Protein Resistance Mechanism

In order to understand why bacteria are becoming immune to previously well-functioning drugs, scientists are penetrating ever deeper into the molecular structure of cells. [24]

Proteins rarely work alone, they interact, form protein complexes or bind DNA and RNA to control what a cell does. [23]

Using tiny micromotors to diagnose and treat disease in the human body could soon be a reality. [22]

Scientists at the University of Illinois at Urbana-Champaign have produced the most precise picture to date of population dynamics in fluctuating feast-or-famine conditions. [21]

For planetary protection, this indicates that more stringent cleaning steps may be needed for missions focused on life detection and highlights the potential need to use differing and rotating cleaning reagents that are compatible with the spacecraft to control the biological burden. [20]

Now an international team of researchers has found a new way to investigate how Tb bacteria inactivate an important family of antibiotics: They watched the process in action for the first time using an X-ray free-electron laser, or XFEL. [19]

A protein complex called facilitates chromatin transcription (FACT) plays a role in DNA packing within a nucleus, as well as in oncogenesis. [18]

An LMU team now reveals the inner workings of a molecular motor made of proteins which packs and unpacks DNA. [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 rate and the Weak and Strong Interactions by the diffraction *patterns. The Weak Interaction changes the diffraction patterns by moving the electric charge from one side to the other side of the diffraction pattern, which violates the CP and Time reversal symmetry.*

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

Contents

Author: George Rajna

Preface

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.

Bacteria: Protein researchers decipher resistance mechanism

Worldwide, resistance to antibiotics is on the rise. In order to understand why bacteria are becoming immune to previously well-functioning drugs, scientists are penetrating ever deeper into the molecular structure of cells. A research group at Martin Luther University Halle-Wittenberg (MLU) has now succeeded in isolating a membrane protein from the E. coli bacterium and shed light on its molecular structure. Armed with this information, they have been able to show how the bacterium manages to rid itself of the antibiotic by forcing out the drug. The paper has been published in *Nature Communications*.

Antibiotic resistance of bacteria is one of the most important medical issues of our time. Left unchecked, previously treatable bacterial diseases are at risk of taking such severe turns that patients might die. "This is a real threat," says Professor Milton T. Stubbs, director of the Centre for Innovation Competence (ZIK) HALOmem, where the work was conducted. According to Stubbs, who has been researching the biosynthesis of antibiotics for many years, the danger this poses means it is crucial to understand the mechanisms of antibiotic resistance.

The current study is the result of work by a junior research group at ZIK HALOmem, led at the time by Dr. Mikio Tanabe. Tanabe is now an Associate Professor at the KEK Research Facility in Tsukuba, Japan. The group succeeded in isolating a membrane protein called MdfA from E. coli bacteria and were able to determine its molecular structure. The protein first had to be produced in the laboratory, isolated in its pure form and crystallised. "Dealing with sensitive membrane proteins is a very complicated process. Optimal conditions must be maintained in the laboratory so that the protein remains stable and keeps its native structure," explains Stubbs.

X-ray crystallography made it possible to visualise the structure of the material produced. Using this precise physical process, researchers are able to penetrate the Ångström range—one Ångström corresponds to one tenth of a nanometre, i.e. one ten billionth (10-10) of a metre, allowing researchers to work at a level at which individual atoms become visible. The ability to locate individual atoms in a molecule at this resolution holds the key to understanding how the protein works.

The process has revealed the three-dimensional structure of the membrane protein MdfA in the E. coli bacterium. The researchers from Halle utilised the results of a study that a rival group in China had recently published on the same protein and thereby succeeded in determining the mechanism that the membrane protein MdfA uses to help the bacterium become resistant.

The principle is reminiscent of a kind of pump mechanism. Although the drug is initially absorbed by the bacteria, it is ejected from the cell by MdfA before it becomes lethal to the bacteria.

"We assume that the mechanism discovered in this research applies to many other antibiotics," explains Milton Stubbs. This information will also provide the basis for later practical applications. "It is not until we understand the mechanisms of how resistances develop that we can look for solutions to prevent them." [24]

You are the company you keep—A new screening method detects direct biomolecule interactions

Proteins are the building blocks of the cell. They do most of the work and are essential for the structure, function and dynamic regulation of the cell and body's tissues and organs. Proteins rarely work alone, they interact, form protein complexes or bind DNA and RNA to control what a cell does. These complexes are key pieces of many important reactions within the cell, such as energy metabolism or gene regulation. Any change in those interactions, which can for example be caused by a mutation, can make the difference between health and disease. Hence, for understanding how cells operate, or what might go wrong in ill cells, it is essential to know how their building blocks interact.

New technologies allowed scientists during the last decades to understand the genetic information an organism possess, which of this information is actively used and which proteins are made by the cell in different circumstances. Now it is a big challenge to understand how biomolecules such as proteins and RNA messenger molecules combine to form the complexes required for a functional cell. In other words, we know the ten thousands of parts a cell is build off, but we don't know how they belong together.

In a paper published in *Nature Communications*, scientists at the Centre for Genomic Regulation (CRG) describe the development of a new method, named "rec-YnH", which was designed to understand the complexes formed between hundreds of proteins and RNAs at the same time.

The method, whose development was led by Sebastian Maurer in collaboration with the Luis Serrano laboratory, is the first technique that allows the detection of interactions between a large number of proteins and RNA molecules at the same time. The researchers put emphasis on the development of a doable and affordable method which is widely applicable.

"Our method reliably measures interactions between many proteins or many proteins and RNA fragments without the need for expensive, specialized equipment," explains Sebastian Maurer. "This methodology can be used by any standard biomedical research laboratory and will be useful for studying a particular process in the cell but also for researchers having to explore millions of protein interactions at a time to look for a complex involved in a particular disease," he concludes.

