Living Machines

It sounds like something out of the Borg in Star Trek. Nano-sized robots self-assemble to form biological machines that do the work that keeps one alive. And yet something like this really does go on. [13]

In a landmark experiment at SLAC National Accelerator Laboratory, scientists used an X-ray laser to capture the first snapshots of a chemical interaction between two biomolecules in real time and at an atomic level. [12]

An international team of scientists has learned how to determine the spatial structure of a protein obtained with an X-ray laser using the sulfur atoms it contains. This development is the next stage in the project of a group led by Vadim Cherezov to create an effective method of studying receptor proteins. [11]

When cryoEM images are obtained from protein nanocrystals the images themselves can appear to be devoid of any contrast. A group of scientists from the Netherlands have now demonstrated that lattice information can be revealed and enhanced by a specialized filter. [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.

Contents

Author: George Rajna

Preface

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.

How to see living machines

It sounds like something out of the Borg in Star Trek. Nano-sized robots self-assemble to form biological machines that do the work that keeps one alive. And yet something like this really does go on.

Every cell in our body - be they flesh and blood, brain and everything in between - has identical DNA, the twisted staircase of nucleic acids uniquely coded to each organism. Complex assemblages that resemble molecular machines take pieces of DNA called genes and make a brain cell when needed, instead of, say, a bone cell. These molecular machines are so complex, yet so tiny, that scientists today are just starting to understand their structure and function using the latest microscopes and supercomputers. Biological molecular machines could lay the foundation for developing cures to diseases like cancer. How small can one see, and what will one find?

Cryo-electron microscopy combined with supercomputer simulations have created the best model yet, with near atomic-level detail, of a vital molecular machine, the human pre-initiation complex (PIC). A science team from Northwestern University, Berkeley National Laboratory, Georgia State University, and UC Berkeley published their results on the PIC May 2016 in the journal Nature.

"For the first time, structures have been detailed of the complex groups of molecules that open up human DNA," said study co-author Ivaylo Ivanov, associate professor of chemistry at Georgia State University. Ivanov led the computational work that modeled the atoms of the different proteins that act like cogs of the PIC molecular machine.

The PIC finds genes associated with making a specific protein, such as an antibody or an enzyme. There the PIC pulls apart the two strands of DNA and feeds the coding strand to the workhorse enzyme RNA polymerase II. This starts transcription, where DNA bits are copied by RNA polymerase II into a single strand of messenger RNA. The RNA makes its way to 'protein factories' in the cell called ribosomes that take them as orders for which protein to make. If DNA is like the blueprint of a new house, RNAs are instructions to the 'contractors' at the ribosome work station. The manufactured proteins are like the nails, wood, plaster, and just about everything else in the house.

The experiment began with images painstakingly taken of PIC. They were made by a group led by study co-author Eva Nogales, a professor in the Department of Molecular and Cellular Biology at UC Berkeley and also Senior Faculty Scientist at the Lawrence Berkeley National Laboratory and Howard Hughes Medical Investigator.

Nogales' group used cryo-electron microscopy (cryo-EM), a rising star in lab techniques. They cryogenically froze human PIC bound to DNA. The freezing kept it in a chemically-active, near-natural

environment. Next they zapped it with electron beams. Thanks to recent advances in direct electron detector technology, cryo-EM can now image at near atomic resolution large and complicated biological structures that have proven too difficult to crystalize. The go-to technique, X-ray crystallography, requires crystallized specimens, and cryo-EM avoids this hard step.

Over 1.4 million cryo-EM 'freeze frames' of PIC were processed using supercomputers at the National Energy Research for Scientific Computing Center to sift out background noise and reconstructed three-dimensional density maps that show details in the shape of the molecule that had never been seen before.

