Mystery of DNA Organization

Stretched out, the DNA from all the cells in our body would reach Pluto. So how does each tiny cell pack a two-meter length of DNA into its nucleus, which is just one-thousandth of a millimeter across? [18]

Scientists have long been able to make specific changes in the DNA code. Now, they're taking the more radical step of starting over, and building redesigned life forms from scratch. [17]

For the first time in the United States, scientists have edited the genes of human embryos, a controversial step toward someday helping babies avoid inherited diseases. [16]

The stage is set for a new era of data-driven protein molecular engineering as advances in DNA synthesis technology merge with improvements in computational design of new proteins. [15]

Scientists at the Technical University of Munich (TUM) have succeeded at measuring these forces for the very first time on the level of single base pairs. This new knowledge could help to construct precise molecular machines out of DNA. The researchers published their findings in the journal Science. [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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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.

Scientists solve longstanding biological mystery of DNA organization

Stretched out, the DNA from all the cells in our body would reach Pluto. So how does each tiny cell pack a two-meter length of DNA into its nucleus, which is just one-thousandth of a millimeter across?

The answer to this daunting biological riddle is central to understanding how the three-dimensional organization of DNA in the nucleus influences our biology, from how our genome orchestrates our cellular activity to how genes are passed from parents to children.

Now, scientists at the Salk Institute and the University of California, San Diego, have for the first time provided an unprecedented view of the 3D structure of human chromatin—the combination of DNA and proteins—in the nucleus of living human cells.

In the tour de force study, described in Science on July 27, 2017, the Salk researchers identified a novel DNA dye that, when paired with advanced microscopy in a combined technology called ChromEMT, allows highly detailed visualization of chromatin structure in cells in the resting and mitotic (dividing) stages. By revealing nuclear chromatin structure in living cells, the work may help rewrite the textbook model of DNA organization and even change how we approach treatments for disease.

"One of the most intractable challenges in biology is to discover the higher-order structure of DNA in the nucleus and how is this linked to its functions in the genome," says Salk Associate Professor Clodagh O'Shea, a Howard Hughes Medical Institute Faculty Scholar and senior author of the paper. "It is of eminent importance, for this is the biologically relevant structure of DNA that determines both gene function and activity."

Salk scientists have solved a longstanding biological mystery of DNA organization. Credit: Salk Institute/Clodagh O'Shea

Ever since Francis Crick and James Watson determined the primary structure of DNA to be a double helix, scientists have wondered how DNA is further organized to allow its entire length to pack into the nucleus such that the cell's copying machinery can access it at different points in the cell's cycle of activity. X-rays and microscopy showed that the primary level of chromatin organization involves 147 bases of DNA spooling around proteins to form particles approximately 11 nanometers (nm) in diameter called nucleosomes. These nucleosome "beads on a string" are then thought to fold into discrete fibers of increasing diameter (30, 120, 320 nm etc.), until they form chromosomes. The problem is, no one has seen chromatin in these discrete intermediate sizes in cells that have not been broken apart and had their DNA harshly processed, so the textbook model of chromatin's hierarchical higher-order organization in intact cells has remained unverified.

To overcome the problem of visualizing chromatin in an intact nucleus, O'Shea's team screened a number of candidate dyes, eventually finding one that could be precisely manipulated with light to undergo a complex series of chemical reactions that would essentially "paint" the surface of DNA with a metal so that its local structure and 3D polymer organization could be imaged in a living cell. The team partnered with University of California, San Diego, professor and microscopy expert Mark Ellisman, one of the paper's coauthors, to exploit an advanced form of electron microscopy that tilts samples in an electron beam enabling their 3D structure to be reconstructed. O'Shea's team called

the technique, which combines their chromatin dye with electron-microscope tomography, ChromEMT.

The team used ChromEMT to image and measure chromatin in resting human cells and during cell division (mitosis) when DNA is compacted into its most dense form—the 23 pairs of mitotic chromosomes that are the iconic image of the human genome. Surprisingly, they did not see any of the higher-order structures of the textbook model anywhere.