Two CRG laboratories successfully combined their expertise in bioinformatics, biochemistry and molecular biology to implement and validate the method. "Our collaboration resulted in an affordable and feasible method that produces high-quality maps of protein-protein and protein-RNA interactions", says Jae-Seong Yang, postdoctoral researcher and co-first author of the paper.

"Interactions between proteins and RNA are key for many biological processes including gene regulation, and our method is the first that can detect interactions between hundreds of proteins and RNAs at the same time. Having such an efficient new tool at hand will be extremely helpful to answer important questions related to many diseases," states co-first author of the study and CRG researcher Mireia Garriga. [23]

A pill for delivering biomedical micromotors

Using tiny micromotors to diagnose and treat disease in the human body could soon be a reality. But keeping these devices intact as they travel through the body remains a hurdle. Now in a study appearing in *ACS Nano*, scientists report that they have found a way to encapsulate micromotors into pills. The pill's coating protects the devices as they traverse the digestive system prior to releasing their drug cargo.

About the width of a human hair, micromotors are self-propelled microscopic robots designed to perform a host of biomedical tasks. In previous research, Joseph Wang, Liangfang Zhang and colleagues used micromotors coated with an antibiotic to treat ulcers in laboratory mice. They found that this approach produced better results than just taking the drugs by themselves. However, the researchers noted that body fluids, such as gastric acid and intestinal fluids, can compromise the effectiveness of micromotors and trigger early release of their payloads. In addition, when taken orally in fluid, some of the micromotors can get trapped in the esophagus. To overcome these issues, Wang and Zhang sought to develop a way to protect and carry these devices into the stomach without compromising their mobility or effectiveness.

The researchers created a pill composed of a pair of sugars—lactose and maltose—that encapsulated tens of thousands of micromotors made of a magnesium/titanium dioxide core loaded with a fluorescent dye cargo. These sugars were chosen because they are easy to mold into tablet, can disintegrate when needed and are nontoxic. When given to laboratory mice, these pills improved the release and retention of the micromotors in the stomach compared to those encapsulated in silica-based tablets or in a liquid solution. The researchers concluded that encapsulating micromotors in traditional pill form improves their ability to deliver medicines to specific targets without diminishing their mobility or performance. [22]

High precision microbial population dynamics under cycles of feast and famine

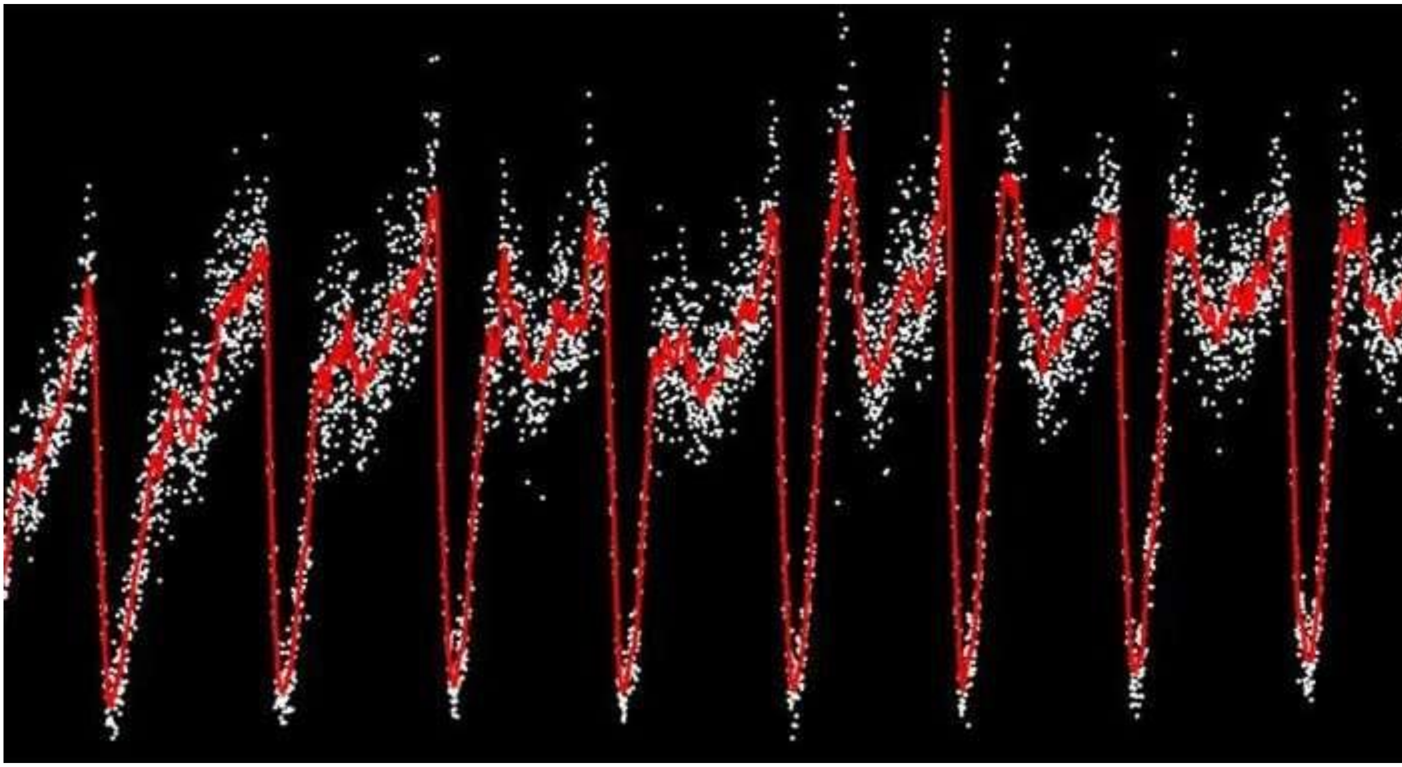
Scientists at the University of Illinois at Urbana-Champaign have produced the most precise picture to date of population dynamics in fluctuating feast-or-famine conditions. Professor Seppe Kuehn, a biological physicist, and his graduate student Jason Merritt found that bacterial population density is a function of both the frequency and the amplitude of nutrient fluctuations. They found that the more frequent the feast cycles and the longer a feast cycle, the more rapid the population recovery from a famine state. This result has important implications for understanding how microbial populations cope with the constant nutrient fluctuations they experience in nature.