"Cryo-EM is going through a great expansion as are all the computer software used to generate both the density maps and also to interpret them like we've done in this study," Nogales said. "It is allowing us to get higher resolution of more structures in different states so that we can describe not just one picture of how they look, but several pictures showing how they are moving. We don't see a continuum, but we see snapshots through the process of action."

Study scientists next built an accurate model that made physical sense of the density maps of PIC using XSEDE, the eXtream Science and Engineering Discovery Environment, funded by the National Science Foundation. XSEDE allows scientists to interactively share computing resources, data and expertise via a single virtual system. Ivaylo Ivanov's team has run over four million core hours of simulations on the Stampede supercomputer at the Texas Advanced Computing Center to model complex molecular machines, including those for this study. Ivanov's broader molecular machine work also includes an XSEDE allocation of 1.7 million core hours on the Comet supercomputer at the San Diego Supercomputing Center.

"I have been using XSEDE resources for more than 12 years now," Ivanov said. "Without the availability of XSEDE resources, all of our research would have been much more limited in terms of the systems that we can address. For us, XSEDE has been absolutely essential."

The goal of all this computational effort is to produce atomic models that tell the full story of the structure and function of the protein complex of molecules. To get there Ivanov's team took the twelve components of the PIC assembly and created homology models for each component that accounted for their amino acid sequences and their relation to similar known protein 3-D structures.

Next they approximated the experimental densities Nogales' team found onto a grid. "We can use a method called molecular dynamics flexible fitting," explained Ivanov, "where you essentially run a molecular dynamics simulation. And you use the experimental density to bias the atoms in the molecular dynamics simulation to move into the denser regions of the EM map. That's the process of flexible fitting to the EM map."

They refined the model with the Phoenix crystallographic refinement package. "That is a complimentary technique that allows us to position side chains and improve the model so that we can capture all the details that are present in the density map," Ivanov said.

XSEDE was "absolutely necessary" for this modeling, said Ivanov. "When we include water and counter ions in addition to the PIC complex in a molecular dynamics simulation box, we get the simulation system size of over a million atoms. One cannot run that on a work station or even on a

modest cluster. For that we really need to go to a thousand cores. In this case, we went up to two thousand and forty-eight cores. And for that we needed access to Stampede," Ivanov said.

One of the insights gained in the study is a working model of how PIC opens the otherwise stable DNA double helix for transcription. Nogales explained that one could imagine a cord made of two threads twisted around each other. Hold one end very tightly. Grab the other and twist it in the opposite direction of the threading to unravel the cord. That's basically how the living machines that keep us alive do it.

"The DNA needs to be opened and moved into the polymerase active site to encode for the first RNA nucleotide," explained Nogales. "The pre-initiation complex is holding the two strands of the DNA very tightly together at one end, so that they cannot move and they cannot open. On the other side of the PIC there is a machine that uses energy to push the DNA, twisting it in the opposite direction in which the two strands are threaded. And when this happens, in between the two sides, the strands will open," said Nogales.

This study resolved the structure of that molecular machine that acts like the twisting fingers, the transcription factor component TFIIH. "TFIIH has a translocase sub-unit, whose role is to simultaneously push the DNA toward the active site of the polymerase and unwind the DNA. By the combined pushing and unwinding, effectively you are separating the two strands of the DNA," Ivanov said.

Both scientists said that they are just beginning to get an atomic-level understanding of transcription, crucial to gene expression and ultimately disease. "Many disease states come about because there are errors in how much a certain gene is being read and how much a certain protein with a certain activity in the cell is present," Nogales said. "Those disease states could be due to excess production of the protein, or conversely not enough. It is very important to understand the molecular process that regulates this production so that we can understand the disease state."

"This work illustrates well two general principles that will drive science in the next few years," commented Peter Preusch, program officer with the National Institutes of Health (NIH). "One is the application of hybrid methods – combinations of biophysical methods including x-ray crystallography and cryoEM along with large scale computational methods to integrate information on larger molecular complexes. Two, there's the requirement for team science drawing the expertise of multiple investigators to solve problems that cannot be tackled by any single lab working alone." Peter Preusch is the Biophysics Branch Chief, Cell Biology and Biophysics Division, National Institute of General Medical Sciences, NIH.