"The textbook model is a cartoon illustration for a reason," says Horng Ou, a Salk research associate and the paper's first author. "Chromatin that has been extracted from the nucleus and subjected to processing in vitro—in test tubes—may not look like chromatin in an intact cell, so it is tremendously important to be able to see it in vivo."

What O'Shea's team saw, in both resting and dividing cells, was chromatin whose "beads on a string" did not form any higher-order structure like the theorized 30 or 120 or 320 nanometers. Instead, it formed a semi-flexible chain, which they painstakingly measured as varying continuously along its length between just 5 and 24 nanometers, bending and flexing to achieve different levels of compaction. This suggests that it is chromatin's packing density, and not some higher-order structure, that determines which areas of the genome are active and which are suppressed.

With their 3D microscopy reconstructions, the team was able to move through a 250 nm x 1000 nm x 1000 nm volume of chromatin's twists and turns, and envision how a large molecule like RNA polymerase, which transcribes (copies) DNA, might be directed by chromatin's variable packing density, like a video game aircraft flying through a series of canyons, to a particular spot in the genome. Besides potentially upending the textbook model of DNA organization, the team's results suggest that controlling access to chromatin could be a useful approach to preventing, diagnosing and treating diseases such as cancer.

"We show that chromatin does not need to form discrete higher-order structures to fit in the nucleus," adds O'Shea. "It's the packing density that could change and limit the accessibility of chromatin, providing a local and global structural basis through which different combinations of DNA sequences, nucleosome variations and modifications could be integrated in the nucleus to exquisitely fine-tune the functional activity and accessibility of our genomes."

Future work will examine whether chromatin's structure is universal among cell types or even among organisms. [18]

Scientists build DNA from scratch to alter life's blueprint

At Jef Boeke's lab, you can whiff an odor that seems out of place, as if they were baking bread here.

But he and his colleagues are cooking up something else altogether: yeast that works with chunks of man-made DNA.

Scientists have long been able to make specific changes in the DNA code. Now, they're taking the more radical step of starting over, and building redesigned life forms from scratch. Boeke, a researcher at New York University, directs an international team of 11 labs on four continents working to "rewrite" the yeast genome, following a detailed plan they published in March.

Their work is part of a bold and controversial pursuit aimed at creating custom-made DNA codes to be inserted into living cells to change how they function, or even provide a treatment for diseases. It could also someday help give scientists the profound and unsettling ability to create entirely new organisms.

The genome is the entire genetic code of a living thing. Learning how to make one from scratch, Boeke said, means "you really can construct something that's completely new."

The research may reveal basic, hidden rules that govern the structure and functioning of genomes. But it also opens the door to life with new and useful characteristics, like microbes or mammal cells that are better than current ones at pumping out medications in pharmaceutical factories, or new vaccines. The right modifications might make yeast efficiently produce new biofuels, Boeke says.

Some scientists look further into the future and see things like trees that purify water supplies and plants that detect explosives at airports and shopping malls.

Also on the horizon is redesigning human DNA. That's not to make genetically altered people, scientists stress. Instead, the synthetic DNA would be put into cells, to make them better at pumping out pharmaceutical proteins, for example, or perhaps to engineer stem cells as a safer source of lab-grown tissue and organs for transplanting into patients.

Some have found the idea of remaking human DNA disconcerting, and scientists plan to get guidance from ethicists and the public before they try it.

Still, redesigning DNA is alarming to some. Laurie Zoloth of Northwestern University, a bioethicist who's been following the effort, is concerned about making organisms with "properties we cannot fully know." And the work would disturb people who believe creating life from scratch would give humans unwarranted power, she said.

"It is not only a science project," Zoloth said in an email. "It is an ethical and moral and theological proposal of significant proportions."

Rewritten DNA has already been put to work in viruses and bacteria. Australian scientists recently announced that they'd built the genome of the Zika virus in a lab, for example, to better understand it and get clues for new treatments.

At Harvard University, Jeffrey Way and Pamela Silver are working toward developing a harmless strain of salmonella to use as a vaccine against food poisoning from salmonella and E. coli, as well as the diarrhea-causing disease called shigella.

