they take every next time period because this accelerated motion. The same thing happens on the atomic scale giving a dp impulse difference and a dx way difference between the different part of the not point like particles.

Relativistic effect

Another bridge between the classical and quantum mechanics in the realm of relativity is that the charge distribution is lowering in the reference frame of the accelerating charges linearly: ds/dt = at (time coordinate), but in the reference frame of the current it is parabolic: $s = a/2 t^2$ (geometric coordinate).

Heisenberg Uncertainty Relation

In the atomic scale the Heisenberg uncertainty relation gives the same result, since the moving electron in the atom accelerating in the electric field of the proton, causing a charge distribution on delta x position difference and with a delta p momentum difference such a way that they product is about the half Planck reduced constant. For the proton this delta x much less in the nucleon, than in the orbit of the electron in the atom, the delta p is much higher because of the greater proton mass.

This means that the electron and proton are not point like particles, but has a real charge distribution.

Wave - Particle Duality

The accelerating electrons explains the wave – particle duality of the electrons and photons, since the elementary charges are distributed on delta x position with delta p impulse and creating a wave packet of the electron. The photon gives the electromagnetic particle of the mediating force of the electrons electromagnetic field with the same distribution of wavelengths.

Atomic model

The constantly accelerating electron in the Hydrogen atom is moving on the equipotential line of the proton and it's kinetic and potential energy will be constant. Its energy will change only when it is changing its way to another equipotential line with another value of potential energy or getting free with enough kinetic energy. This means that the Rutherford-Bohr atomic model is right and only that changing acceleration of the electric charge causes radiation, not the steady acceleration. The steady acceleration of the charges only creates a centric parabolic steady electric field around the charge, the magnetic field. This gives the magnetic moment of the atoms, summing up the proton and electron magnetic moments caused by their circular motions and spins.

The Relativistic Bridge

Commonly accepted idea that the relativistic effect on the particle physics it is the fermions' spin - another unresolved problem in the classical concepts. If the electric charges can move only with accelerated motions in the self maintaining electromagnetic field, once upon a time they would

reach the velocity of the electromagnetic field. The resolution of this problem is the spinning particle, constantly accelerating and not reaching the velocity of light because the acceleration is radial. One origin of the Quantum Physics is the Planck Distribution Law of the electromagnetic oscillators, giving equal intensity for 2 different wavelengths on any temperature. Any of these two wavelengths will give equal intensity diffraction patterns, building different asymmetric constructions, for example proton - electron structures (atoms), molecules, etc. Since the particles are centers of diffraction patterns they also have particle – wave duality as the electromagnetic waves have. [2]

The weak interaction

The weak interaction transforms an electric charge in the diffraction pattern from one side to the other side, causing an electric dipole momentum change, which violates the CP and time reversal symmetry. The Electroweak Interaction shows that the Weak Interaction is basically electromagnetic in nature. The arrow of time shows the entropy grows by changing the temperature dependent diffraction patterns of the electromagnetic oscillators.

Another important issue of the quark model is when one quark changes its flavor such that a linear oscillation transforms into plane oscillation or vice versa, changing the charge value with 1 or -1. This kind of change in the oscillation mode requires not only parity change, but also charge and time changes (CPT symmetry) resulting a right handed anti-neutrino or a left handed neutrino.

The right handed anti-neutrino and the left handed neutrino exist only because changing back the quark flavor could happen only in reverse, because they are different geometrical constructions, the u is 2 dimensional and positively charged and the d is 1 dimensional and negatively charged. It needs also a time reversal, because anti particle (anti neutrino) is involved.

The neutrino is a 1/2spin creator particle to make equal the spins of the weak interaction, for example neutron decay to 2 fermions, every particle is fermions with ½ spin. The weak interaction changes the entropy since more or less particles will give more or less freedom of movement. The entropy change is a result of temperature change and breaks the equality of oscillator diffraction intensity of the Maxwell–Boltzmann statistics. This way it changes the time coordinate measure and makes possible a different time dilation as of the special relativity.

The limit of the velocity of particles as the speed of light appropriate only for electrical charged particles, since the accelerated charges are self maintaining locally the accelerating electric force. The neutrinos are CP symmetry breaking particles compensated by time in the CPT symmetry, that is the time coordinate not works as in the electromagnetic interactions, consequently the speed of neutrinos is not limited by the speed of light.