While this fundamental work does not directly produce cures, it does lay the foundation to help develop them in the future, said Ivanov. "In order to understand disease, we have to understand how these complexes function in the first place… A collaboration between computational modelers and experimental structural biologists could be very fruitful in the future. "

The May 2016 Nature Articles study (DOI: 10.1038/nature17970), "Near-atomic resolution visualization of human transcription promoter opening," was authored by Yuan He, Lawrence Berkeley National Laboratory and now at Northwestern University; Chunli Yan and Ivaylo Ivanov, Georgia State University; Jie Fang, Carla Inouye, Robert Tjian, Eva Nogales, UC Berkeley. Funding

came from the National Institute of General Medical Sciences (NIH) and the National Science Foundation. [13]

X-ray laser gets first real-time snapshots of a chemical flipping a biological switch

In a landmark experiment at SLAC National Accelerator Laboratory, scientists used an X-ray laser to capture the first snapshots of a chemical interaction between two biomolecules in real time and at an atomic level.

Scientists have used the powerful X-ray laser at the Department of Energy's SLAC National Accelerator Laboratory to make the first snapshots of a chemical interaction between two biomolecules - one that flips an RNA "switch" that regulates production of proteins, the workhorse molecules of life.

The results, published today in Nature, show the game-changing potential of X-ray free-electron lasers, or XFELs, for studying RNA, which guides protein manufacturing in the cell, serves as the primary genetic material in retroviruses such as HIV and also plays a role in most forms of cancer.

And because this particular type of RNA switch, known as a riboswitch, is found only in bacteria, a deeper understanding of its function may offer a way to turn off protein production and kill harmful germs without causing side effects in the humans they infect.

"Previous experiments at SLAC's X-ray laser have studied biological reactions like photosynthesis that are triggered by light. But this is the first to observe one that is triggered by the chemical interaction of two biomolecules in real time and at the atomic scale," said Yun-Xing Wang, a structural biologist at the National Cancer Institute's Center for Cancer Research who led the international research team.

"This really demonstrates the unique capability that X-ray free-electron lasers offer that no current technology, or any other technology on the horizon, can do. It's like you have a camera with a very fast shutter speed, so you can catch every move of the biomolecules in action."

The experiments were carried out at SLAC's Linac Coherent Light Source (LCLS), a DOE Office of Science User Facility. They are the first to demonstrate how XFELs can take snapshots and potentially make movies of RNA and other biomolecules as they chemically interact - offering glimpses into fundamental workings of the cell that can't be obtained any other way.

Seeing RNA Shape Shifting

RNA is a key part of the genetic material in all living cells. It comes in several types that work together to guide the production of proteins by the cell's ribosomes, according to blueprints encoded in DNA.

But both DNA and RNA also contain extensive regions that don't code for any protein - the so-called genetic "dark matter." Scientists thought for many years that these regions didn't do anything. Now they know that they play an important role in determining where and when genes turn on and off and otherwise fine-tuning their function. The vast majority of cancers are due to mutations in these

non-coding regions, Wang said, so understanding how these regions work is important for cancer research as well as fundamental biology.

However, figuring out what the RNA non-coding regions do is difficult. RNA molecules are wobbly and flexible, so it's hard to incorporate them into the large crystals typically needed to study their atomic structure at X-ray light sources.

LCLS removes this barrier by allowing scientists to get structural information from much smaller, nanosized crystals, which are much easier to make. Its powerful X-ray laser pulses, a billion times brighter than any available before, are so short that they collect data from each crystal in a few millionths of a billionth of a second, before damage from the X-rays sets in.