The team's findings were made possible by extraordinarily precise measurements of population dynamics in bacterial communities. The measurement, based on automated imaging of hundreds of millions of single cells, allowed the team to capture population dynamics over periods of more than a week with a temporal resolution of one minute. Those numbers and the extended duration of the experiment couldn't have happened without Merritt's continuous-culture systems, coupled to automated-sampling fluorescence microscopes.

These findings are published in the August 28 issue of *Physical Review Letters*.

The experimental setup took about two years and many prototypes to develop. Merritt built six identical systems for the experiment, each one automated to continuously pump in fresh media and pump out bacterial cultures for sampling. The samples were continuously imaged to track changes in population density and structure. Software developed by Merritt automatically segments images to count bacterial cells, producing massive data sets. The software takes advantage of machine learning to resolve otherwise difficult-to-solve problems in image recognition and processing.

Kuehn comments, "Scientists studying populations of bacteria typically take samples manually and do their counting offline, in person. What Jason's systems do is automatically remove a sample, pass it in front of a microscope to be imaged, and then put it back. And they do that once a minute, 24 hours a day, with no input, for up to a month. His software counts the cells in the images, extracting information in real time."



Graph illustrating population density as a function of the frequency and amplitude of available nutrients. Credit: Kuehn Lab, University of Illinois at Urbana-Champaign

He continues, "So that's a big step forward—this has never been achieved before. Short-timescale quantitative studies have been done using microfluidic devices, but these are limited to about three days' runtime. We can run for 30 days, producing long-timescale highly quantitative measurements. We can easily run replicate experiments, reproducing the same results. Because of this, we were able to use the system to test hypotheses about the underlying mechanisms governing the dynamics we observed."

Merritt comments, "The idea for the system grew out of previous work Seppe had done. The device I built is basically a metal block with glass vials within it. The most important part of our system and the part that was the most difficult to get to work reliably is the coupling to a fluorescence microscope."

The system continuously draws samples out of the liquid culture into flexible tubing and then into a thin glass capillary in the path of the microscope. The bacteria pass through the capillary many at a time, but are spaced apart from one another. The biggest challenge overall was on the software side, doing proper image segmentation to convert the images to data.

The main finding, that populations apparently recovery faster from more frequent or larger pulses of nutrients, puzzled the team at first. However, the precision of the measurement allowed them to uncover the mechanism.

Merritt continues, "What we found out is that the fast recovery rates for the planktonic population are driven by dispersal from aggregated cells (biofilms) during feast conditions. So basically when there's a lot of food, these cell aggregates start shedding cells rapidly, and the cells that shed off start growing rapidly. But during famine conditions when there's not very much food, these cells start coming back together and forming the aggregates again. This is the mechanism driving the frequency and amplitude dependence."

Kuehn adds, "Variations in a natural population may be the result of any one or a combination of many different variables—the amount of nutrients, temperature, competition and predation, etc.—so it's difficult to measure cause and effect. In the lab, we tightly control all of the parameters of our experiment. And now we can make a really robust and reproducible quantitative measurement. Going forward, we would like to modify these systems to study topics in evolutionary history. We also plan to do studies in which we use feedback control of microbial communities, to see whether we can push the communities back into a particular state. These are studies that wouldn't be possible without an automated system like the one we used in this study." [21]

Team discover how microbes survive clean rooms and contaminate spacecraft

Rakesh Mogul, a Cal Poly Pomona professor of biological chemistry, was the lead author of an article in the journal *Astrobiology* that offers the first biochemical evidence explaining the reason the contamination persists.

Chemistry professor Gregory A. Barding, Jr., was a collaborator and second author on the paper. The remaining 22 coauthors are all Cal Poly Pomona students—14 undergraduates in chemistry, three chemistry graduate students and five undergraduates in biological sciences.

"We designed the project to give students hands-on experience – and to support the learn-by-doing philosophy of Cal Poly Pomona. The students did the research, mostly as thesis projects in the areas of enzymology, molecular microbiology and analytical chemistry," said Mogul.

In the clean room facilities, NASA implements a variety of planetary protection measures to minimize biological contamination of spacecraft. These steps are important because contamination by Earth-based microorganisms could compromise life-detection missions by providing false positive results.

Despite extensive cleaning procedures, however, molecular genetic analyses show that the clean rooms harbor a diverse collection of microorganisms, or a spacecraft microbiome, that includes bacteria, archaea and fungi, explained Mogul. The Acinetobacter, a genus of bacteria, are among the dominant members of the spacecraft microbiome.

To figure out how the spacecraft microbiome survives in the cleanroom facilities, the research team analyzed several Acinetobacter strains that were originally isolated from the Mars Odyssey and Phoenix spacecraft facilities.

They found that under very nutrient-restricted conditions, most of the tested strains grew on and biodegraded the cleaning agents used during spacecraft assembly. The work showed that cultures grew on ethyl alcohol as a sole carbon source while displaying reasonable tolerances towards oxidative stress. This is important since oxidative stress is associated with desiccating and high radiation environments similar to Mars.

The tested strains were also able to biodegrade isopropyl alcohol and Kleenol 30, two other cleaning agents commonly used, with these products potentially serving as energy sources for the microbiome.