A key goal is to prevent the strain from turning harmful as a result of picking up DNA from other bacteria. That requires changing its genome in 30,000 places.

"The only practical way to do that," Way says, "is to synthesize it from scratch."

The cutting edge for redesigning a genome, though, is yeast. Its genome is bigger and more complex than the viral and bacterial codes altered so far. But it's well-understood and yeast will readily swap man-made DNA for its own.

Still, rewriting the yeast genome is a huge job.

It's like a chain with 12 million chemical links, known by the letters, A, C, G and T. That's less than one-hundredth the size of the human genome, which has 3.2 billion links. But it's still such a big job that Boeke's lab and scientists in the United States, Australia, China, Singapore, and the United Kingdom are splitting up the work. By the time the new yeast genome is completed, researchers will have added, deleted or altered about a million DNA letters.

Boeke compares a genome to a book with many chapters, and researchers are coming out with a new edition, with chapters that allow the book to do something it couldn't do before.

To redesign a particular stretch of yeast DNA, scientists begin with its sequence of code letters—nature's own recipe. They load that sequence into a computer, then tell the computer to make specific kinds of changes. For example one change might let them rearrange the order of genes, which might reveal strategies to make yeast grow better, says NYU researcher Leslie Mitchell.

Once the changes are made, the new sequence used as a blueprint. It is sent to a company that builds chunks of DNA containing the new sequence. Then these short chunks are joined together in the lab to build ever longer strands.

The project has so far reported building about one-third of the yeast genome. Boeke hopes the rest of the construction will be done by the end of the year. But he says it will take longer to test the new DNA and fix problems, and to finally combine the various chunks into a complete synthetic genome.

Last year, Boeke and others announced a separate effort, what is now called Genome Project-write or GP-write . It is chiefly focused on cutting the cost of building and testing large genomes, including human ones, by more than 1,000-fold within 10 years. The project is still seeking funding.

In the meantime, leaders of GP-write have started discussions of ethical, legal and social issues. And they realize the idea of making a human genome is a sensitive one.

"The notion that we could actually write a human genome is simultaneously thrilling to some and not so thrilling to others," Boeke said. "So we recognize this is going to take a lot of discussion." [17]

In US first, scientists edit genes of human embryos

For the first time in the United States, scientists have edited the genes of human embryos, a controversial step toward someday helping babies avoid inherited diseases.

The experiment was just an exercise in science—the embryos were not allowed to develop for more than a few days and were never intended to be implanted into a womb, according to MIT Technology Review, which first reported the news.

Officials at Oregon Health & Science University confirmed Thursday that the work took place there and said results would be published in a journal soon. It is thought to be the first such work in the U.S.; previous experiments like this have been reported from China. How many embryos were created and edited in the experiments has not been revealed.

The Oregon scientists reportedly used a technique called CRISPR, which allows specific sections of DNA to be altered or replaced. It's like using a molecular scissors to cut and paste DNA, and is much more precise than some types of gene therapy that cannot ensure that desired changes will take place exactly where and as intended. With gene editing, these so-called "germline" changes are permanent and would be passed down to any offspring.

The approach holds great potential to avoid many genetic diseases, but has raised fears of "designer babies" if done for less lofty reasons, such as producing desirable traits.

Last year, Britain said some of its scientists could edit embryo genes to better understand human development.

And earlier this year in the U.S., the National Academy of Sciences and National Academy of Medicine said in a report that altering the genes of embryos might be OK if done under strict criteria and aimed at preventing serious disease.

"This is the kind of research that the report discussed," University of Wisconsin-Madison bioethicist R. Alta Charo said of the report of Oregon's work. She co-led the National Academies panel but was not commenting on its behalf Thursday.

"This was purely laboratory-based work that is incredibly valuable for helping us understand how one might make these germline changes in a way that is precise and safe. But it's only a first step," she said.

"We still have regulatory barriers in the United States to ever trying this to achieve a pregnancy. The public has plenty of time" to weigh in on whether that should occur, she said.