Wang's team studied a riboswitch from Vibrio vulnificus, a bacterium related to the one that causes cholera. The riboswitch sits in a long strand of messenger RNA (mRNA), which copies DNA's instructions for making a protein so they can be read and carried out by the ribosome. The switch acts like a thermostat that regulates protein production.

In this case, the mRNA guides production of a protein that in turn helps to produce a small molecule called adenine. When there is too much adenine in the bacterial cell, adenine molecules enter pockets in the riboswitches and flip the riboswitches into a different shape, and this changes the pace of protein and adenine production.

First Stills of an Elegant Film

For the LCLS experiments, the researchers made nanocrystals that incorporated millions of copies of the riboswitch and mixed them with a solution containing adenine molecules. Each crystal was so small that adenine could quickly and uniformly penetrate into every corner of it, enter riboswitch pockets and flip them almost instantaneously, as if they were millions of synchronized swimmers executing a single flawless move.

The scientists took snapshots of this interaction by hitting the crystals with X-ray laser pulses at carefully timed intervals after the mixing started. This gave them the first glimpse of a fleeting intermediate stage in the process, which occurred 10 seconds in. Separately, they obtained the first images of the riboswitch in its initial, empty-pocket state, and discovered that it existed in two slightly different configurations, only one of which participates in switching.

The researchers were surprised to discover that the sudden change in the shape of the riboswitches was so dramatic that it changed the shape of the entire crystal, too. Normally a major change like this would crack the crystal and spoil the experiment. But because these crystals were so small they held together, so the X-ray laser could still get structural information from them.

"To me it's still a mystery how the crystal managed to do that," said Soichi Wakatsuki, a professor at SLAC and at the Stanford School of Medicine and head of the lab's Biosciences Division, who was not part of the research team. "This actually opens up a lot of new possibilities and gives us a new way to look at how RNA and proteins interact with small molecules, so this is very exciting." [12]

X-ray laser speeds up the process of determining protein structures

An international team of scientists has learned how to determine the spatial structure of a protein obtained with an X-ray laser using the sulfur atoms it contains. This development is the next stage in the project of a group led by Vadim Cherezov to create an effective method of studying receptor proteins. A detailed description of the study has been published in the journal Science Advances.

Receptor proteins (GPCRs) allow signals to be transmitted within cells, which, in turn, enables the cells to obtain information about their environment and interact with one another. As a result, we are able to see, feel, maintain blood pressure, etc. Any disorders in the way these proteins work can result in serious consequences, such as blindness. Developing medicines to restore the normal function of receptors is not possible without a precise understanding of the way in which GPCRs operate, which, as with other proteins, is determined by their spatial structure, i.e., the way in which the protein folds.

The best method of doing this is to use X-ray crystallography. For X-rays, a crystal is a three-dimensional diffraction lattice in which the radiation is scattered on the atoms.

A particular problem with this method is obtaining protein crystals. In order to do this, receptor proteins have to be extracted from a cell membrane and placed in a special lipid environment. Then, by selecting the temperature and using substances to speed up the nucleation process, the protein crystallizes.

One challenge with GPCRs is that they are highly mobile and dynamic molecules that frequently change their spatial structure. This means that it is difficult for them to grow large crystals that are needed for the classical diffraction procedure. This procedure involves exposing the crystal to radiation at different angles for a relatively long period of time. X-rays ionize the atoms, which destroys the protein molecules. Large crystals of a few dozen microns are needed to compensate for this effect.

Thanks to the new experimental method of Serial Femtosecond Crystallography, it is now possible to solve this problem. The method has been developed over the past few years by an international team of scientists. One of the leaders is Vadim Cherezov, a professor at the University of Southern California and MIPT. The method is based on the use of a new X-ray source generator– a free-electron laser. The radiation these emit is so powerful that it fully ionizes atoms in a crystal as it passes through, essentially destroying it. However, as the laser pulse has a very short duration (a few femtoseconds, 10-15 s), a diffraction pattern can be recorded before the atoms move from their position. This means that the scientists are able to avoid the difficulties associated with radiation damage.