"We're giving the planetary protection community a baseline understanding of why these microorganisms remain in the clean rooms," said Mogul. "There's always stuff coming into the clean rooms, but one of the questions has been why do the microbes remain in the clean rooms, and why is there a set of microorganisms that are common to the clean rooms."

For planetary protection, this indicates that more stringent cleaning steps may be needed for missions focused on life detection and highlights the potential need to use differing and rotating cleaning reagents that are compatible with the spacecraft to control the biological burden. [20]

X-ray laser scientists develop a new way to watch bacteria attack antibiotics

Tuberculosis, a lung disease that spreads in the air through coughs or sneezes, now kills more people worldwide than any other infectious agent, according to the World Health Organization's latest global tuberculosis report. And in hundreds of thousands of cases each year, treatment fails because the bacteria that cause Tb have become resistant to antibiotics.

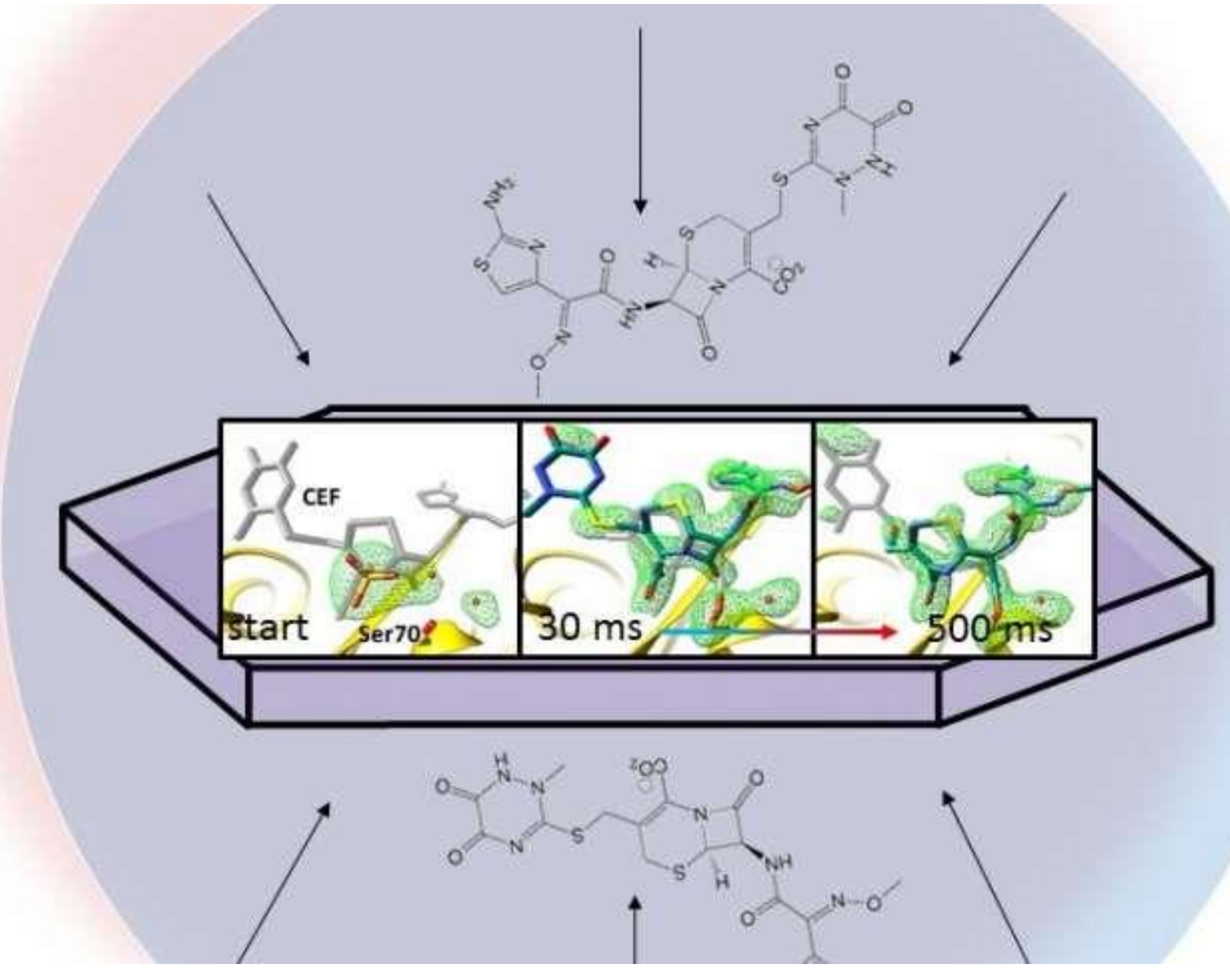
Now an international team of researchers has found a new way to investigate how Tb bacteria inactivate an important family of antibiotics: They watched the process in action for the first time using an X-ray free-electron laser, or XFEL.

In experiments at the Department of Energy's SLAC National Accelerator Laboratory, they mixed an antibiotic with an enzyme called beta-lactamase that Tb bacteria use, and then watched in real time as the enzyme attacked the antibiotic to deactivate it.

The researchers' method, called mix-and-inject serial crystallography, takes advantage of the brilliant, ultrafast pulses produced by SLAC's Linac Coherent Light Source (LCLS). X-ray snapshots taken 30 milliseconds to 2 seconds after the reaction began showed lactamase binding to the antibiotic, ceftriaxone, and bursting one of its chemical bonds.

The results of the experiment were published today in *BMC Biology*.

"This proof-of-concept study shows that we're able to see the shape and intermediate stages of the molecules during the process," says Marius Schmidt, a University of Wisconsin Milwaukee professor who led the experiment. "After decades of trying other techniques in the field of crystallography, the technology is here."