One prominent genetics expert, Dr. Eric Topol, director of the Scripps Translational Science Institute in La Jolla, California, said gene editing of embryos is "an unstoppable, inevitable science, and this is more proof it can be done."

Experiments are in the works now in the U.S. using gene-edited cells to try to treat people with various diseases, but "in order to really have a cure, you want to get this at the embryo stage," he said. "If it isn't done in this country, it will be done elsewhere." [16]

Feedback from thousands of designs could transform protein engineering

The stage is set for a new era of data-driven protein molecular engineering as advances in DNA synthesis technology merge with improvements in computational design of new proteins.

This week's Science reports the largest-scale testing of folding stability for computationally designed proteins, made possible by a new high-throughput approach.

The scientists are from the UW Medicine Institute for Protein Design at the University of Washington in Seattle and the University of Toronto in Ontario.

The lead author of the paper is Gabriel Rocklin, a postdoctoral fellow in biochemistry at the University of Washington School of Medicine. The senior authors are Cheryl Arrowsmith, of the

Princess Margaret Cancer Center, the Structural Genomics Consortium and the Department of Medical Biophysics at the University of Toronto, and David Baker, UW professor of biochemistry and a Howard Hughes Medical Institute investigator.

Proteins are biological workhorses. Researchers want to build new molecules, not found naturally, that can perform tasks in preventing or treating disease, in industrial applications, in energy production, and in environmental cleanups.

"However, computationally designed proteins often fail to form the folded structures that they were designed to have when they are actually tested in the lab," Rocklin said.

In the latest study, the researchers tested more than 15,000 newly designed mini-proteins that do not exist in nature to see whether they form folded structures. Even major protein design studies in the past few years have generally examined only 50 to 100 designs.

An animation of a computationally designed mini protein from a UW Medicine Institute for Protein Design large-scale study to assess molecular folding and structural stability. Credit: UW Medicine Institute for Protein Design

"We learned a huge amount at this new scale, but the taste has given us an even larger appetite," said Rocklin. "We're eager to test hundreds of thousands of designs in the next few years."

The most recent testing led to the design of 2,788 stable protein structures and could have many bioengineering and synthetic biology applications. Their small size may be advantageous for treating diseases when the drug needs to reach the inside of a cell.

Proteins are made of amino acid chains with specific sequences, and natural protein sequences are encoded in cellular DNA. These chains fold into 3-dimensional conformations. The sequence of the amino acids in the chain guide where it will bend and twist, and how parts will interact to hold the structure together.

For decades, researchers have studied these interactions by examining the structures of naturally occurring proteins. However, natural protein structures are typically large and complex, with thousands of interactions that collectively hold the protein in its folded shape. Measuring the contribution of each interaction becomes very difficult.

The scientists addressed this problem by computationally designing their own, much simpler proteins. These simpler proteins made it easier to analyze the different types of interactions that hold all proteins in their folded structures.

"Still, even simple proteins are so complicated that it was important to study thousands of them to learn why they fold," Rocklin said. "This had been impossible until recently, due to the cost of DNA. Each designed protein requires its own customized piece of DNA so that it can be made inside a cell. This has limited previous studies to testing only tens of designs."

To encode their designs of short proteins in this project, the researchers used what is called DNA oligo library synthesis technology. It was originally developed for other laboratory protocols, such as large gene assembly. One of the companies that provided their DNA is Custom Array in Bothell,

Wash. They also used DNA libraries made by Agilent in Santa Clara, Calif., and Twist Bioscience in San Francisco.

By repeating the cycle of computation and experimental testing over several iterations, the researchers learned from their design failures and progressively improved their modeling. Their design success rate rose from 6 percent to 47 percent. They also produced stable proteins in shapes where all of their first designs failed.

Their large set of stable and unstable mini-proteins enabled them to quantitatively analyze which protein features correlated with folding. They also compared the stability of their designed proteins to similarly sized, naturally occurring proteins.

The most stable natural protein the researchers identified was a much-studied protein from the bacteria Bacillus stear other mophilus. This organism basks in high temperatures, like those in hot springs and ocean thermal vents. Most proteins lose their folded structures under such high temperature conditions. Organisms that thrive there have evolved highly stable proteins that stay folded even when hot.

