# Machine Learning Metal Compounds

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*A research team at The University of Tokyo has developed a powerful machine learning algorithm that predicts the properties and structures of unknown samples from an electron spectrum. [25]*

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*Researchers at Oregon State University have used deep learning to decipher which ribonucleic acids have the potential to encode proteins. [23]*

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*Bacterial systems are some of the simplest and most effective platforms for the expression of recombinant proteins. [21]*

*Now, in a new paper published in Nature Structural & Molecular Biology, Mayo researchers have determined how one DNA repair protein gets to the site of DNA damage. [20]*

*A microscopic thread of DNA evidence in a public genealogy database led California authorities to declare this spring they had caught the Golden State Killer, the rapist and murderer who had eluded authorities for decades. [19]*

*Researchers at Delft University of Technology, in collaboration with colleagues at the Autonomous University of Madrid, have created an artificial DNA blueprint for the replication of DNA in a cell-like structure. [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.

# Researchers use machine learning technique to rapidly evaluate new transition metal compounds

In recent years, machine learning has been proving a valuable tool for identifying new materials with properties optimized for specific applications. Working with large, well-defined data sets, computers learn to perform an analytical task to generate a correct answer and then use the same technique on an unknown data set.

While that approach has guided the development of valuable new materials, they've primarily been organic compounds, notes Heather Kulik Ph.D. '09, an assistant professor of chemical engineering. Kulik focuses instead on inorganic compounds—in particular, those based

on [transition metals](), a family of elements (including iron and copper) that have unique and useful properties. In those compounds—known as transition metal complexes—the metal atom occurs at the center with chemically bound arms, or ligands, made of carbon, hydrogen, nitrogen, or oxygen atoms radiating outward.

Transition metal complexes already play important roles in areas ranging from [energy storage]()to catalysis for manufacturing fine chemicals—for example, for pharmaceuticals. But Kulik thinks that machine learning could further expand their use. Indeed, her group has been working not only to apply machine learning to inorganics—a novel and challenging undertaking—but also to use the technique to explore new territory. "We were interested in understanding how far we could push our models to do discovery—to make predictions on compounds that haven't been seen before," says Kulik.

## Sensors and computers

For the past four years, Kulik and Jon Paul Janet, a graduate student in chemical engineering, have been focusing on transition metal complexes with "spin"—a quantum mechanical property of electrons. Usually, electrons occur in pairs, one with spin up and the other with spin down, so they cancel each other out and there's no net spin. But in a transition metal, electrons can be unpaired, and the resulting net spin is the property that makes inorganic complexes of interest, says Kulik. "Tailoring how unpaired the electrons are gives us a unique knob for tailoring properties."

A given complex has a preferred spin state. But add some energy—say, from light or heat—and it can flip to the other state. In the process, it can exhibit changes in macroscale properties such as size or color. When the energy needed to cause the flip—called the spin-splitting energy—is near zero, the complex is a good candidate for use as a sensor, or perhaps as a fundamental component in a quantum computer.

Chemists know of many metal-ligand combinations with spin-splitting energies near zero, making them potential "spin-crossover" (SCO) complexes for such practical applications. But the full set of possibilities is vast. The spin-splitting energy of a transition metal complex is determined by what ligands are combined with a given metal, and there are almost endless ligands from which to choose. The challenge is to find novel combinations with the desired property to become SCOs—without resorting to millions of trial-and-error tests in a lab.

