

ORNL Neutrons for Magnetic Materials

Two of the world's most powerful sources for neutron scattering at the US Department of Energy's (DOE's) Oak Ridge National Laboratory (ORNL) are getting upgrades. [23]

Direct observations of the structure and catalytic mechanism of a prototypical kinase enzyme—protein kinase A or PKA—will provide researchers and drug developers with significantly enhanced abilities to understand and treat fatal diseases and neurological disorders such as cancer, diabetes, and cystic fibrosis. [22]

The ability to grow large protein crystals is the single biggest bottleneck that limits the use of neutron protein crystallography in structural biology. [21]

The conclusion that proteins have a terrible conductance tallies well with their general physical characteristics – they lack both electronic conduction bands and high levels of structural order. [20]

In their proof-of-concept study, the protein nanowires formed an electrically conductive network when introduced into the polymer polyvinyl alcohol. [19]

Nanocages are highly interesting molecular constructs, from the point of view of both fundamental science and possible applications. [18]

DNA flows inside a cell's nucleus in a choreographed line dance, new simulations reveal. [17]

Chemist Ivan Huc finds the inspiration for his work in the molecular principles that underlie biological systems. [16]

What makes particles self-assemble into complex biological structures? [15]

Scientists from Moscow State University (MSU) working with an international team of researchers have identified the structure of one of the key regions of telomerase—a so-called "cellular immortality" ribonucleoprotein. [14]

Researchers from Tokyo Metropolitan University used a light-sensitive iridium-palladium catalyst to make "sequential" polymers, using visible light to change how building blocks are combined into polymer chains. [13]

Researchers have fused living and non-living cells for the first time in a way that allows them to work together, paving the way for new applications. [12]

UZH researchers have discovered a previously unknown way in which proteins interact with one another and cells organize themselves. [11]

Dr Martin Sweatman from the University of Edinburgh's School of Engineering has discovered a simple physical principle that might explain how life started on Earth. [10]

Nearly 75 years ago, Nobel Prize-winning physicist Erwin Schrödinger wondered if the mysterious world of quantum mechanics played a role in biology. A recent finding by Northwestern University's Prem Kumar adds further evidence that the answer might be yes. [9]

A UNSW Australia-led team of researchers has discovered how algae that survive in very low levels of light are able to switch on and off a weird quantum phenomenon that occurs during photosynthesis. [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 ratio and the Weak and Strong Interactions by the diffraction patterns. The Weak Interaction changes the diffraction patterns by moving the electric charge from one side to the other side of the diffraction pattern, which violates the CP and Time reversal symmetry.

The diffraction patterns and the locality of the self-maintaining electromagnetic potential explains also the Quantum Entanglement, giving it as a natural part of the

Relativistic Quantum Theory and making possible to understand the Quantum Biology.

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Author: George Rajna

Preface

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.

ORNL neutrons add advanced polarization capability for measuring magnetic materials

Understanding magnetism at its most fundamental level is vital to developing more powerful electronics, but materials with more complex magnetic structures require more complex tools for studying them—powerful tools simply referred to as "neutrons."

Two of the world's most powerful sources for [neutron scattering](#) at the US Department of Energy's (DOE's) Oak Ridge National Laboratory (ORNL) are getting upgrades. Adding an advanced capability called spherical neutron polarimetry will enable researchers using ORNL's High Flux Isotope Reactor (HFIR) and Spallation Neutron Source (SNS) to make measurements of materials featuring exotic magnetic structures and quantum states that were previously inaccessible in the United States.

"Neutrons are ideal for studying magnetic phenomena," said ORNL post-masters researcher Nicolas Silva. "They're electrically neutral, or have no charge, and exhibit magnetic moments, which sort of make them like tiny magnets themselves."

When neutrons pass through a material and scatter off magnetic fields generated by a material's atoms, they paint an atomic portrait or even a 3-D model of the material's atomic arrangement and reveal how the atoms within the system are behaving.

Neutrons have a "spin," or orientation, like the north and south poles of refrigerator magnets. In a typical neutron beam, the neutrons within the beam have spins that are arranged randomly. Measuring certain highly dynamic or complex magnetic systems, however, requires more uniformity, which is provided by a polarized neutron beam in which each neutron spin is aligned in parallel and with the same orientation.

"Neutron polarization filters allow us to see through the stuff we don't want to see that might be muddying up the signal we're interested in," said instrument scientist Barry Winn. "Similar to how polarized lenses allow anglers to see fish swimming below that would be otherwise blocked by the water's reflection."

Neutrons will change their spins in predictable ways when they scatter. Using a polarized beam enables researchers to better understand what's happening in a material by establishing the neutron

spin before and measuring the neutron spin after the beam strikes the sample. For example, a neutron's spin could be flipped in the opposite direction during scattering.

"In the US, most of the measurements we've been doing with polarized neutrons until now have been based on whether the neutron, after being scattered from the material or its [magnetic field](#), gets rotated 180 degrees or preserves its orientation. We call that spin-flip and non-spin-flip," said Winn.

"But there's a problem with that. If we get any scattering off the sample that's something other than a non-spin-flip or spin-flip—or something other than 0 and 180 degrees—then the strategy blows up in our face."

The strategy works well for conventional magnetic materials such as ferromagnets and antiferromagnets, in which all the magnetic atoms are pointing either in the same direction or in alternate directions, but remain parallel to their neighbors. However, the strategy does not work for more complex magnetic structures.

For example, the technique is limited when it comes to investigating exotic particles such as skyrmions—quasi-particles that exhibit chiral motion, or tangled vortices, or whirlpools of asymmetric field lines. Such particles provide exciting potential for materials used in advanced data storage and quantum computing applications.

To tackle the problem, polarization scientist Peter Jiang is leading an ORNL team including Winn and Silva in a laboratory directed research and development project to develop spherical neutron polarimetry for multiple ORNL beamlines. The technology will enable neutron measurements of materials that don't conform to the traditional spin-flip and non-spin-flip domains, or, in other words, will enable researchers to see the dynamical magnetic behavior that exists in between.

"The traditional techniques are not sophisticated enough to study certain complex magnetic systems," said Jiang. "Now, we're no longer restricted to spin-flips. This allows us to look at magnetic arrangements that we weren't able to figure out before."

Spherical neutron polarimetry has been used in Europe, and now Jiang and the ORNL team are adapting the technology to instruments at SNS and HFIR. They're building the technology based on ongoing research conducted by Tianhao Wang, first as a graduate student at Indiana University, Bloomington, and later as a postdoctoral research on the ORNL team.

The basic technology incorporates additional optical devices installed on both the incoming beam that hits the sample—the incident beam—and the outgoing beam that scatters off it, which enables measurements of scattered neutrons oriented in any direction. The ORNL technology builds on previous prototype designs and will offer several innovations.

With the ORNL spherical neutron polarimetry devices, the scattered beam trajectory need not be in line with the incident beam but instead can be angled around the sample.

"That means if the neutron doesn't experience a full flip, we can adjust the field on the other end, or move the apparatus to detect neutrons scattering in different directions," explained Silva.