As the crystal is destroyed immediately, it is not possible to measure it at different orientations. To solve this problem, scientists collect and process data from several crystals. Using a special injector, the lipid environment in which the crystals are situated is exposed to an X-ray pulse. The whole process is similar to squeezing toothpaste out of a tube.

The result is millions of diffraction images that need to be processed by selecting images with crystals, finding their orientation, and then putting them together in a three-dimensional diffraction pattern. Two parameters must be known in order to decipher the structure: the amplitude and the

phase of the reflected radiation. The amplitude value is measured on a detector during the experiment, but determining the phase is a complex task; however, there are a number of ways of solving the problem. For example, if a certain protein is known to have a similar structure, it can be used as a first approximation. Of course, this is not possible in all cases.

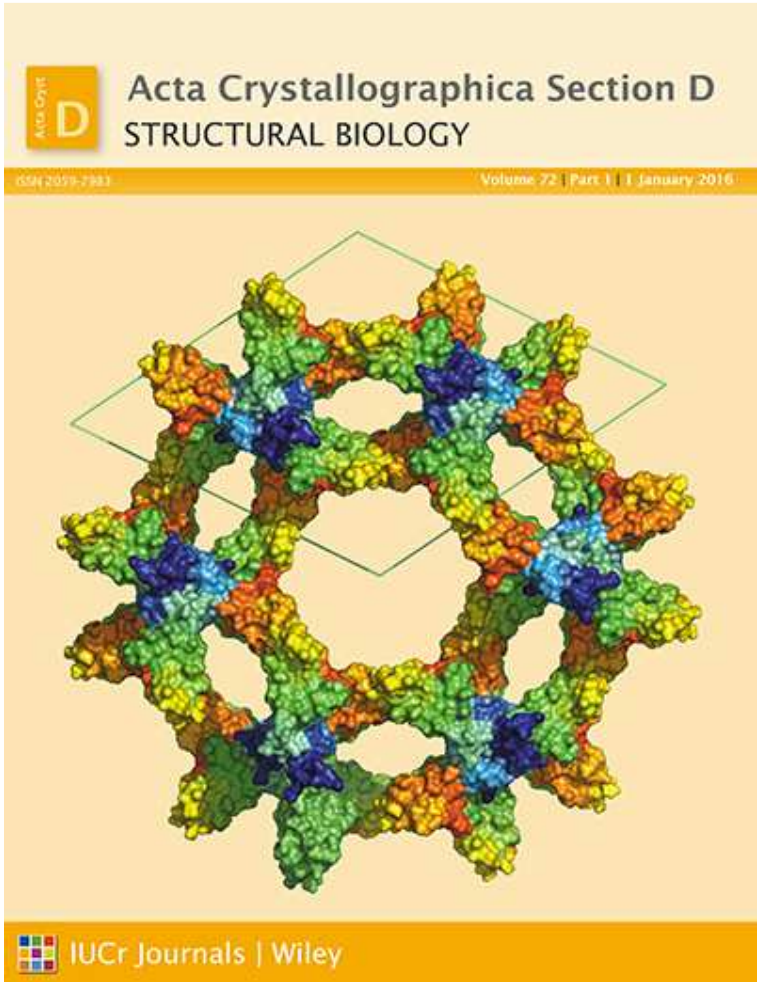
Another popular method is to use an effect known as anomalous scattering. This occurs when the X-ray wavelength is close to the electron transition energy in the atoms, which results in the wave being absorbed and re-emitted. This causes a change in the amplitudes and phases. If the amplitudes are measured very precisely, the differences between them can be used to reconstruct the phases. However, most of the atoms that make up proteins (carbon, oxygen and nitrogen) are not suitable for this. A relatively heavy element found in almost all proteins is sulfur, which the researchers used in their most recent study to reconstruct the phases.