The weak interaction T-asymmetry is in conjunction with the T-asymmetry of the second law of thermodynamics, meaning that locally lowering entropy (on extremely high temperature) causes the weak interaction, for example the Hydrogen fusion.

Probably because it is a spin creating movement changing linear oscillation to 2 dimensional oscillation by changing d to u quark and creating anti neutrino going back in time relative to the

proton and electron created from the neutron, it seems that the anti neutrino fastest then the velocity of the photons created also in this weak interaction?

A quark flavor changing shows that it is a reflection changes movement and the CP- and T- symmetry breaking!!! This flavor changing oscillation could prove that it could be also on higher level such as atoms, molecules, probably big biological significant molecules and responsible on the aging of the life.

Important to mention that the weak interaction is always contains particles and antiparticles, where the neutrinos (antineutrinos) present the opposite side. It means by Feynman's interpretation that these particles present the backward time and probably because this they seem to move faster than the speed of light in the reference frame of the other side.

Finally since the weak interaction is an electric dipole change with ½ spin creating; it is limited by the velocity of the electromagnetic wave, so the neutrino's velocity cannot exceed the velocity of light.

The General Weak Interaction

The Weak Interactions T-asymmetry is in conjunction with the T-asymmetry of the Second Law of Thermodynamics, meaning that locally lowering entropy (on extremely high temperature) causes for example the Hydrogen fusion. The arrow of time by the Second Law of Thermodynamics shows the increasing entropy and decreasing information by the Weak Interaction, changing the temperature dependent diffraction patterns. A good example of this is the neutron decay, creating more particles with less known information about them.

The neutrino oscillation of the Weak Interaction shows that it is a general electric dipole change and it is possible to any other temperature dependent entropy and information changing diffraction pattern of atoms, molecules and even complicated biological living structures.

We can generalize the weak interaction on all of the decaying matter constructions, even on the biological too. This gives the limited lifetime for the biological constructions also by the arrow of time. There should be a new research space of the Quantum Information Science the 'general neutrino oscillation' for the greater then subatomic matter structures as an electric dipole change. There is also connection between statistical physics and evolutionary biology, since the arrow of time is working in the biological evolution also.

The Fluctuation Theorem says that there is a probability that entropy will flow in a direction opposite to that dictated by the Second Law of Thermodynamics. In this case the Information is growing that is the matter formulas are emerging from the chaos. So the Weak Interaction has two directions, samples for one direction is the Neutron decay, and Hydrogen fusion is the opposite direction.

Fermions and Bosons

The fermions are the diffraction patterns of the bosons such a way that they are both sides of the same thing.

Van Der Waals force

Named after the Dutch scientist Johannes Diderik van der Waals – who first proposed it in 1873 to explain the behaviour of gases – it is a very weak force that only becomes relevant when atoms and molecules are very close together. Fluctuations in the electronic cloud of an atom mean that it will

have an instantaneous dipole moment. This can induce a dipole moment in a nearby atom, the result being an attractive dipole—dipole interaction.

Electromagnetic inertia and mass

Electromagnetic Induction

Since the magnetic induction creates a negative electric field as a result of the changing acceleration, it works as an electromagnetic inertia, causing an electromagnetic mass. [1]

Relativistic change of mass

The increasing mass of the electric charges the result of the increasing inductive electric force acting against the accelerating force. The decreasing mass of the decreasing acceleration is the result of the inductive electric force acting against the decreasing force. This is the relativistic mass change explanation, especially importantly explaining the mass reduction in case of velocity decrease.

The frequency dependence of mass

Since E = hv and $E = mc^2$, $m = hv/c^2$ that is the m depends only on the v frequency. It means that the mass of the proton and electron are electromagnetic and the result of the electromagnetic induction, caused by the changing acceleration of the spinning and moving charge! It could be that the m_0 inertial mass is the result of the spin, since this is the only accelerating motion of the electric charge. Since the accelerating motion has different frequency for the electron in the atom and the proton, they masses are different, also as the wavelengths on both sides of the diffraction pattern, giving equal intensity of radiation.