The team also developed two independent cooling systems to enable researchers to study how [magnetic structures](#) change as a function of temperature. The first system cools two spherical neutron polarization components located on either side of the sample to make them superconducting. The second system introduces an extra cryostat with [liquid helium auto-refilling](#) capability that allows researchers to more easily explore materials under a range of temperatures without interfering with the temperatures required for superconductivity in the first system.

Finally, the spherical neutron polarimetry devices are made with more efficient materials. Whereas previous designs use niobium for the superconducting sheets, the new design uses an yttrium-barium-copper-oxide (YBCO) that superconducts at 93 Kelvin (-292° F), a significantly higher temperature than its niobium predecessor. Additionally, the superconducting films are coupled with Mu-metal yokes that combine to shield all other magnetic fields and establish a zero field around the sample to study the materials' spins in their natural state.

"Reaching superconductivity requires a significant amount of cooling power. Niobium needs to be cooled to below 10 K to maintain superconductivity, so the European designs required extensive cooling systems that had to be manually refilled with liquid helium often," said Jiang.

"With the high-temperature YBCO films, we can use a single-stage closed-cycle refrigerator to cool the film to far below its critical temperature, so we're not worried about any loss in superconductivity. And, with the added liquid helium autofill system for the cryostat and the closed-cycle refrigeration system, the device will be easier to use and more efficient."

What's more, the system is compact by comparison with previous systems—the high-temperature superconductors that negate the need for a large cooling system make it mobile.

"If anything, there's a testament to how portable the device is. We've moved it to the [nuclear reactor at the University of Missouri](#), then back to HFIR, and from HFIR to SNS," said Silva. "I've put it together and taken it apart multiple times, and each time I've found easier ways to connect the pieces—just little quality-of-life changes we're making to enhance its utility."

The system has been successfully tested, wherein full polarization measurements were made using several known materials including silicon, manganese-oxide, and bismuth-iron-oxide.

The team plans to implement the system at HFIR's PTAX triple axis spectrometer and the GP-SANS diffractometer, which will be optimized for the reactor's steady-state neutron beam, with full capabilities expected by the end of 2020.

Subsequently, the team will develop a similar spherical [neutron](#) polarimetry device exclusively for the HYSPEC instrument at SNS which will make it the only instrument in the world that couples a [super-mirror array](#) and wide-angle capability. The device will also benefit from the unique capabilities enabled by the SNS pulsed-source accelerator.

"In the meantime," said Winn, "we're going to have a workhorse in PTAX that's going to knock our socks off." [23]

Neutrons paint atomic portrait of prototypical cell signaling enzyme

Direct observations of the structure and catalytic mechanism of a prototypical kinase enzyme—protein kinase A or PKA—will provide researchers and drug developers with significantly enhanced abilities to understand and treat fatal diseases and neurological disorders such as cancer, diabetes, and cystic fibrosis.

The discovery was made by an international team of researchers using macromolecular neutron crystallography at the Department of Energy's Oak Ridge National Laboratory and the Institut Laue-Langevin in Grenoble, France. Building on a decade-long investigation, the combined efforts revealed previously unknown characteristics of the archetypal protein [kinase](#), including a complete map of the atomic [structure](#) and the underpinnings of the enzyme's chemistry used in cellular signaling. The details are published in the journal *Science Advances*.

Kinases are a large group of hundreds of enzymes responsible for initiating and regulating myriad cellular processes. Kinases send signals to proteins by way of phosphorylation—adding a reactive chemical group consisting of phosphorus and oxygen to a specific location on a substrate protein to activate its specific biological function.

Problems arise when gene mutations cause kinases to work improperly, which in turn leads to disease. A malfunctioning kinase, or one that can't be deactivated, could be responsible for the overexpression of proteins that lead to the uncontrollable propagation of cancer cells. The opposite is also true in neurological disorders in which a malfunctioning kinase simply causes cells to die.

"Creating drugs that target specific kinases is extremely important," said co-author Andrey Kovalevsky. "This detailed understanding of the PKA structure and its dynamics will tell us more about other kinds of kinases and should help drug developers design new drugs with better specificity, which would ultimately translate to more precise therapeutics with fewer side effects."

Changes in the [protein structure](#) due to mutations can be difficult to detect even though the effects of mutations on the protein dynamical behavior can be quite profound. However, these dynamical behaviors become more apparent by examining the overall hydrogen bonding network throughout the protein.

Neutrons are uniquely sensitive to light elements such as hydrogen. Because approximately 50 percent of all atoms in proteins are hydrogen, and most of the chemical reactions that enzymes catalyze involve hydrogen, neutrons are an ideal and unsurpassed probe for detecting the positions of hydrogen atoms within the protein structure and tracking their movement during catalysis.

Neutron diffraction using the IMAGINE diffractometer at ORNL's High Flux Isotope Reactor, a DOE Office of Science User Facility, and the LADI-III diffractometer at ILL enabled researchers to see the exact positions of hydrogen atoms to reveal the complete kinase structure as well as the protonation

states of all amino acids in PKA and the ligands bound to its active site, many of which were previously unknown.

"Neutrons enabled us to validate X-ray predictions of hydrogen atom positions, as well as determining the protonation states of chemical groups that were not known, or in places where we didn't expect to find them. This major chemical advance paves the way for more sophisticated molecular modeling and simulation studies of protein kinase structure and function," said corresponding author Susan Taylor.

"Neutrons offer an unprecedented view of the [hydrogen](#) bond network surrounding and within the [active site](#) of PKA and give crucial insights on how allosteric transmission of information through the [protein](#) structure occurs," added co-author Gianluigi Veglia. "Combining [neutron](#) crystallography with [nuclear magnetic resonance spectroscopy](#) will provide a comprehensive understanding of how enzymes work." [22]

Methods for large protein crystal growth for neutron protein crystallography

The ability to grow large protein crystals is the single biggest bottleneck that limits the use of neutron protein crystallography in structural biology. Protein crystals need to have volumes in the region of at least 0.1mm^3 . Theoretically there is no particular reason why crystals of this size cannot be grown. If they can be, neutron protein crystallography can provide crucial information on the location of hydrogen atoms details relating to hydration hydrogen bonding and ligand interactions. This type of information is of direct relevance to academic and pharmacologically driven research in the life sciences.

The challenge is thus to achieve large crystal growth in a reproducible, time-saving, labour-saving way. It would be ideal if in the future, neutron crystallographers can, after suitable pre-characterisation work, submit their solutions to an automated or semi-automated platform that would allow the exploration of a large range of conditions in a highly systematic way and to allow users to monitor growth from their remote computers.

Ashley Jordan at the Institut Laue-Langevin (ILL) in Grenoble, France, has been investigating two new crystal growth methods: the development of a module that could allow larger scale automated approaches in the future (task 1), and a flow crystallization system (task 2).