In a liquid droplet (represented by the light blue circle), an antibiotic disperses through a crystallized protein, beta-lactamase, and binds to it. X-ray snapshots of the bound pair allowed researchers to create maps of the electron …more

In crystallography, scientists form a crystal from many copies of a protein and hit the crystal with X-rays to produce a diffraction pattern on a detector, which reveals the protein's atomic structure. This structure is key to understanding how enzymes and other proteins function.

In the past this only worked with relatively large crystals, which have limited value in this method because the solution containing the antibiotic would take a long time to diffuse into the crystal and react with the enzyme. It is important that the diffusion is faster than the reaction, so that the many protein molecules in the crystal start the chemical process together.

But LCLS and other XFELs have such intense beams that they can capture diffraction patterns from much tinier crystals, a millionth of a meter across or less, Schmidt said, so the antibiotic can get to the enzyme quickly, and the reaction can be recorded with X-rays.

"While there have been elegant studies to observe protein motions with light-induced changes, our work illustrates that a larger class of proteins, namely enzymes, can be investigated in a time-resolved fashion at LCLS and other XFELs," says Jose Olmos, a doctoral student at Rice University who is one of the principal authors of the publication.

In this study, the research team delivered tiny crystals of beta-lactamase while mixing them with the antibiotic just fractions of a second before they were hit with X-ray pulses.

Credit: CC0 Public Domain

The team took millions of X-ray snapshots during the reaction and stitched them together to create a map that shows changes in the three-dimensional structure of the antibiotic as it interacts with the enzyme at room temperature.

"For structural biologists, this is how we learn exactly how biology functions," says Mark Hunter, staff scientist at SLAC and co-author on the study. "We decipher a molecule's structure at a certain point in time, and it gives us a better idea of how the molecule works."

In future experiments, taking even more snapshots during the course of the reaction could provide greater detail of the structure and chemical behavior of lactamase. With more information scientists could manipulate the design of antibiotics to prevent such attacks. The experimental method could also be applied to learn the fine details of other types of biological processes where enzymes initiate or steer reactions.

"There's a large amount of excitement building over this method, because it opens up this new time realm for structural biologists," Hunter says. Previous work using this technique captured the flipping of an RNA "switch," important for studies into retroviruses and cancer.

The scientists plan to use the method to look at additional antibiotics. They also intend to take advantage of higher repetition rates – more rapid firing of X-ray pulses – expected at a future upgrade to LCLS and at the recently opened European XFEL. This will allow scientists to capture the data they need in just minutes, compared to days. They could also take more closely spaced snapshots of the reactions, which could give an even more complete picture of the swift chemistry as it happens. [19]

Molecular biologists compared human and yeast FACT

A protein complex called facilitates chromatin transcription (FACT) plays a role in DNA packing within a nucleus, as well as in oncogenesis. A team of scientists from MSU, working in cooperation with foreign colleagues, have reported similarities between the work of this complex in humans and yeast. This discovery led to the prediction that a new protein assists the FACT complex in humans. An article about the study was published in *Journal of Biological Chemistry*.

In eukaryotes, hereditary information is encoded in DNA, which is about one meter long, but is packed within the nucleus. The DNA molecule is extremely thin, and if it were chaotically crumpled, it would be impossible to detangle it without damage. In order to read the genetic code, it has to be unpacked. Histones, the proteins that bind to DNA, help to pack the genome in the cell nuclei. This complex is called chromatin. A minimal unit of chromatin is called a nucleosome; chromatin looks like a sequence of sewing spools (nucleosomes) with two DNA loops tightly wrapped on each of them.

However, the work of this system also includes lots of other proteins. One of the protein complexes that control this process is FACT . It secures more effective RNA reading from the DNA template packed in chromatin.

"On the molecular level, yeast FACT can both stabilize nucleosomes in the genome during RNA reading and unfold nucleosomes," said study co-author Vasily Suditsky, the head of the laboratory for the regulation of transcription and replication of the Faculty of Biology, MSU. "The balance between these two functions is determined by the presence of the yeast protein Nhp6, which helps FACT unfold nucleotides. Until recently, the second function was unknown for human FACT, despite the considerable similarity of the structure of these protein complexes in yeast and humans."

Surprisingly, FACT straightens the DNA looped around the spools without expending energy. Previously, such studies were conducted using yeast material. In the new article, Vasily Suditsky and his colleagues analyzed the mechanism of operation of this complex in humans. They were the first to prove that the Nhp6 protein from yeast in combination with human FACT complex is able to unfold nucleosomes.

"The critical data were obtained at the Faculty of Biology, MSU using a modern biophysical approach—single-particle FRET (spFRET is a method that allows the measurement of the interatomic distance within one DNA-protein complex," said Studitsky. "The information we received led to the assumption that humans may possess a homologue of the yeast protein Nhp6 helping FACT unfold nucleosomes and regulate gene transcription."

The team also found important differences between human and yeast FACT complexes, though the activity of both varieties appeared to be relatively similar. The scientists found that in vitro yeast FACT cannot work without Nhp6, but in vivo (in cells), it functions. However, in this case, the functions of the FACT complex may be compensated with other proteins. Therefore, it is still unknown whether yeast FACT can function without Nhp6. On the contrary, human FACT is not stably associated with nucleosomes without additional proteins that haven't been studied in humans yet.

FACT complex is evolutionarily conserved. Scientists tried adding yeast Nhp6 to human FACT complex, and it functioned. Therefore, it can be assumed that humans also have a still unknown protein that helps FACT function.

"In the future, we plan to search for this hypothetical Nhp6-like human protein and to determine the role of nucleosome unfolding by FACT in gene regulation and detection of regions with damaged chromatin structure in the genome," said Studitsky. [18]

Study reveals the inner workings of a molecular motor that packs and unpacks DNA

DNA is tightly packed into the nucleus of a cell. Nevertheless, the cellular machinery needs to constantly access the genomic information. An LMU team now reveals the inner workings of a molecular motor made of proteins which packs and unpacks DNA.