Electron - Proton mass rate

The Planck distribution law explains the different frequencies of the proton and electron, giving equal intensity to different lambda wavelengths! Also since the particles are diffraction patterns they have some closeness to each other – can be seen as a gravitational force. [2]

There is an asymmetry between the mass of the electric charges, for example proton and electron, can understood by the asymmetrical Planck Distribution Law. This temperature dependent energy distribution is asymmetric around the maximum intensity, where the annihilation of matter and antimatter is a high probability event. The asymmetric sides are creating different frequencies of electromagnetic radiations being in the same intensity level and compensating each other. One of these compensating ratios is the electron – proton mass ratio. The lower energy side has no compensating intensity level, it is the dark energy and the corresponding matter is the dark matter.

Gravity from the point of view of quantum physics

The Gravitational force

The gravitational attractive force is basically a magnetic force.

The same electric charges can attract one another by the magnetic force if they are moving parallel in the same direction. Since the electrically neutral matter is composed of negative and positive

charges they need 2 photons to mediate this attractive force, one per charges. The Bing Bang caused parallel moving of the matter gives this magnetic force, experienced as gravitational force.

Since graviton is a tensor field, it has spin = 2, could be 2 photons with spin = 1 together.

You can think about photons as virtual electron – positron pairs, obtaining the necessary virtual mass for gravity.

The mass as seen before a result of the diffraction, for example the proton – electron mass rate Mp=1840 Me. In order to move one of these diffraction maximum (electron or proton) we need to intervene into the diffraction pattern with a force appropriate to the intensity of this diffraction maximum, means its intensity or mass.

The Big Bang caused acceleration created radial currents of the matter, and since the matter is composed of negative and positive charges, these currents are creating magnetic field and attracting forces between the parallel moving electric currents. This is the gravitational force experienced by the matter, and also the mass is result of the electromagnetic forces between the charged particles. The positive and negative charged currents attracts each other or by the magnetic forces or by the much stronger electrostatic forces!?

The gravitational force attracting the matter, causing concentration of the matter in a small space and leaving much space with low matter concentration: dark matter and energy. There is an asymmetry between the mass of the electric charges, for example proton and electron, can understood by the asymmetrical Planck Distribution Law. This temperature dependent energy distribution is asymmetric around the maximum intensity, where the annihilation of matter and antimatter is a high probability event. The asymmetric sides are creating different frequencies of electromagnetic radiations being in the same intensity level and compensating each other. One of these compensating ratios is the electron – proton mass ratio. The lower energy side has no compensating intensity level, it is the dark energy and the corresponding matter is the dark matter.

The Higgs boson

By March 2013, the particle had been proven to behave, interact and decay in many of the expected ways predicted by the Standard Model, and was also tentatively confirmed to have + parity and zero spin, two fundamental criteria of a Higgs boson, making it also the first known scalar particle to be discovered in nature, although a number of other properties were not fully proven and some partial results do not yet precisely match those expected; in some cases data is also still awaited or being analyzed.

Since the Higgs boson is necessary to the W and Z bosons, the dipole change of the Weak interaction and the change in the magnetic effect caused gravitation must be conducted. The Wien law is also important to explain the Weak interaction, since it describes the T_{max} change and the diffraction patterns change. [2]

Higgs mechanism and Quantum Gravity

The magnetic induction creates a negative electric field, causing an electromagnetic inertia. Probably it is the mysterious Higgs field giving mass to the charged particles? We can think about the photon as an electron-positron pair, they have mass. The neutral particles are built from negative and positive charges, for example the neutron, decaying to proton and electron. The wave – particle duality makes sure that the particles are oscillating and creating magnetic induction as an inertial mass, explaining also the relativistic mass change. Higher frequency creates stronger magnetic induction, smaller frequency results lesser magnetic induction. It seems to me that the magnetic induction is the secret of the Higgs field.

In particle physics, the Higgs mechanism is a kind of mass generation mechanism, a process that gives mass to elementary particles. According to this theory, particles gain mass by interacting with the Higgs field that permeates all space. More precisely, the Higgs mechanism endows gauge bosons in a gauge theory with mass through absorption of Nambu–Goldstone bosons arising in spontaneous symmetry breaking.

The simplest implementation of the mechanism adds an extra Higgs field to the gauge theory. The spontaneous symmetry breaking of the underlying local symmetry triggers conversion of components of this Higgs field to Goldstone bosons which interact with (at least some of) the other fields in the theory, so as to produce mass terms for (at least some of) the gauge bosons. This mechanism may also leave behind elementary scalar (spin-0) particles, known as Higgs bosons.