Task 1: A module for automated large crystal growth exploration

This SINE2020 project has focused on the development of a temperature controllable multi-well module in which crystal growth can be optimized. The idea of designing this module was to scale up the approach so that multiple crystallization wells with individual (programmable) [temperature control](#) could be used to explore a wide range of growth conditions. A prototype module was made that consisted of a custom plate design containing 6×4 wells where the individual crystallisation experiments can occur. Each well can be adapted to different conditions, with each having independent temperature control. The wells are heated using Peltier heating elements with a temperature feedback system that allows each well to be heated and cooled over a temperature

range of 4 degrees C to 60 degrees C, with an accuracy of 0.1 degree. The set-up was designed to allow crystal growth to be monitored and recorded photographically.

Ashley Jordan, Ryo Mizuta and John Allibon (who developed the software) have built and tested the prototype system. Crystallization tests have been carried out using trypsin and rubredoxin.

Post-SINE2020, the idea would be to make these modules "plug and play" so that a more extended 'robotic' approach could be used. Crystallography runs could be removed by the user on completion and other runs installed using another module – the module would be the working unit of a larger array – with all being camera visualisable and providing time-lapse information to a user portal.

Task 2: Flow crystallization

Another way of pursuing large crystal growth is the idea of a flow crystallization system. The idea is to maintain steady-state batch conditions around a crystal at all times during its growth, by providing a constant supply of fresh protein stock to the crystallization environment. This will maintain optimal solution conditions at all times and help minimize accumulation of impurities on crystal surfaces – such impurities may hinder crystal growth.

A Dolomite Mito P-Pump was chosen to maintain the extremely low flow rate (between 70-1500 nl min⁻¹) required to regulate the system. A suitable crystallization chamber that can connect to the pump was designed and made using a 3-D printer. This chamber creates a sealed environment and provides ready access to the [crystals](#) once they have grown. [21]

STM measurements redefine protein conductances

“Properly connected, proteins are the world’s best molecular wires,” says [Stuart Lindsay](#), Director and Professor at the Biodesign Center for Single Molecule Biophysics at Arizona State University (ASU). His comments refer to recent experiments at ASU to measure the conductance of single proteins between electrodes for the first time with what he describes as “staggering” results that may have uses for direct, label-free, sensitive, and very selective (background-free) single-molecule detection as well as protein motion sensing. “Measurements on peptides (small protein chains) show they are the world’s worst molecular wires,” he adds. So what changed?

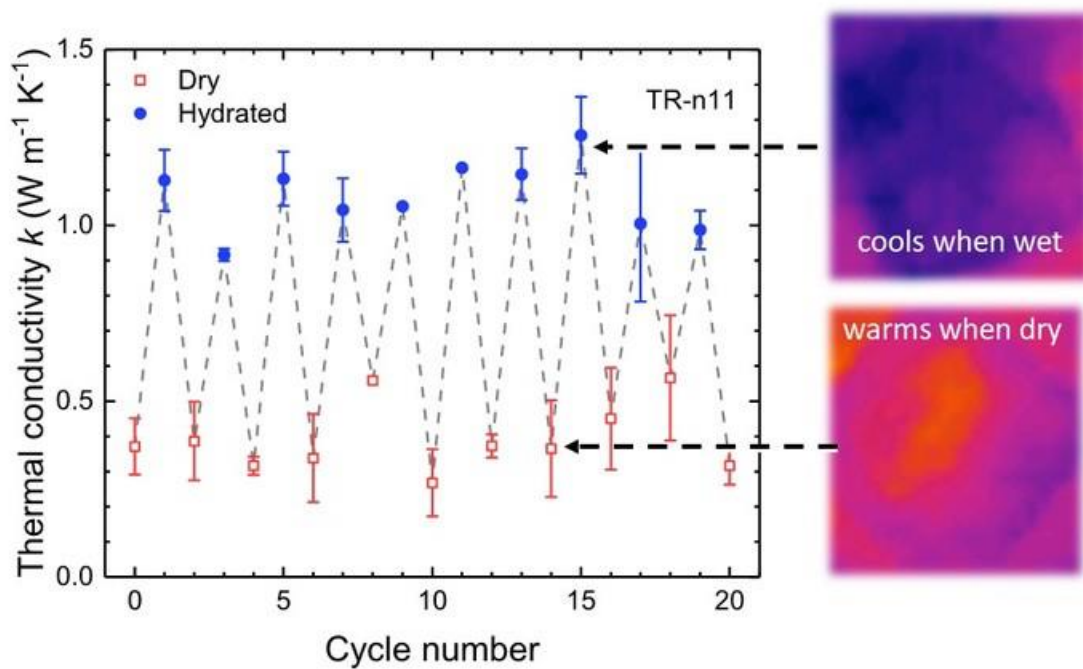
Contact control

The conclusion that proteins have a terrible conductance tallies well with their general physical characteristics – they lack both electronic conduction bands and high levels of structural order. Previous experiments have attempted to investigate the conductance of proteins by injecting electrons from optically excited chromophores, but contacting the molecule to an electrode allows studies of the response to injection of electrons with much lower energies. However so far these have struggled against the uncertainty in the number of molecules contacted, the size of the gap, the nature of the contacts, and possible ionic contributions to the current measured.

Here scanning tunnelling measurements present significant advantages over macroscopic contact devices as Lindsay explains because they allow for single-molecule contacts. “In addition, we carry out the experiments under electrochemical potential control so we can be certain there are no ionic

currents and we use chemically well-defined contacts, so that we know (and can control) the metal-molecule interface.”

The resulting conductances measured in the nanosiemens range over distances of several nanometres. Having ruled out ionic currents the researchers were also able to eliminate possible meaningful contributions from tunnelling, which would be five orders of magnitude weaker. Crucially, while the conductance varied little with the length of the protein, the conductance was highly dependent on the chemistry of the electrodes, which the researchers functionalized with specific ligands for different proteins.



Squid-inspired proteins make new thermal switch

Current pathways

The researchers found that the chemistry of the contacts was so significant that weaker coupling to the hydrophobic interior of the protein provided a stronger current than a stronger coupling to the hydrophilic exterior. The researchers describe the role of contact chemistry in terms of the path the current takes either across the surface or through the interior. “We hypothesize that the hydrophobic

interior of proteins is a wonderful place for electrons to propagate and that electrons are injected into the interior of the protein using specific ligands,” Lindsay tells *Physics World*.

The experiments also reveal fluctuations that set in above a threshold applied bias of 100 mV in magnitude. Comparison of the lifetime of the on states with the peak current magnitude indicate a single barrier that determines both the current and bonding strength at the contact. The magnitude of this barrier within the relevant exponential expression matches that of a hydrogen bond suggesting that a hydrogen bond may be playing the role of “weak link in the circuit”. The conductance values measured are also compatible with those calculated for thermally activated hopping over a 0.22–0.47-V barrier, the size of the hydrogen bond. “We have devised and implemented a new scheme to extract the electronic decay length, and temperature dependent measurements are underway as well,” adds Lindsay.