Special software had to be developed specifically for the task. Out of 7 million images obtained, the researchers had to select those with diffracted reflections. They then had to determine the orientation of the crystal and the intensity of all reflections and subsequently collate all the data obtained. 600,000 diffraction patterns were found and then used to successfully reconstruct the structure of a protein with a resolution of 2.5Å. By combining the data with the results obtained at a different X-ray wavelength, the researchers were able to increase the resolution to 1.9Å. This level of precision not only enables the structure of receptor proteins to be determined with high accuracy, but also allows scientists to see molecules of water, ions and lipids that surround them, which is extremely important for understanding how proteins function and for modeling their interaction with other substances.

"When I participated in a study to determine the structure of the first receptor protein, it took me about a year to obtain crystals that were large enough to conduct classical X-ray diffraction. We hope that the method we have developed will help to greatly increase the speed of this process," said Prof. Cherezov commenting on the significance of the research.

Of the 800 receptor proteins that exist, the structures of only 34 are currently known. The experimental method developed by the scientists will significantly speed up the studies of the remaining proteins. This, in turn, will contribute to the development of new and more effective drugs to treat a vast number of diseases. [11]

Digital enhancement of cryoEM photographs of protein Nanocrystals



The procedure described by van Genderen et al. [(2016). Acta Cryst. D71, 34-39] paves the way towards full three-dimensional structure determination at high resolution for protein crystals. The authors report on how lattice information can be enhanced by means of a wave finder in combination with Wiener-type maximum-likelihood filtering. The lattice filter is a very powerful tool for selecting and analysing extremely low contrast cryo-images of three dimensional protein/peptide nanocrystals. It confirms that the three-dimensional crystals are made up from multiple domains that are slightly differently oriented. Indeed, the algorithm can comfortably deal with multiple crystals with very different orientations, unit cells and/or space groups.

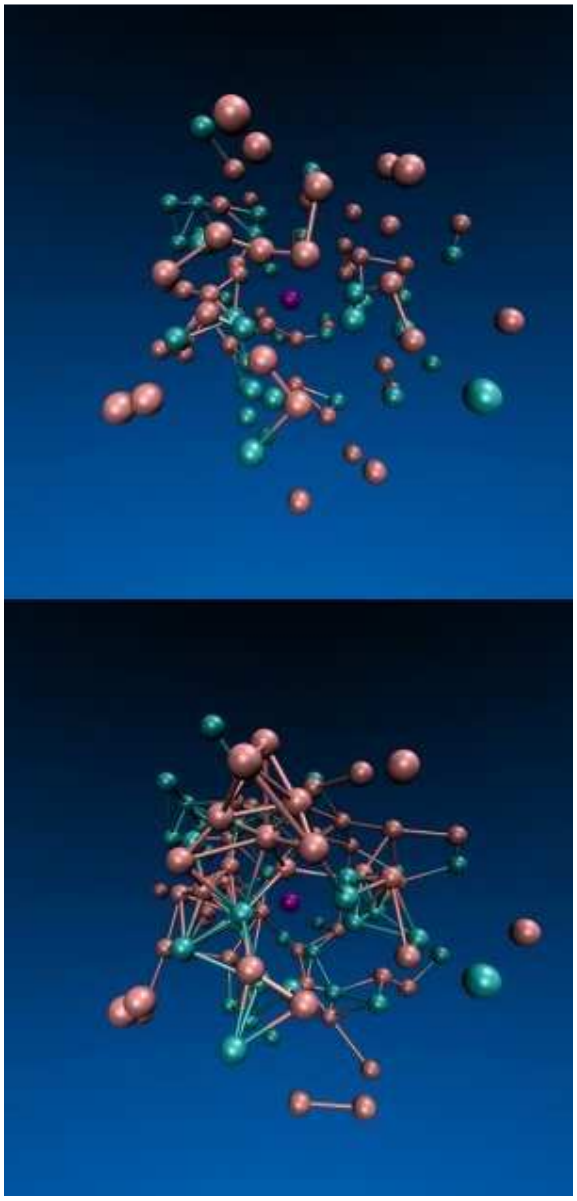
The authors of the paper propose the new lattice filter as a powerful tool for processing very noisy images with crystal factors (and thus the phase information) hidden within them. The filter is able to discriminate between noise images and the very noisy images with very low contrast which contain crystal-like structures. The lattice filter retains the shape of the spots in Fourier space and also retains any phase gradients within the Bragg spots (which determine the domain structure within the crystal). Thus, it retains all of the significant information from the Bragg spots. This will open the way to combining the phases acquired from stationary, two-dimensional images with intensities of rotation diffraction data taken from the same type of crystals. In this way, the authors expect to be able to phase the diffraction information of protein and peptide crystals. [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.