"A total of 774 designed proteins had a higher stability scores than this most protease-resistant monomeric protein," the researchers noted. Proteases are enzymes that break down proteins, and were essential tools the researchers used to measure stability for their thousands of proteins.

The researchers predict that, as DNA synthesis technology continues to improve, high-throughput protein design will become possible for larger, more complex protein structures.

"We are moving away from the old style of protein design, which was a mix of computer modeling, human intuition, and small bits of evidence about what worked before." Rocklin said. "Protein designers were like master craftsmen who used their experience to hand-sculpt each piece in their workshop. Sometimes things worked, but when they failed it was hard to say why. Our new approach lets us collect an enormous amount of data on what makes proteins stable. This data can now drive the design process." [15]

Measuring forces in the DNA molecule

DNA, our genetic material, normally has the structure of a twisted rope ladder. Experts call this structure a double helix. Among other things, it is stabilized by stacking forces between base pairs. Scientists at the Technical University of Munich (TUM) have succeeded at measuring these forces for the very first time on the level of single base pairs. This new knowledge could help to construct precise molecular machines out of DNA. The researchers published their findings in the journal Science.

Over 60 years ago, the researchers Crick and Watson identified the structure of deoxyribonucleic acid, which is more commonly known as DNA. They compared the double helix to a rope ladder that had been twisted into a spiral. The rungs of this ladder consisted of guanine/cytosine and thymine/adenine base pairs. But what keeps the DNA strands in that spiral structure?

Special measuring system for molecular interactions

Prof. Hendrik Dietz from the Chair of Experimental Biophysics uses DNA as construction material to create molecular structures. Hence, he is greatly interested in gaining a better understanding of this material. "There are two types of interactions which stabilize double helices", he explains. For one, DNA contains hydrogen bonds.

For another, there are what experts call base pair stacking forces, which act between the stacked base pairs along the spiral axis. The forces of the hydrogen bonds, on the other hand, act perpendicular to the axis. "So far, it is not quite clear to which extent these two forces each contribute to the overall stability of the DNA double helix", explains Dietz.

Directly measuring the weak stacking forces between base pairs was a big technical challenge for the researchers, who worked on the problem for six years. In collaboration with the TUM Chair of Molecular Biophysics (Prof. Matthias Rief) and the TUM Chair of Theoretical Biophysics - Biomolecular Dynamics (Prof. Martin Zacharias), they succeeded in developing a special experimental setup that now makes it possible to measure extremely weak contact interactions between individual molecules.

A trillionth of a bar of chocolate

To put it simply, the measurement system is designed hierarchically and involves microscopic beams, at the tips of which one or more double helix structures running in parallel are located. These have been modified such that each end carries one base pair. Two of these microscopic beams are connected with a flexible polymer. On the other side, the beams are coupled to microscopic spheres which can be pulled apart using optical laser tweezers. In solution, the base pairs on the end of one of the beam can now interact with the base pairs on the end of the other beam. This also makes it possible to measure how long a stacking bond between them lasts before they fall apart again, as well as the force acting between the base pairs.

The forces measured by the researchers were in the range of piconewtons. "A newton is the weight of a bar of chocolate", explains Dietz. "What we have here is a thousandth of a billionth of that, which is practically nothing." Forces in the range of two piconewtons are sufficient to separate the bond created by stacking forces.

Furthermore, the scientists also observed that the bonds spontaneously broke up and formed again within just a few milliseconds. The strength and the lifetime of the interactions depends to a great extent on which base pairs are stacked on each other.

Creating DNA machines

The results of the measurements may help to better understand mechanical aspects of fundamental biological processes such as DNA replication, i.e. the reproduction of genetic material. For example, the short life of the stacking interactions could mean that an enzyme tasked with separating the base pairs during this process just needs to wait for the stacking bonds break up on their own - instead of having to apply force to separate them.