Significant findings

Further experiments demonstrated the potential for using the strong ligand specific conductance for single-molecule, highly specific, label- and background free electronic detection of IgG antibodies to HIV and Ebola viruses, and the researchers are now working on technological applications of the results. “The wonderful thing about sorting out the connections issue is that we have a “tool kit” for bioelectronics mapped out,” says Lindsay as he lists them. “(1) For wires, use ligand connected proteins. This not only makes a fantastic contact, but it also makes a self-assembling, directed contact. (2) Multivalent proteins complete circuits and can generate branched wiring. (3) Since the conductivity “reads” the internal state of the protein, enzymes can be wired as single molecule sensors with an exquisite response. Future results from the lab will illustrate this.”

What may take a little longer to unravel is the biological role of protein conductances. Here Lindsay points towards [theoretical calculations by Gabor Vattay](#), which show that the calculated energy level distribution in a number of proteins matches that expected for a very unusual state of matter called “quantum critical”, which also matches certain [previous observations of giant protein conductance fluctuations](#). “If this is true, then proteins must have evolved a rather special structure. So why?” asks Lindsay. “I don’t know, but it is very interesting that ligand mediated contacts allow for sharing of electrons. Does this play a role in recognition?” he adds, highlighting the weaker contacts forged by strong, covalent modifications of residues on the outside of a protein compared with weaker contacts made by ligands that reach into the protein. In terms of biological significance, it seems these latest results raise at least as many questions as they answer.

Full details are reported in the [Proceedings of the National Association of Science](#). [20]

Scientists make new 'green' electronic polymer-based films with protein nanowires

An interdisciplinary team of scientists at the University of Massachusetts Amherst has produced a new class of electronic materials that may lead to a "green," more sustainable future in biomedical

and environmental sensing, say research leaders microbiologist Derek Lovley and polymer scientist Todd Emrick.

They say their new work shows it is possible to combine protein [nanowires](#) with a [polymer](#) to produce a flexible electronic composite material that retains the electrical conductivity and unique sensing capabilities of protein nanowires. Results appear in the journal *Small*.

Protein nanowires have many advantages over the [silicon nanowires](#) and carbon nanotubes in terms of their biocompatibility, stability, and potential to be modified to sense a wide range of biomolecules and chemicals of medical or environmental interest, says Lovley. However, these sensor applications require that the protein nanowires be incorporated into a flexible matrix suitable for manufacturing wearable sensing devices or other types of electronic devices.

As Lovley explains, "We have been studying the biological function of protein nanowires for over a decade, but it is only now that we can see a path forward for their use in practical fabrication of electronic devices." Postdoctoral research Yun-Lu Sun, now at the University of Texas at Austin, discovered the proper conditions for mixing protein nanowires with a non-conductive polymer to yield the electrically conductive composite material. He demonstrated that although the wires are made of protein, they are very durable and easy to process into new [materials](#).

"An additional advantage is that protein nanowires are a truly 'green,' sustainable material," Lovley adds. "We can mass-produce protein nanowires with microbes grown with renewable feedstocks. The manufacture of more traditional nanowire materials requires high energy inputs and some really nasty chemicals." By contrast, he says, "Protein nanowires are thinner than silicon wires, and unlike silicon are stable in water, which is very important for biomedical applications, such as detecting metabolites in sweat."

Emrick adds, "These electronic protein nanowires bear surprising resemblance to polymer fibers and we're trying to figure out how to combine the two most effectively."

In their proof-of-concept study, the protein nanowires formed an electrically conductive network when introduced into the polymer polyvinyl alcohol. The material can be treated with harsh conditions, such as heat, or extreme pH such as high acidity, that might be expected to ruin a protein-based composite, but it continued to work well.

The conductivity of the protein nanowires embedded in the polymer changed dramatically in response to pH. "This is an important biomedical parameter diagnostic of some serious medical conditions," Lovley explains. "We can also genetically modify the structure of the protein nanowires in ways that we expect will enable detection of a wide range of other molecules of biomedical significance."

The electrically conductive protein nanowires are a natural product of the microorganism *Geobacter* discovered in Potomac River mud by Lovley more than 30 years ago. *Geobacter* uses the protein nanowires to make electrical connections with other microbes or minerals. He notes, "Material science experts like Todd Emrick and Thomas Russell on our team deserve the credit for bringing [protein](#) nanowires into the materials field. It's not just about mud anymore."

In this work supported by UMass Amherst campus funds for exploratory research, next steps for the collaborative materials-microbiology team include scaling up production of nanowire-polymer matrices, Lovley says.

He points out, "Materials scientists need a lot more nanowires than we're used to making. We're were making thimblefuls for our biological studies. They need buckets full, so we are now concentrating on producing larger amounts and on tailoring the nanowires so they'll respond to other molecules." The researchers have also applied for a patent on the idea of a conductive polymer made with [protein nanowires](#). [19]

Nanocages in the lab and in the computer: how DNA-based dendrimers transport nanoparticles

How to create nanocages, i.e., robust and stable objects with regular voids and tunable properties? Short segments of DNA molecules are perfect candidates for the controllable design of novel complex structures. Physicists from the University of Vienna, the Technical University of Vienna, the Jülich Research Center in Germany and Cornell University in the U.S.A., investigated methodologies to synthesize DNA-based dendrimers in the lab and to predict their behavior using detailed computer simulations. Their results are published in *Nanoscale*.

Nanocages are highly interesting molecular constructs, from the point of view of both fundamental science and possible applications. The cavities of these nanometer-sized objects can be employed as carriers of smaller molecules, which is of critical importance in medicine for drug or gene delivery in living organisms. This idea brought together researchers from various interdisciplinary fields who have been investigating dendrimers as promising candidates for creating such nano-carriers. Their tree-like architecture and step-wise growth with repeating self-similar units results in dendrimers containing cavities, hollow objects with controllable design. Nevertheless, decades of research have showed that vast number of different dendrimer types experience back-folding of outer branches with growing dendrimer generations, giving rise to a higher density of constituents in the molecule's interior. The effect of back-folding is enhanced upon addition of salt in the solution, whereby flexible dendrimers undergo significant shrinking, becoming compact objects with no hollow spaces in their interior.

The team of collaborators consisted of Nataša Adžić and Christos Likos (University of Vienna), Clemens Jochum and Gerhard Kahl (TU Wien), Emmanuel Stiakakis (Jülich) as well as Thomas Derrien and Dan Luo (Cornell). The researchers found a way to create dendrimers rigid enough to prevent back-folding of outer arms even in the case of high branching generations, preserving regular voids in their interior. Moreover, their novel macromolecules are characterized by remarkable resistance to added salt: they showed that the morphology and conformational characteristics of these systems stay unaffected even upon of addition of salt even at high concentration. The nanocages they created, in the lab and studied computationally are DNA-based dendrimers, or so-called, dendrimer-like DNAs (DL-DNA). The building block they are composed of is a Y-shaped double-stranded DNA unit, a three-armed structure consisting of double-stranded DNA (ds-DNA), formed via hybridization of three single-stranded DNA chains (ss-DNA), each of which has partially complementary sequences to the other two. Each arm is made up of 13 base pairs and a single-stranded sticky end with four nucleobases which acts as a glue. While a single Y-DNA corresponds to the first dendrimer generation,

the attachment of further Y-DNA elements yields DL-DNA of higher generations. The resulting dendrimer is a charged and hollow-containing macromolecular assembly with tree-like architecture. Due to the rigidity of dsDNA, the branches of DL-DNA are stiff so that the whole molecule is rigid. Since DNA is charged, the electrostatic repulsion enhances the rigidity of the molecule.