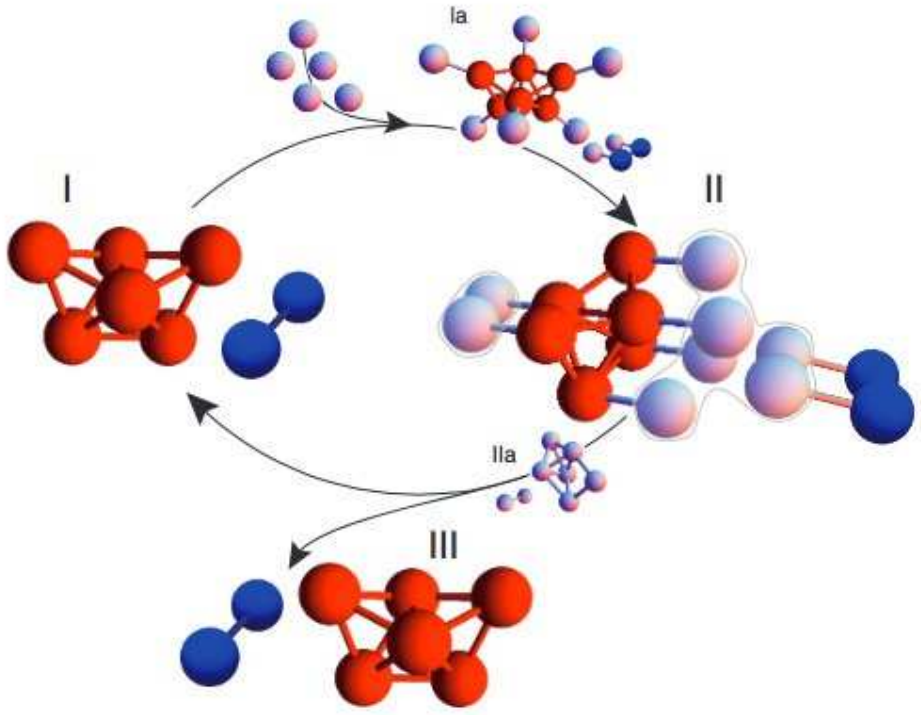
Thus, as particles in a system move around and interact, they will, through sheer chance, tend to adopt configurations in which the energy is spread out. Eventually, the system arrives at a state of maximum entropy called “thermodynamic equilibrium,” in which energy is uniformly distributed. A cup of 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.