The genomic DNA of higher organisms is compacted in a highly condensed form known as chromatin. The DNA is tightly wound around a myriad of tiny histone spools called nucleosomes. A single human cell, for instance, accommodates in this manner about two meters of DNA. However, genes must be constantly transcribed into messenger RNAs to direct protein synthesis. Moreover, the entire DNA must be replicated before cell division and DNA damage needs to be repaired. Thus, there must be way to actively grant access to the genome.

This is when chromatin remodelers come into play. Chromatin remodelers have an essential role as they are molecular machines: they unpick and unpack segments of the DNA by sliding nucleosome spools back and forth, replacing individual histones, freeing up the DNA for transcription, and finally compacting it again, when the job is done. Since all of this happens in a highly dynamic fashion, chromatin remodelers enable cells to react rapidly to alterations in their environment – and this holds for brewer's yeast as well as for human cells. In mediating gene accessibility, chromatin remodelers are vital for development and cell differentiation; cell types are defined by the sets of genes they express, remodelers help to determine cell identity.

So far, however, very little is known about what remodeling proteins look like and how they go about doing what they do. In molecular terms, functional remodelers are often very large complexes comprising many different protein components, whose coordinated action makes them akin to molecular machines. These features also make it very difficult to determine their detailed structure. But a team led by Professor Karl-Peter Hopfner, who holds a Chair in Structural Molecular Biology at LMU's Gene Center, has now used cryo-electron microscopy to reconstruct the three-dimensional structure of the nucleosome-sliding remodeler INO80 (which itself consists of 15 subunits) bound to a single nucleosome. "Even with innovative approaches, the best available technology and intensive teamwork, we were always working at the cutting edge," says Dr. Sebastian Eustermann, who worked out the molecular structure of the complex on the basis of electron micrographs of thousands of individual complexes.

By analyzing images of randomly oriented views of the complex formed between INO80 and a nucleosome in the electron micrographs, Hopfner and his team have pieced together its structure at a resolution which has seldom been achieved for a chromatin complex of comparable size. This allowed the researchers to unravel the intricate interaction of the remodeler with its substrate DNA spooled around histones and dissect how the whole machinery works.

From a biochemical point of view, remodelers are responsible for heavy-duty reorganizational tasks. To perform these tasks, they must execute "large-scale conformational changes, which are carried out with astounding precision," says Eustermann. In order to alter the relative positions of nucleosomes, the INO80 complex must first weaken the contacts between the nucleosomal histones and the DNA. A molecular motor which is part of the INO80 complex segmentally detaches the double-stranded DNA from the nucleosome. In doing so, it progressively breaks the contacts that normally keep the DNA tightly wound around the histone particle.

The motor subunit feeds DNA it into the nucleosome. This results in the transient formation of a double-stranded DNA loop that is likely an important intermediate in complex remodeling reactions on the nucleosome. On one hand, the loop exposes some histone proteins that could be replaced by other histones to form a different type of nucleosome. On the other hand, the loop is eventually passed over another subunit and the machine then acts as a ratchet, allowing the nucleosome to "move" on the DNA. Throughout this unpacking process, other subunits in the complex serve to support and stabilize the partially 'denuded' nucleosome itself.

The structure of the complex revealed in the new study sheds new light on the function and mode of action of chromatin remodelers in general. These molecular machines play an essential part in the workings of the cell by maintaining the flexibility of the chromatin, thus enabling the genetic apparatus to respond dynamically to changing metabolic demands. "Our results provide the first well-founded picture of how they do that," says Hopfner. "Moreover, it has recently become clear that remodelers play a central role in tumorigenesis, because they often misregulated in tumor tissue. So structural and mechanistic insights into their functions will be vital for the future development of new therapies for cancer," he adds. [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 cellsfrom 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 selfreproducing 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.