However, Dietz also intends to apply the data directly to his current research: He uses DNA as programmable building material to construct machines on the order of nanometers. When doing so, he draws inspiration from the complex structures which can e.g. be found in cells and, among other

things, serve as molecular "factories" to synthesize important compounds such as ATP, which stores energy. "We now know what would be possible if we could just build structures that were sufficiently sophisticated", says Dietz. "Naturally, when we have a better understanding of the properties of the molecular interactions, we are better able to work with these molecules."

At the moment, the lab is building a molecular rotational motor out of DNA, the components of which interlock and are held together via stacking forces. The goal is to be able to control a directed rotation via chemical or thermal stimuli. To do so, the timing of the movement of the rotor in the stator is crucial, and this task has now been made significantly easier with the new findings on the stacking forces. [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.

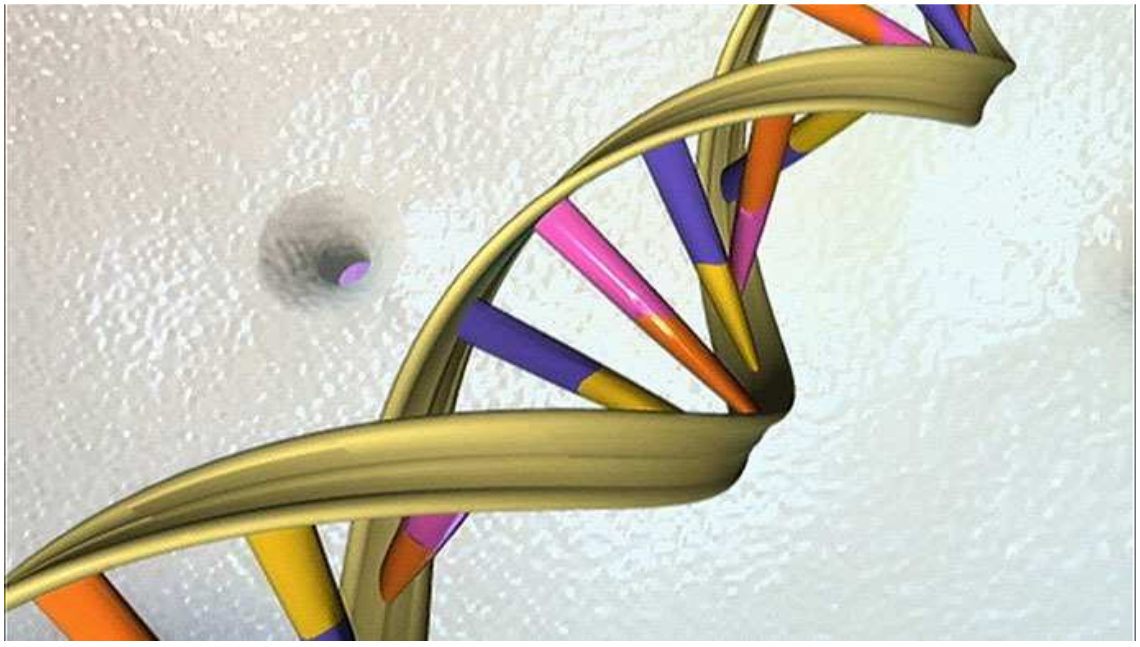
Simulation

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]