DL-DNA molecules have been assembled in the laboratory by the Jülich and Cornell partners with remarkable control and sub-nanometer precision through programmable sticky-end cohesions. Their step-wise growth is highly controllable, unidirectional and non-reversible. This property is of high importance, as it has been shown that DNA-based dendrimers have been envisioned to play a promising role in developing nanoscale-barcodes, DNA-based vaccine technologies, as well as a structural probes involving multiplexed molecular sensing processes. Sizes, shapes as well as additional conformational details invisible to the experimentalists, such as the size of voids and the degree of branches back-folding, have been analyzed by computer simulations in Vienna. To describe the complex structure of DNA units, the group used a simple monomer-resolved model with interactions carefully chosen to mimic the equilibrium properties of DNA in physiological solution. The excellent agreement obtained between experiments and simulations for the [dendrimer](#) characteristics validates the theoretical models employed and paves the way for further investigation of the nanocages' properties and their applications as functional and smart nanocarriers and as building blocks for engineering biocompatible artificial materials. [18]

DNA 'dances' in first explanation of how genetic material flows through a nucleus

DNA flows inside a cell's nucleus in a choreographed line dance, new simulations reveal. The finding is the first large-scale explanation of genetic material moving within a working cell.

"Previous work mostly focused on what was going on at the microscale of DNA," says study co-author Michael Shelley, group leader for biophysical modeling at the Flatiron Institute's Center for Computational Biology in New York City and co-director of the Courant Institute's Applied Mathematics Laboratory at New York University. "People didn't really think about what was going on at the larger scale."

Shelley and colleagues simulated the motions of chromatin, the functional form of DNA inside the nucleus. Chromatin looks like beads on a string, with ball-like clusters of [genetic material](#) linked by strands of DNA. The researchers propose that molecular machines along the DNA cause segments of the chromatin to straighten and pull taut. This activity aligns neighboring strands to face the same direction. That alignment, in turn, results in a cascading waltz of genetic material shimmying across the nucleus.

[The dancing DNA may play a role in gene expression, replication and remodeling](#), though the exact effects remain unclear, the researchers reported online October 22 in *Proceedings of the National Academy of Sciences*.

The findings help explain [measurements reported in 2013](#) by scientists, including Alexandra Zidovska, at Harvard University. Besides previously known small-scale motions of individual genes, the

scientists' experiment revealed large regions of chromatin that shifted in unison through a cell's nucleus at a rate of a fraction of a micron every few seconds. The scientists, though, couldn't identify the cause or details of the movement.

Shelley's had experience studying how microbes swim. The similar physics involved made him curious about the mechanism behind the migrating DNA. He partnered with David Saintillan of the University of California, San Diego, and Zidovska, now of New York University, to investigate.

The researchers investigated two ways a molecular machine along a DNA molecule might move nearby genetic material: pulling and pushing. A molecular machine can't exert a net force, which means that by pulling on one piece of DNA, it must hold onto and pull something else. The two inward-pulling forces will cancel, giving zero net force and causing the DNA segment to contract. If the machine instead pushes outward, the forces will similarly cancel, and the DNA segment will extend.

These contractions and extensions take place within a gooey liquid that fills a cell's nucleus. The movement of the DNA generates a flow in the liquid that can reorient nearby lengths of molecules.

Using computer simulations, the researchers modeled how contraction and extension affected a jumble of chromatin confined within a spherical nucleus. When the lengths of DNA contracted, the resulting flow pointed nearby strands in a different direction, blocking any choreographed movements. Extension created streams of fluid that aligned nearby DNA in the same direction. That alignment resulted in a cascading effect that shifted large patches of DNA in the same direction.

"It's like part of the nucleus suddenly decides that we're all going to move over this way a little, then another bit says we're all going to move over this way," Shelley says. "The chromatin sort of wanders around."

This DNA shimmy could help distribute throughout the [nucleus](#) the molecular machinery responsible for expressing a particular gene, Shelley proposes. Finding out for sure, he says, will require more complex simulations as well as additional experiments into how [chromatin](#) cuts a rug. [17]

Biomimetic chemistry—DNA mimic outwits viral enzyme

Not only can synthetic molecules mimic the structures of their biological models, they can also take on their functions and may even successfully compete with them, as an artificial DNA sequence designed by Ludwig-Maximilians-Universitaet (LMU) in Munich chemist Ivan Huc now shows.

Chemist Ivan Huc finds the inspiration for his work in the molecular principles that underlie biological systems. As the leader of a research group devoted to biomimetic supramolecular chemistry, he creates 'unnatural' molecules with defined, predetermined shapes that closely resemble the major biological polymers, proteins and DNA found in cells. The backbones of these molecules are referred to as 'foldamers' because, like origami patterns, they adopt predictable shapes and can be easily modified. Having moved to LMU from his previous position at Bordeaux University last summer, Huc has synthesized a helical molecule that mimics surface features of the DNA double helix so closely that bona fide DNA-binding proteins interact with it.

This work is described in a paper published in *Nature Chemistry*. The new study shows that the synthetic compound is capable of inhibiting the activities of several DNA-processing enzymes, including the 'integrase' used by the [human immunodeficiency virus](#) (HIV) to insert its genome into that of its host cell. The successful demonstration of the efficacy of the synthetic DNA mimic might lead to a new approach to the treatment of AIDS and other retroviral diseases.

The new paper builds on advances described in two previous publications in *Nature Chemistry* published earlier this year. In the first of these papers, Huc and his colleagues developed a pattern of binding interactions required to enable synthetic [molecules](#) to assume stable forms similar to the helical backbones of proteins. In the second, they worked out the conditions required to append their synthetic helix to natural proteins during synthesis by cellular ribosomes. "As always in biology, shape determines function," he explains. In the new study, he introduces a synthetic molecule that folds into a helical structure that mimics surface features of the DNA double helix, and whose precise shape can be altered in a modular fashion by the attachment of various substituents. This enables the experimenter to imitate in detail the shape of natural DNA double helix, in particular the position of negative charges. The imitation is so convincing that it acts as a decoy for two DNA-binding enzymes, including the HIV integrase, which readily bind to it and are essentially inactivated.

However, the crucial question is whether or not the foldamer can effectively compete for the enzymes in the presence of their normal DNA substrate. "If the enzymes still bind to the foldamer under competitive conditions, then the mimic must be a better binder than the natural DNA itself," Huc says. And indeed, the study demonstrates that the HIV integrase binds more strongly to the foldamer than to natural DNA. "Furthermore, although initially designed to resemble DNA, the foldamer owes its most useful and valuable properties to the features that differentiate it from DNA," Huc points out.