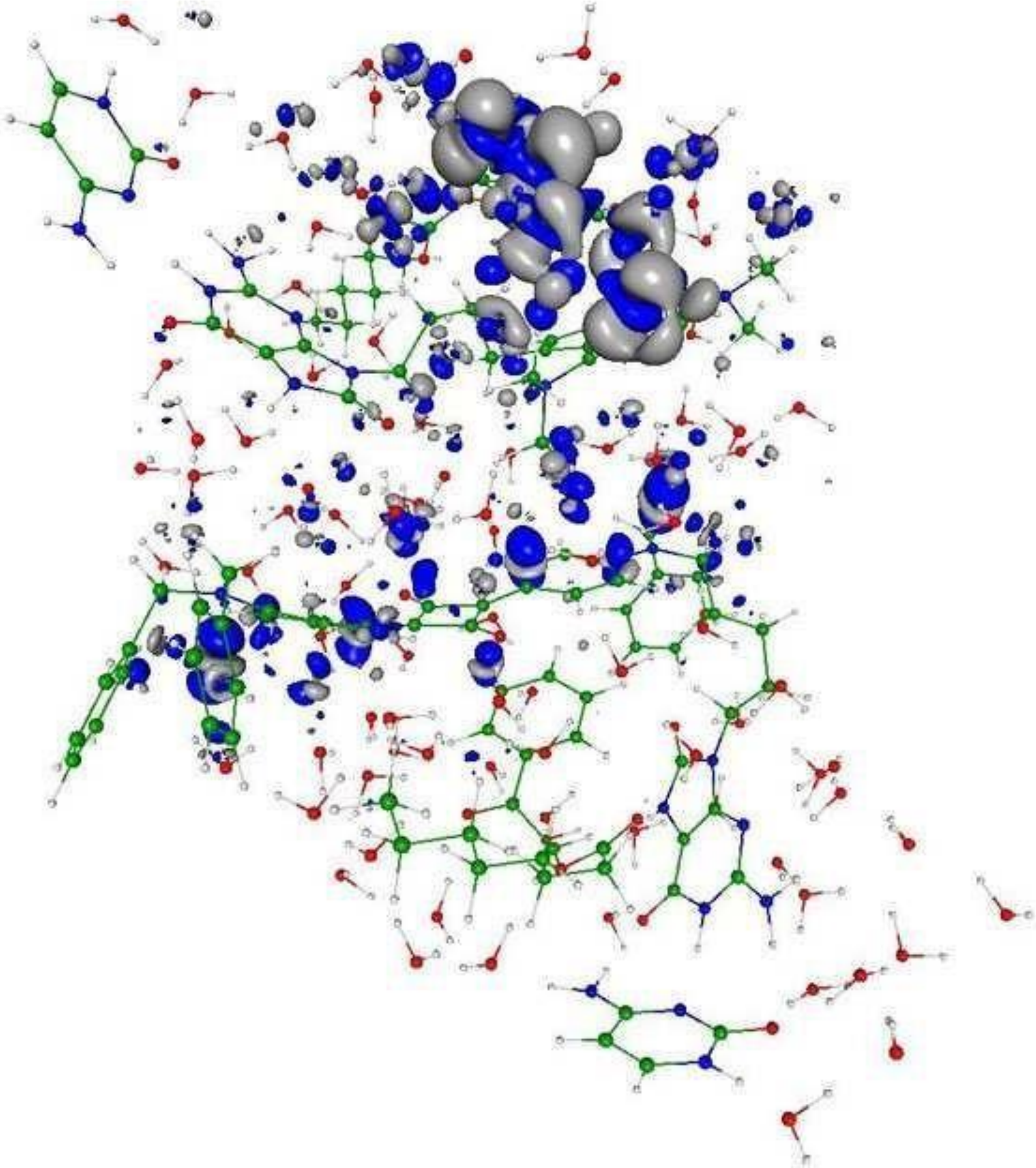
Our discovered phenomenon of the quantum entanglement in the prebiotic systems enhance the photosynthesis in the proposed systems because simultaneously excite two prebiotic kernels in the system by appearance of two additional quantum entangled excited states (Tamulis A, Grigalavicius M, Baltrusaitis 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 selfassembled two synthesized protocell system due to the photo excited electron charge transfer from one protocell to another that leads to closer self-assembly and exchange of energy and information.

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

As a result, these nonlinear quantum interactions compressed the overall molecular system resulting in a smaller gap between the HOMO and LUMO electron energy levels which allows enhanced tunneling of photo excited electrons from the sensitizer squarine and (1,4bis(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 electrodynamics field within the living system.

What this means is that each living cell is giving off, or resonating, a biophoton field of coherent energy. If each cell is emitting this field, then the whole living system is, in effect, a resonating field-a ubiquitous nonlocal field. And since biophotons are the entities through which the living system communicates, there is near-instantaneous intercommunication throughout. And this, claims Popp, is the basis for coherent biological organization -- referred to as quantum coherence. This discovery led Popp to state that the capacity for evolution rests not on aggressive struggle and rivalry but on the capacity for communication and cooperation. In this sense the built-in capacity for species evolution is not based on the individual but rather living systems that are interlinked within a coherent whole: Living systems are thus neither the subjects alone, nor objects isolated, but both subjects and objects in a mutually communicating universe of meaning. . . . Just as the cells in an organism take on different tasks for the whole, different populations enfold information not only for themselves, but for all other organisms, expanding the consciousness of the whole, while at the same time becoming more and more aware of this collective consciousness.

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

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

Creating quantum technology

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

Quantum Entanglement

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

The Bridge

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

Accelerating charges

The moving charges are self maintain the electromagnetic field locally, causing their movement and this is the result of their acceleration under the force of this field. In the classical physics the charges will distributed along the electric current so that the electric potential lowering along the current, by linearly increasing the way they take every next time period because this accelerated motion. The same thing happens on the atomic scale giving a dp impulse difference and a dx way difference between the different part of the not point like particles.

Relativistic effect

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

Heisenberg Uncertainty Relation

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

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

Wave – Particle Duality

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

Atomic model

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

The Relativistic Bridge

Commonly accepted idea that the relativistic effect on the particle physics it is the fermions' spin - another unresolved problem in the classical concepts. If the electric charges can move only with accelerated motions in the self maintaining electromagnetic field, once upon a time they would reach the velocity of the electromagnetic field. The resolution of this problem is the spinning particle, constantly accelerating and not reaching the velocity of light because the acceleration is radial. One origin of the Quantum Physics is the Planck Distribution Law of the electromagnetic oscillators, giving equal intensity for 2 different wavelengths on any temperature. Any of these two wavelengths will give equal intensity diffraction patterns, building different asymmetric constructions, for example proton - electron structures (atoms), molecules, etc. Since the particles are centers of diffraction patterns they also have particle – wave duality as the electromagnetic waves have. [2]

The weak interaction

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

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

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

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

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

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

Probably because it is a spin creating movement changing linear oscillation to 2 dimensional oscillation by changing d to u quark and creating anti neutrino going back in time relative to the proton and electron created from the neutron, it seems that the anti neutrino fastest then the velocity of the photons created also in this weak interaction?

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

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

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

The General Weak Interaction

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

The neutrino oscillation of the Weak Interaction shows that it is a general electric dipole change and it is possible to any other temperature dependent entropy and information changing diffraction pattern of atoms, molecules and even complicated biological living structures. We can generalize the weak interaction on all of the decaying matter constructions, even on the biological too. This gives the limited lifetime for the biological constructions also by the arrow of time. There should be a new research space of the Quantum Information Science the 'general neutrino oscillation' for the greater then subatomic matter structures as an electric dipole change.