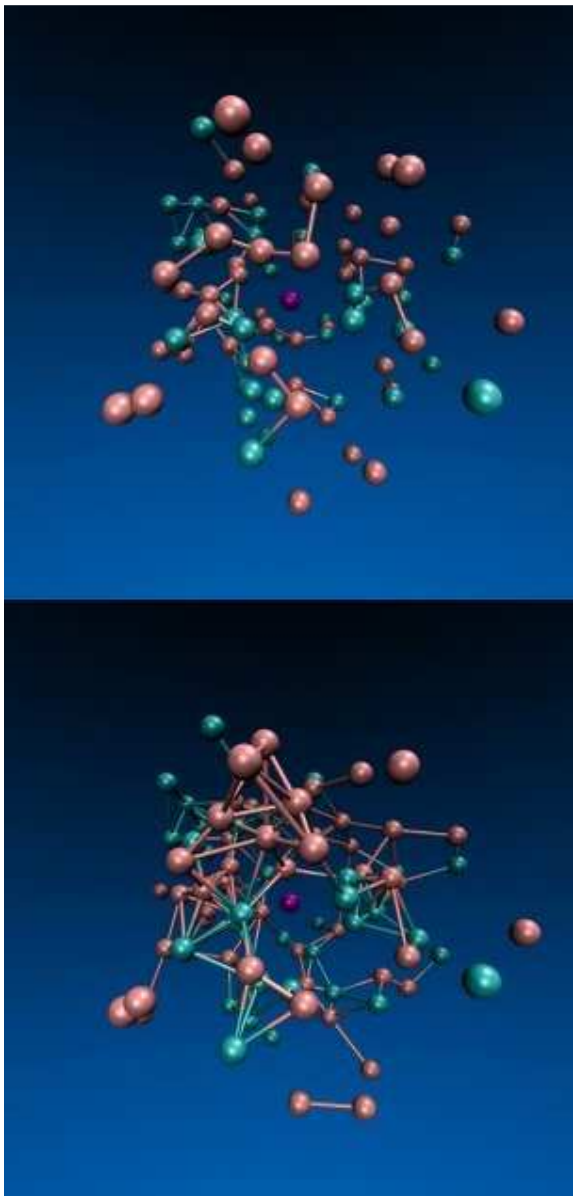
This Physicist Has a Groundbreaking Idea about Why Life Exists

“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.

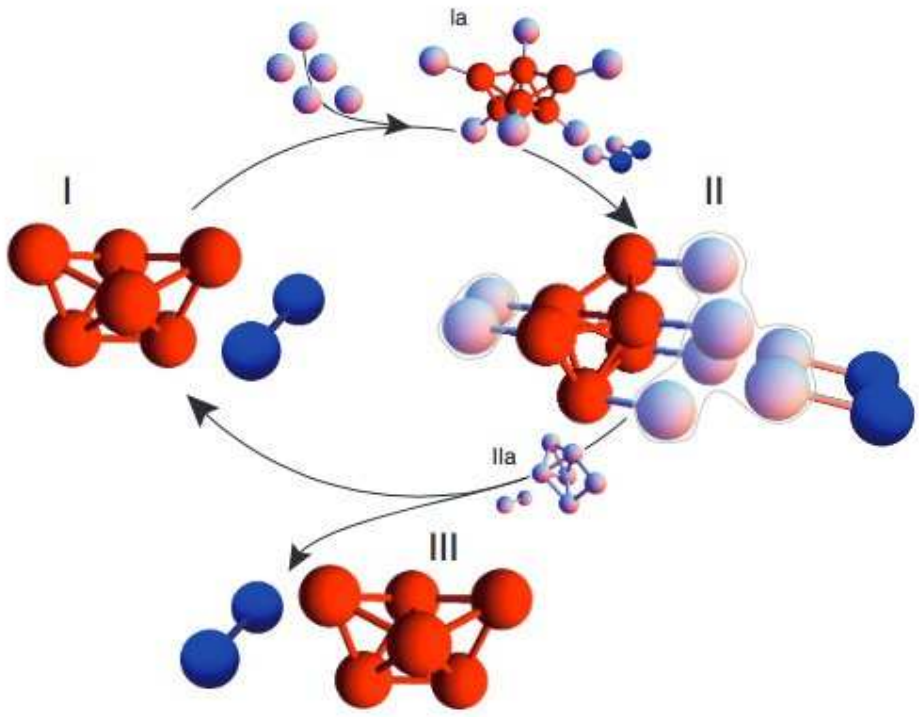
Thus, as particles in a system move around and interact, they will, through sheer chance, tend to adopt configurations in which the energy is spread out. Eventually, the system arrives at a state of maximum entropy called “thermodynamic equilibrium,” in which energy is uniformly distributed. A cup of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