In the Standard Model, the phrase "Higgs mechanism" refers specifically to the generation of masses for the W[±], and Z weak gauge bosons through electroweak symmetry breaking. The Large Hadron Collider at CERN announced results consistent with the Higgs particle on July 4, 2012 but stressed that further testing is needed to confirm the Standard Model.

What is the Spin?

So we know already that the new particle has spin zero or spin two and we could tell which one if we could detect the polarizations of the photons produced. Unfortunately this is difficult and neither ATLAS nor CMS are able to measure polarizations. The only direct and sure way to confirm that the particle is indeed a scalar is to plot the angular distribution of the photons in the rest frame of the centre of mass. A spin zero particles like the Higgs carries no directional information away from the original collision so the distribution will be even in all directions. This test will be possible when a much larger number of events have been observed. In the mean time we can settle for less certain indirect indicators.

The Graviton

In physics, the graviton is a hypothetical elementary particle that mediates the force of gravitation in the framework of quantum field theory. If it exists, the graviton is expected to be massless (because the gravitational force appears to have unlimited range) and must be a spin-2 boson. The spin follows from the fact that the source of gravitation is the stress-energy tensor, a second-rank tensor (compared to electromagnetism's spin-1 photon, the source of which is the four-current, a first-rank tensor). Additionally, it can be shown that any massless spin-2 field would give rise to a force indistinguishable from gravitation, because a massless spin-2 field must couple to (interact with) the stress-energy tensor in the same way that the gravitational field does. This result suggests that, if a massless spin-2 particle is discovered, it must be the graviton, so that the only experimental verification needed for the graviton may simply be the discovery of a massless spin-2 particle. [3]

Conclusions

"The fact that the genetic code can simultaneously write two kinds of information means that many DNA changes that appear to alter protein sequences may actually cause disease by disrupting gene control programs or even both mechanisms simultaneously," said Stamatoyannopoulos.

Speaking about the discovery, Stamatoyannopoulos said that the "new findings highlight that DNA is an incredibly powerful information storage device, which nature has fully exploited in unexpected ways." [10]

There is also connection between statistical physics and evolutionary biology, since the arrow of time is working in the biological evolution also.

Prentiss, who runs an experimental biophysics lab at Harvard, says England's theory could be tested by comparing cells with different mutations and looking for a correlation between the amount of energy the cells dissipate and their replication rates. [8]

Exists experimental evidence for quantum-coherent is used for more efficient light-harvesting in plant photosynthesis. Quantum entanglement exists in supramolecules determining the sense of smell and in the brain neurons microtubules due to quantum vibrations.

In the work presented here, we started to design and quantum mechanical investigations of the molecular logical devices which are useful for construction of nano medicine biorobots against the molecular diseases such a cancer tumors, and against the new kinds of synthesized microorganisms and nano guns. [7]

One of the most important conclusions is that the electric charges are moving in an accelerated way and even if their velocity is constant, they have an intrinsic acceleration anyway, the so called spin, since they need at least an intrinsic acceleration to make possible they movement.

The accelerated charges self-maintaining potential shows the locality of the relativity, working on the quantum level also. [1]

The bridge between the classical and quantum theory is based on this intrinsic acceleration of the spin, explaining also the Heisenberg Uncertainty Principle. The particle – wave duality of the electric charges and the photon makes certain that they are both sides of the same thing.

The Secret of Quantum Entanglement that the particles are diffraction patterns of the electromagnetic waves and this way their quantum states every time is the result of the quantum state of the intermediate electromagnetic waves. [2]

These relatively new developments in biophysics have discovered that all biological organisms are constituted of a liquid crystalline medium. Further, DNA is a liquid-crystal, lattice-type structure (which some refer to as a liquid crystal gel), whereby body cells are involved in a holographic instantaneous communication via the emitting of biophotons (a source based on light). This implies that all living biological organisms continuously emit radiations of light that form a field of coherence and communication. Moreover, biophysics has discovered that living organisms are permeated by quantum wave forms. [5]

Basing the gravitational force on the accelerating Universe caused magnetic force and the Planck Distribution Law of the electromagnetic waves caused diffraction gives us the basis to build a Unified Theory of the physical interactions also.

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