There is also connection between statistical physics and evolutionary biology, since the arrow of time is working in the biological evolution also.
The Fluctuation Theorem says that there is a probability that entropy will flow in a direction opposite to that dictated by the Second Law of Thermodynamics. In this case the Information is growing that is the matter formulas are emerging from the chaos. So the Weak Interaction has two directions, samples for one direction is the Neutron decay, and Hydrogen fusion is the opposite direction.

Fermions and Bosons

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

Van Der Waals force

Named after the Dutch scientist Johannes Diderik van der Waals – who first proposed it in 1873 to explain the behaviour of gases – it is a very weak force that only becomes relevant when atoms and molecules are very close together. Fluctuations in the electronic cloud of an atom mean that it will have an instantaneous dipole moment. This can induce a dipole moment in a nearby atom, the result being an attractive dipole–dipole interaction.

Electromagnetic inertia and mass

Electromagnetic Induction

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

Relativistic change of mass

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

The frequency dependence of mass

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

Electron – Proton mass rate

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

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

Gravity from the point of view of quantum physics

The Gravitational force

The gravitational attractive force is basically a magnetic force.

The same electric charges can attract one another by the magnetic force if they are moving parallel in the same direction. Since the electrically neutral matter is composed of negative and positive charges they need 2 photons to mediate this attractive force, one per charges. The Bing Bang caused parallel moving of the matter gives this magnetic force, experienced as gravitational force.

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

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

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

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

The gravitational force attracting the matter, causing concentration of the matter in a small space and leaving much space with low matter concentration: dark matter and energy.
There is an asymmetry between the mass of the electric charges, for example proton and electron, can understood by the asymmetrical Planck Distribution Law. This temperature dependent energy

distribution is asymmetric around the maximum intensity, where the annihilation of matter and antimatter is a high probability event. The asymmetric sides are creating different frequencies of electromagnetic radiations being in the same intensity level and compensating each other. One of these compensating ratios is the electron – proton mass ratio. The lower energy side has no compensating intensity level, it is the dark energy and the corresponding matter is the dark matter.

The Higgs boson

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

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

Higgs mechanism and Quantum Gravity

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

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

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

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

What is the Spin?

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

The Graviton

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

Conclusions

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.

References

[1] The Magnetic field of the Electric current and the Magnetic induction

http://academia.edu/3833335/The_Magnetic_field_of_the_Electric_current

[2] 3 Dimensional String Theory http://academia.edu/3834454/3_Dimensional_String_Theory

[3] Graviton Production By Two Photon and Electron-Photon Processes In Kaluza-Klein Theories With
Large Extra Dimensions http://arxiv.org/abs/hep-ph/9909392

[4] Quantum Entanglement

http://en.wikipedia.org/wiki/Quantum_entanglemen

t

[5] Quantum Consciousness

https://realitysandwich.com/155783/quantum_consciousness_0/

[6] Quantum Biology http://www.nature.com/news/2011/110615/pdf/474272a.pdf [7]

Quantum entanglement in photoactive prebiotic systems

https://globalmedicaldiscovery.com/key-drug-discovery-articles/quantum-entanglementphotoactive-prebiotic-systems/
[8] Quantum biology: Algae evolved to switch quantum coherence on and off

http://phys.org/news/2014-06-quantum-biology-algae-evolved-coherence.html

[9] Experiment demonstrates quantum mechanical effects from biological systems

https://phys.org/news/2017-12-quantum-mechanical-effects-biological.html

[10] Particles in charged solution form clusters that reproduce

https://phys.org/news/2017-12-particles-solution-clusters.html

[11] New interaction mechanism of proteins discovered

https://phys.org/news/2018-02-interaction-mechanism-proteins.html

[12] Artificial and biological cells work together as mini chemical factories

https://phys.org/news/2018-03-artificial-biological-cells-mini-chemical.html

[13] Custom sequences for polymers using visible light

https://phys.org/news/2018-03-custom-sequences-polymers-visible.html

[14] Scientists explore the structure of a key region of longevity protein telomerase

https://phys.org/news/2018-03-scientists-explore-key-region-longevity.html

[15] Simulations document self-assembly of proteins and DNA

https://phys.org/news/2018-03-simulations-document-self-assembly-proteins-dna.html

[16] Biomimetic chemistry—DNA mimic outwits viral enzyme

https://phys.org/news/2018-04-biomimetic-chemistrydna-mimic-outwits-viral.html

[17] Study reveals the inner workings of a molecular motor that packs and unpacks DNA

https://phys.org/news/2018-04-reveals-molecular-motor-dna.html

[18] Molecular biologists compared human and yeast FACT

https://phys.org/news/2018-05-molecular-biologists-human-yeast-fact.html

[19] X-ray laser scientists develop a new way to watch bacteria attack antibiotics

https://phys.org/news/2018-06-x-ray-laser-scientists-bacteria-antibiotics.html

[20] Team discover how microbes survive clean rooms and contaminate spacecraft

https://phys.org/news/2018-06-team-microbes-survive-rooms-contaminate.html

[21] High precision microbial population dynamics under cycles of feast and famine

https://phys.org/news/2018-09-high-precision-microbial-population-dynamics.html

[22] A pill for delivering biomedical micromotors

https://phys.org/news/2018-09-pill-biomedical-micromotors.html

[23] You are the company you keep—A new screening method detects direct biomolecule interactions

https://phys.org/news/2018-10-company-keepa-screening-method-biomolecule.html

[24] Bacteria: Protein researchers decipher resistance mechanism

https://phys.org/news/2018-10-bacteria-protein-decipher-resistance-mechanism.html