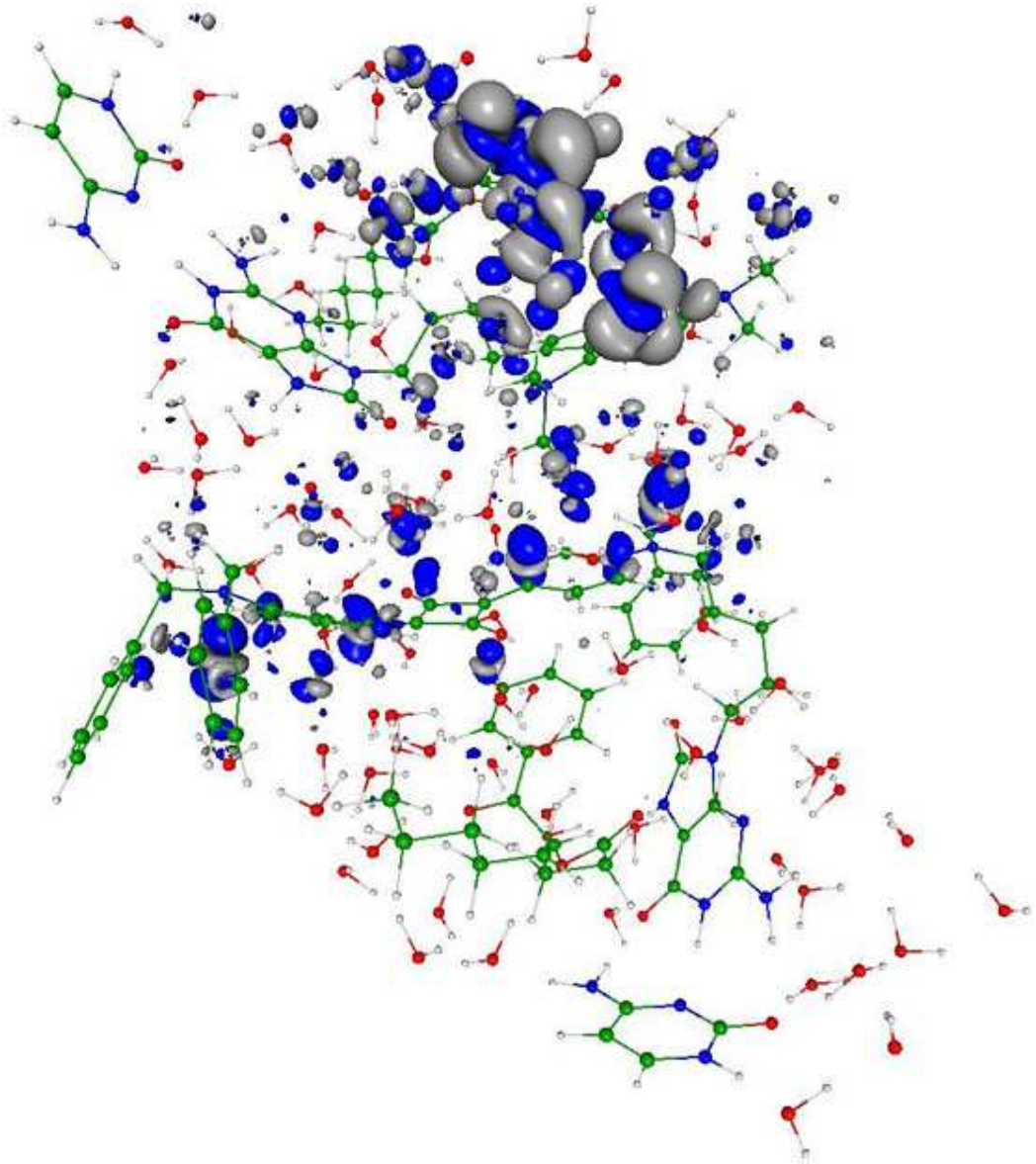
Our discovered phenomenon of the quantum entanglement in the prebiotic systems enhance the photosynthesis in the proposed systems because simultaneously excite two prebiotic kernels in the system by appearance of two additional quantum entangled excited states (Tamulis A, Grigalavicius M, Baltrusaitis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

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

"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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