Thanks to the modular nature of foldamer design, the structures of these artificial DNA mimics can be readily altered, which enables a broad range of variants to be produced using the same basic platform. In the current study, Huc and his colleagues have focused on enzymes that are generically capable of binding to DNA, irrespective of its base sequence. However, it may also be possible to use the foldamer approach to develop DNA mimics that can block the action of the many important DNA-binding proteins whose functions depend on the recognition of specific nucleotide sequences. [16]

Simulations document self-assembly of proteins and DNA

What makes particles self-assemble into complex biological structures? Often, this phenomenon is due to the competition between forces of attraction and repulsion, produced by electric charges in various sections of the particles. In nature, these phenomena often occur in particles that are suspended in a medium—referred to as colloidal particles—such as proteins, DNA and RNA. To facilitate self-assembly, it is possible to "decorate" various sites on the surface of such particles with different charges, called patches.

In a new study published in *EPJE*, physicists have developed an algorithm to simulate the molecular dynamics of these patchy [particles](#). The findings published by Silvano Ferrari and colleagues from the

TU Vienna and the Centre for Computational Materials Science (CMS), Austria, will improve our understanding of what makes self-assembly in biological systems possible.

In this study, the authors model charged patchy particles, which are made up of a rigid body with only two charged patches, located at opposite poles. They then develop the equations governing the dynamics of an ensemble of such colloidal patchy particles.

Based on an existing approach originally developed for molecular particles, their simulation includes additional constraints to guarantee that the electrical charge "decorations" are preserved over time. In this regard, they develop equations for describing the particles' motion; the solutions to these equations describe the trajectories of these colloidal particles. Such [molecular dynamics](#) simulations lend themselves to being run in parallel on a huge number of particles.

With these findings, the authors complement the lessons learned from experimental observations of similar particles recently synthesised in the lab. Recent experiments have demonstrated that [colloidal particles](#) decorated at two interaction sites display a remarkable propensity for self-organising into highly unusual structures that remain stable over a broad temperature range. [15]

Scientists explore the structure of a key region of longevity protein telomerase

Scientists from Moscow State University (MSU) working with an international team of researchers have identified the structure of one of the key regions of telomerase—a so-called "cellular immortality" ribonucleoprotein. Structural and functional studies on this protein are important for the development of potential anticancer drugs. The results of the study have been published in *Nucleic Acids Research*.

Each cell goes through a DNA replication process before division. This is a precise, fine-tuned process controlled by the coordinated work of a sophisticated enzymatic machinery. However, due to the nature of the copying process, the termini of DNA molecules are left uncopied, and DNA becomes shorter with each replication. However, no important data is lost in the process, as the termini of DNA molecules (telomeres) consist of thousands of small, repeated regions that do not carry hereditary information. When the reserve of telomere repetitions is exhausted, the cell ceases to divide, and eventually, it can die. Scientists believe that this is the mechanism of cellular aging, which is necessary for the renewal of cells and tissues of the body.

But how do "immortal" strains and stem cells that give life to a huge number of offspring cope with this? This is where the enzyme [telomerase](#) comes into play. It can restore telomeric termini of chromosomes and therefore compensate for their shortening during mitosis. The telomerase protein catalytic subunit works together with the RNA molecule, and its short fragment is used as a template to synthesize telomeric repetitions. MSU-based scientists discovered the structure of the telomerase fragment that is in charge of this process.

"Our work is aimed at the structural characterization of the telomerase complex. In a living cell, it includes a catalytic subunit, an RNA molecule, a segment of telomeric DNA, and several auxiliary components. Anomalously low activity of telomerase caused by genetics can result in serious pathogenic conditions (telomeropathy), while its anomalous activation is the reason for the cellular "immortality" of most known cancers. Information on the structure of telomerase and the relationships between its components is necessary for understanding the function and regulation of this enzyme, and in the future, for directed control of its activity," said Elena Rodina, assistant professor of the Department for the Chemistry of Natural Products, Faculty of Chemistry, MSU.

Working with thermotolerant yeast, a model eukaryotic organism, the researchers determined the structure of one of the major domains of the telomerase catalytic subunit (the so-called TEN-domain) and determined which parts of it are responsible for the interaction of the enzyme with the RNA molecule and the synthesized DNA. Based on the experimental data obtained, the scientists constructed a theoretical model of the catalytic core of telomerase.

The activity of the enzyme may be described in a simplified way: Telomerase can be represented as a molecular machine containing an RNA molecule. This machine, with the help of a template part of RNA, binds to the end of a long chain of DNA, and synthesizes a fragment of a new DNA chain along the remaining template fragment. After that, the telomerase machine has to move to the newly synthesized end of the DNA in order to continue to build up the chain. The scientists assume that the TEN-domain allows telomerase to synthesize DNA fragments of strictly defined length, after which the RNA template should be detached from the DNA strand to move closer to its edge. Thus, the TEN domain facilitates the movement of the enzyme to building up a new region, i.e. the next telomeric fragment, and this is how the synthesis cycle is repeated.

In addition, the researchers identified the structural core of the TEN domain that remained unchanged in a variety of organisms, despite all the evolutionary vicissitudes, which indicates the important role of this core in the function of the enzyme. The team also revealed the elements specific for different groups of organisms, which interact with own proteins of individual telomerase complex.

"The data obtained bring us closer to an understanding of the structure, function and regulation of telomerase. In the future, this knowledge can be used to create drugs aimed at regulating telomerase activity—either to increase it (for example, to increase the cell life span in biomaterials for transplantology) or to reduce (for instance, for immortal cancer cells to lose their immortality)," concludes Elena Rodina. [14]

Custom sequences for polymers using visible light

Researchers from Tokyo Metropolitan University used a light-sensitive iridium-palladium catalyst to make "sequential" polymers, using visible light to change how building blocks are combined into polymer chains. By simply switching the light on or off, they were able to realize different compositions along the polymer chain, allowing precise control over physical properties and material

function. This may drastically simplify existing polymer production methods, and help overcome fundamental limits in creating new polymers.

The world is full of long, chain-like molecules known as polymers. Famous examples of "sequential" copolymers, i.e. polymers made of multiple [building blocks](#) (or "monomers") arranged in a specific order, include DNA, RNA and proteins; their specific structure imparts the vast range of molecular functionality that underpins biological activity. However, making sequential polymers from scratch is a tricky business. We can design special monomers that assemble in different ways, but the complex syntheses that are required limit their availability, scope and functionality.

To overcome these limits, a team led by Associate Professor Akiko Inagaki from the Department of Chemistry, Tokyo Metropolitan University, applied a light-sensitive catalyst containing iridium and palladium. By switching a light on and off, they were able to control the speed at which two different monomers, styrene and vinyl ether, become part of a [polymer chain](#). When exposed to light, the styrene monomer was found to be incorporated into the copolymer structure much more rapidly than in the dark, resulting in a single copolymer chain with different compositions along its length. Parts that are rich in styrene are more rigid than those rich in vinyl ether; by using different on/off [light](#) sequences, they could create polymers with a range of [physical properties](#) e.g. different "glass transition" temperatures, above which the [polymer](#) becomes softer.