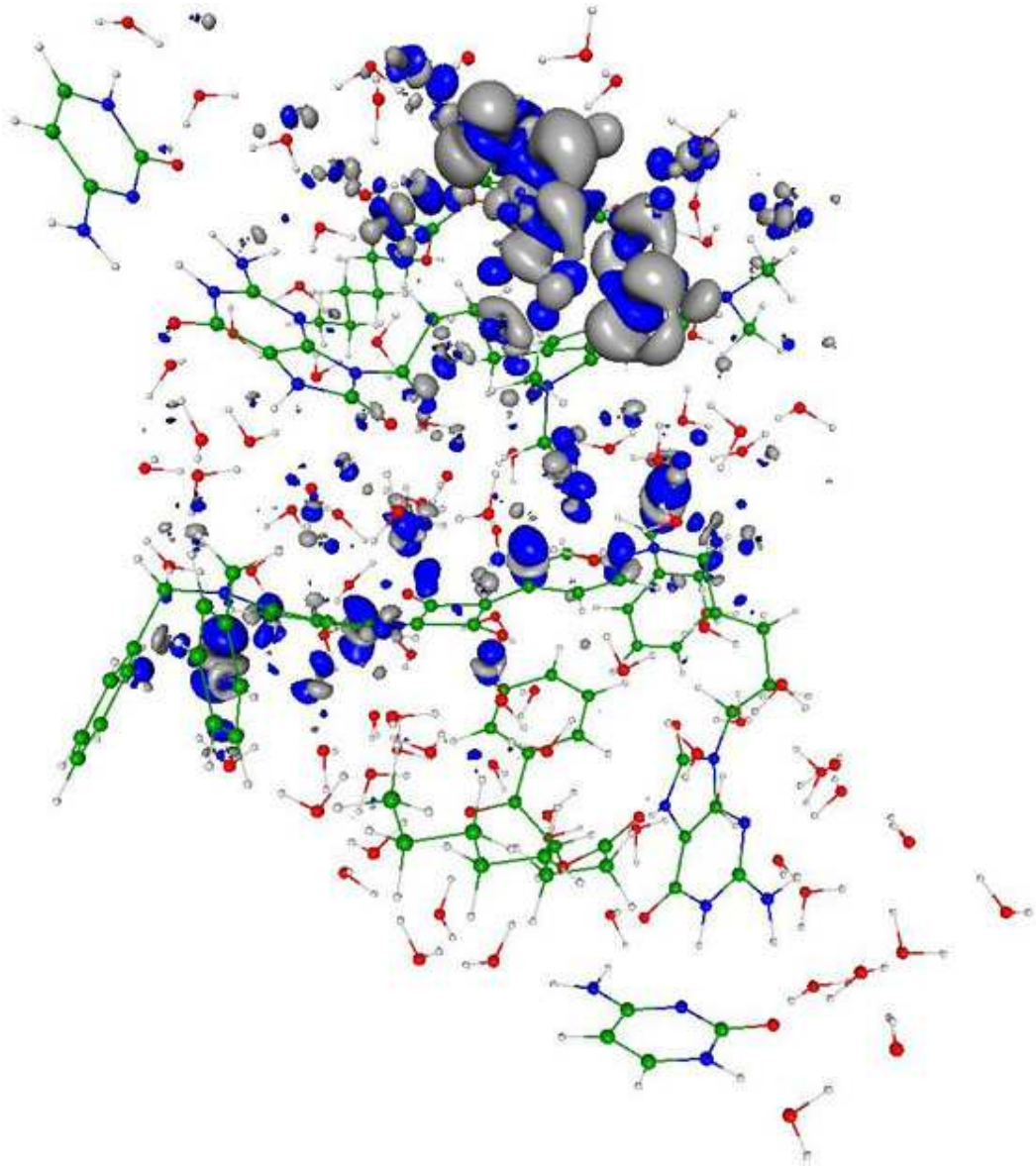
Our discovered phenomenon of the quantum entanglement in the prebiotic systems enhance the photosynthesis in the proposed systems because simultaneously excite two prebiotic kernels in the system by appearance of two additional quantum entangled excited states (Tamulis A, Grigalavicius M, Baltrusaitis 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.

Figure legend



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 $E = h\nu$ and $E = mc^2$, $m = h\nu / c^2$ that is the m depends only on the ν 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_o 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 $W^{\pm}$, 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

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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