The newly developed process is significantly simpler than existing methods. The team also found that both types of monomer were built into the polymer via a mechanism known as non-radical coordination-insertion; this is a generic mechanism, meaning that this new method might be applied to make polymers using a wide range of catalysts and monomers, with the potential to overcome the limited availability of [monomer](#) candidates. [13]

Artificial and biological cells work together as mini chemical factories

Researchers have fused living and non-living cells for the first time in a way that allows them to work together, paving the way for new applications.

The system, created by a team from Imperial College London, encapsulates biological cells within an [artificial cell](#). Using this, researchers can harness the natural ability of biological cells to process chemicals while protecting them from the environment.

This system could lead to applications such as cellular 'batteries' powered by photosynthesis, synthesis of drugs inside the body, and biological sensors that can withstand harsh conditions.

Previous artificial cell design has involved taking parts of biological cell 'machinery' - such as enzymes that support [chemical](#) reactions - and putting them into artificial casings. The new study, published today in *Scientific Reports*, goes one step further and encapsulates entire cells in artificial casings.

The artificial cells also contain enzymes that work in concert with the biological cell to produce new chemicals. In the proof-of-concept experiment, the artificial cell systems produced a fluorescent chemical that allowed the researchers to confirm all was working as expected.

Lead researcher Professor Oscar Ces, from the Department of Chemistry at Imperial, said: "Biological cells can perform extremely complex functions, but can be difficult to control when trying to harness one aspect. Artificial cells can be programmed more easily but we cannot yet build in much complexity.

"Our new system bridges the gap between these two approaches by fusing whole biological cells with artificial ones, so that the machinery of both works in concert to produce what we need. This is a paradigm shift in thinking about the way we design artificial cells, which will help accelerate research on applications in healthcare and beyond."

To create the system, the team used microfluidics: directing liquids through small channels. Using water and oil, which do not mix, they were able to make droplets of a defined size that contained the biological cells and enzymes. They then applied an artificial coating to the droplets to provide protection, creating an artificial cell environment.

They tested these artificial cells in a solution high in copper, which is usually highly toxic to biological cells. The team were still able to detect fluorescent chemicals in the majority of the artificial cells, meaning the biological cells were still alive and functioning inside. This ability would be useful in the human body, where the artificial cell casing would protect the foreign biological cells from attack by the body's immune system.

First author of the study Dr Yuval Elani, an EPSRC Research Fellow also from the Department of Chemistry, said: "The system we designed is controllable and customisable. You can create different sizes of artificial cells in a reproducible manner, and there is the potential to add in all kinds of cell machinery, such as chloroplasts for performing photosynthesis or engineered microbes that act as sensors."

To improve the functionality of these artificial cell systems, the next step is to engineer the artificial coating to act more like a biological membrane, but with special functions.

For example, if the membrane could be designed to open and release the chemicals produced within only in response to certain signals, they could be used to deliver drugs to specific areas of the body. This would be useful for example in cancer treatment to release targeted drugs only at the site of a tumour, reducing side effects.

While a system like that may be a way off yet, the team say this is a promising leap in the right direction. The work is the first example of fusing living and non-living components to emerge from Imperial and King's College's new FABRICELL centre for artificial cell science. [12]

New interaction mechanism of proteins discovered

UZH researchers have discovered a previously unknown way in which proteins interact with one another and cells organize themselves. This new mechanism involves two fully unstructured proteins forming an ultra-high-affinity complex due to their opposite net charge. Proteins usually bind one another as a result of perfectly matching shapes in their three-dimensional structures.

Proteins are among the most important biomolecules and are the key mediators of molecular communication between and within cells. For two proteins to bind, specific regions of their three-dimensional structures have to match one another exactly, as a key fits into a lock. The structure of proteins is extremely important for their functioning and for triggering the required responses in cells. Now, researchers at the University of Zurich, together with colleagues from Denmark and the U.S., have discovered that unstructured proteins can also have ultra-high-affinity interactions.

One of these proteins is histone H1, which, as a component of chromatin, is responsible for DNA packaging. Its binding partner, prothymosin α , acts as a kind of shuttle that deposits and removes the histone from the DNA. This process determines whether or not genes in specific parts of the DNA can be read. Both proteins are involved in several regulatory processes in the body, such as cell division and proliferation, and therefore also play a role when it comes to a number of diseases, including cancer. Ben Schuler, professor at the Department of Biochemistry at UZH and head of the research project published in *Nature*, says, "The interesting thing about these proteins is that they're completely unstructured—like boiled noodles in water." How such disordered proteins should be able to interact according to the key/lock principle had puzzled the team of researchers.

Notably, the two proteins bind to one another much more strongly than the average protein partners. The research team used single-molecule fluorescence and nuclear magnetic resonance spectroscopy to determine the arrangement of the proteins. Observed in isolation, they show extended unstructured protein chains. The chains become more compact as soon as both binding partners come together and form a complex. The strong interaction is caused by the strong electrostatic attraction, since histone H1 is highly positively charged while prothymosin α is highly negatively charged. Even more surprising was the discovery that the protein complex was also fully unstructured, as several analyses confirmed.

To investigate the shape of the protein complex, the researchers labeled both proteins with fluorescent probes, which they then added to selected sites on the proteins. Together with computer simulations, this molecular map yielded the following results: Histone 1 interacts with prothymosin α preferably in its central region, which is the region with the highest charge density. Moreover, it emerged that the complex is highly dynamic: The proteins' position in the complex changes extremely quickly—in a matter of approx. 100 nanoseconds.

The interaction behavior is likely to be fairly common. Cells have many proteins that contain highly charged sequences and may be able to form such protein complexes. There are hundreds of such proteins in the human body alone. "It's likely that the interaction between disordered, highly charged proteins is a basic mechanism for how cells function and organize themselves," concludes Ben Schuler. According to the biophysicist, textbooks will need revision to account for this new way of binding. The discovery is also relevant for developing new therapies, since unstructured proteins are largely unresponsive to traditional drugs, which bind to specific structures on the protein surface. [11]

Particles in charged solution form clusters that reproduce

Dr Martin Sweatman from the University of Edinburgh's School of Engineering has discovered a simple physical principle that might explain how life started on Earth.

He has shown that particles that become charged in solution, like many biological [molecules](#), can form giant clusters that can reproduce. Reproduction is shown to be driven by simple physics—a balance of forces between short-range attraction and long-range repulsion. Once cluster [reproduction](#) begins, he suggests chemical evolution of clusters could follow, leading eventually to life.

Many [biological molecules](#), like DNA and proteins, might show this behaviour. Even the building blocks of life, amino acids and nucleobases, might show this behaviour. Reproduction in modern cells might even be driven by this simple physical mechanism, i.e. chemistry is not so important.

Dr Sweatman's research uses theoretical methods and computer simulations of simple particles. They clearly show giant clusters of molecules with the right balance of forces can reproduce. No chemistry is involved. However, these theoretical predictions have yet to be confirmed by experiment.

Dr Sweatman said, "Although it will be difficult to see this behaviour for solutions of small biomolecules, it should be possible to confirm this behaviour experimentally with much larger particles that can be seen under a microscope, like charged colloids.

"If this [behaviour](#) is confirmed, then we take another step towards Darwin's idea of life beginning in a warm little pond. A simple evaporation and condensation cycle in a pond might be sufficient to drive [cluster](#) reproduction initially. Survival of the fittest clusters of chemicals might then eventually lead to life."

The research has been published in the international journal *Molecular Physics*.

Experiment demonstrates quantum mechanical effects from biological systems

Nearly 75 years ago, Nobel Prize-winning physicist Erwin Schrödinger wondered if the mysterious world of quantum mechanics played a role in biology. A recent finding by Northwestern University's Prem Kumar adds further evidence that the answer might be yes.

Kumar and his team have, for the first time, created quantum entanglement from a biological system. This finding could advance scientists' fundamental understanding of biology and potentially open doors to exploit biological tools to enable new functions by harnessing [quantum mechanics](#).

"Can we apply quantum tools to learn about biology?" said Kumar, professor of electrical engineering and computer science in Northwestern's McCormick School of Engineering and of physics and astronomy in the Weinberg College of Arts and Sciences. "People have asked this question for many, many years—dating back to the dawn of quantum mechanics. The reason we are interested in these new quantum states is because they allow applications that are otherwise impossible."

Partially supported by the Defense Advanced Research Projects Agency, the research was published Dec. 5 in *Nature Communications*.

Quantum entanglement is one of quantum mechanics' most mystifying phenomena. When two particles—such as atoms, photons, or electrons—are entangled, they experience an inexplicable link that is maintained even if the particles are on opposite sides of the universe. While entangled, the particles' behavior is tied one another. If one particle is found spinning in one direction, for example, then the other particle instantaneously changes its spin in a corresponding manner dictated by the entanglement. Researchers, including Kumar, have been interested in harnessing quantum entanglement for several applications, including quantum communications. Because the particles can communicate without wires or cables, they could be used to send secure messages or help build an extremely fast "quantum Internet."

"Researchers have been trying to entangle a larger and larger set of atoms or photons to develop substrates on which to design and build a quantum machine," Kumar said. "My laboratory is asking if we can build these machines on a biological substrate."

In the study, Kumar's team used green fluorescent proteins, which are responsible for bioluminescence and commonly used in biomedical research. The team attempted to entangle the photons generated from the fluorescing molecules within the algae's barrel-shaped protein structure by exposing them to spontaneous four-wave mixing, a process in which multiple wavelengths interact with one another to produce new wavelengths.

Through a series of these experiments, Kumar and his team successfully demonstrated a type of entanglement, called polarization entanglement, between photon pairs. The same feature used to make glasses for viewing 3D movies, polarization is the orientation of oscillations in light waves. A wave can oscillate vertically, horizontally, or at different angles. In Kumar's entangled pairs, the photons' polarizations are entangled, meaning that the oscillation directions of light waves are linked. Kumar also noticed that the barrel-shaped structure surrounding the fluorescing molecules protected the entanglement from being disrupted.

"When I measured the vertical polarization of one particle, we knew it would be the same in the other," he said. "If we measured the horizontal polarization of one particle, we could predict the horizontal polarization in the other particle. We created an entangled state that correlated in all possibilities simultaneously."

Now that they have demonstrated that it's possible to create quantum entanglement from biological particles, next Kumar and his team plan to make a biological substrate of entangled particles, which could be used to build a quantum machine. Then, they will seek to understand if a biological substrate works more efficiently than a synthetic one. [9]

Quantum biology: Algae evolved to switch quantum coherence on and off

A UNSW Australia-led team of researchers has discovered how algae that survive in very low levels of light are able to switch on and off a weird quantum phenomenon that occurs during photosynthesis.

The function in the algae of this quantum effect, known as coherence, remains a mystery, but it is thought it could help them harvest energy from the sun much more efficiently. Working out its role in a living organism could lead to technological advances, such as better organic solar cells and quantum-based electronic devices.

The research is published in the journal *Proceedings of the National Academy of Sciences*.

It is part of an emerging field called quantum biology, in which evidence is growing that quantum phenomena are operating in nature, not just the laboratory, and may even account for how birds can navigate using the earth's magnetic field.

"We studied tiny single-celled algae called cryptophytes that thrive in the bottom of pools of water, or under thick ice, where very little light reaches them," says senior author, Professor Paul Curmi, of the UNSW School of Physics.

"Most cryptophytes have a light-harvesting system where quantum coherence is present. But we have found a class of cryptophytes where it is switched off because of a genetic mutation that alters the shape of a light-harvesting protein.

"This is a very exciting find. It means we will be able to uncover the role of quantum coherence in photosynthesis by comparing organisms with the two different types of proteins."

In the weird world of quantum physics, a system that is coherent – with all quantum waves in step with each other – can exist in many different states simultaneously, an effect known as superposition. This phenomenon is usually only observed under tightly controlled laboratory conditions.

So the team, which includes Professor Gregory Scholes from the University of Toronto in Canada, was surprised to discover in 2010 that the transfer of energy between molecules in the light harvesting systems from two different cryptophyte species was coherent.

The same effect has been found in green sulphur bacteria that also survive in very low light levels.

"The assumption is that this could increase the efficiency of photosynthesis, allowing the algae and bacteria to exist on almost no light," says Professor Curmi.

"Once a light-harvesting protein has captured sunlight, it needs to get that trapped energy to the reaction centre in the cell as quickly as possible, where the energy is converted into chemical energy for the organism.

"It was assumed the energy gets to the reaction centre in a random fashion, like a drunk staggering home. But quantum coherence would allow the energy to test every possible pathway simultaneously before travelling via the quickest route."

In the new study, the team used x-ray crystallography to work out the crystal structure of the lightharvesting complexes from three different species of cryptophytes.

They found that in two species a genetic mutation has led to the insertion of an extra amino acid that changes the structure of the protein complex, disrupting coherence.

"This shows cryptophytes have evolved an elegant but powerful genetic switch to control coherence and change the mechanisms used for light harvesting," says Professor Curmi.

The next step will be to compare the biology of different cryptophytes, such as whether they inhabit different environmental niches, to work out whether the quantum coherence effect is assisting their survival. [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 squaraine molecule of the first protocell situated in the bottom of this bicellular 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 squaraine and (1,4bis(N,Ndimethylamino)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 electrodynamic 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 unfold 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]

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 Δx position difference and with a Δp momentum difference such a way that they product is about the half Planck reduced constant. For the proton this Δx much less in the nucleon, than in the orbit of the electron in the atom, the Δp 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 Δx position with Δp 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 1/2 spin creator particle to make equal the spins of the weak interaction, for example neutron decay to 2 fermions, every particle is fermions with 1/2 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 $\frac{1}{2}$ 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 than 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_0 inertial mass is the result of the spin, since this is the only accelerating motion of the electric charge. Since the accelerating motion has different frequency for the electron in the atom

and the proton, their 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 be 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 Big 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 ratio $M_p = 1840 M_e$. 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.

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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

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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