## Translating molecules into numbers

The standard way to analyze the electronic structure of molecules is using a computational modeling method called density functional theory, or DFT. The results of a DFT calculation are fairly accurate—especially for organic systems—but performing a calculation for a single compound can take hours, or even days. In contrast, a machine learning tool called an artificial neural network (ANN) can be trained to perform the same analysis and then do it in just seconds. As a result, ANNs are much more practical for looking for possible SCOs in the huge space of feasible complexes.
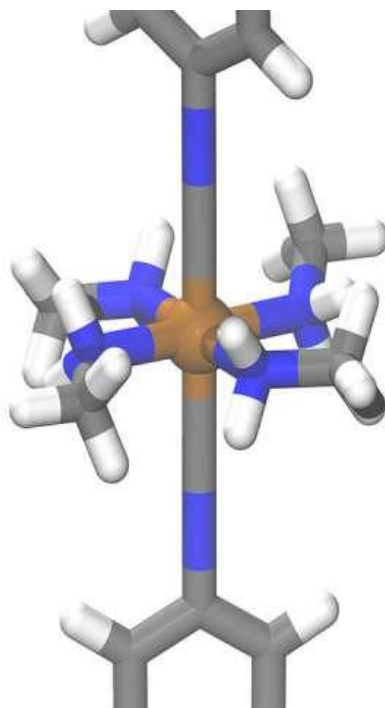
This graphic represents a sample transition metal complex. A transition metal complex consists of a central transition metal atom (orange) surrounded by an array of chemically bound organic molecules in structures known as ligands. Credit: Massachusetts Institute of Technology

Because an ANN requires a numerical input to operate, the researchers' first challenge was to find a way to represent a given transition metal complex as a series of numbers, each describing a selected property. There are rules for defining representations for organic molecules, where the physical structure of a molecule tells a lot about its properties and behavior. But when the researchers followed those rules for transition metal complexes, it didn't work. "The metal-organic bond is very tricky to get right," says Kulik. "There are unique properties of the bonding that are more variable. There are many more ways the electrons can choose to form a bond." So the researchers needed to make up new rules for defining a representation that would be predictive in inorganic chemistry.

Using machine learning, they explored various ways of representing a transition metal complex for analyzing spin-splitting energy. The results were best when the representation gave the most emphasis to the properties of the metal center and the metal-ligand connection and less emphasis to the properties of ligands farther out. Interestingly, their studies showed that representations that gave more equal emphasis overall worked best when the goal was to predict other properties, such as the ligand-metal bond length or the tendency to accept electrons.

## Testing the ANN

As a test of their approach, Kulik and Janet—assisted by Lydia Chan, a summer intern from Troy High School in Fullerton, California—defined a set of transition metal complexes based on four transition metals—chromium, manganese, iron, and cobalt—in two oxidation states with 16 ligands (each molecule can have up to two). By combining those building blocks, they created a "search space" of 5,600 complexes—some of them familiar and well-studied, and some of them totally unknown.

In previous work, the researchers had trained an ANN on thousands of compounds that were well-known in transition metal chemistry. To test the trained ANN's ability to explore a new chemical space to find compounds with the targeted properties, they tried applying it to the pool of 5,600 complexes, 113 of which it had seen in the previous study.

The result was the plot labeled "Figure 1" in the slideshow above, which sorts the complexes onto a surface as determined by the ANN. The white regions indicate complexes with spin-splitting energies within 5 kilo-calories per mole of zero, meaning that they are potentially good SCO candidates. The red and blue regions represent complexes with spin-splitting energies too large to be useful. The green diamonds that appear in the inset show complexes that have iron centers and similar ligands—in other words, related compounds whose spin-crossover energies should be similar. Their appearance in the same region of the plot is evidence of the good correspondence between the researchers' representation and key properties of the complex.

But there's one catch: Not all of the spin-splitting predictions are accurate. If a complex is very different from those on which the network was trained, the ANN analysis may not be reliable—a standard problem when applying machine learning models to discovery in materials science or chemistry, notes Kulik. Using an approach that looked successful in their previous work, the researchers compared the numeric representations for the training and test complexes and ruled out all the test complexes where the difference was too great.

## Focusing on the best options

Performing the ANN analysis of all 5,600 complexes took just an hour. But in the real world, the number of complexes to be explored could be thousands of times larger—and any promising candidates would require a full DFT calculation. The researchers therefore needed a method of evaluating a big data set to identify any unacceptable candidates even before the ANN analysis. To that end, they developed a genetic algorithm—an approach inspired by natural selection—to score individual complexes and discard those deemed to be unfit.
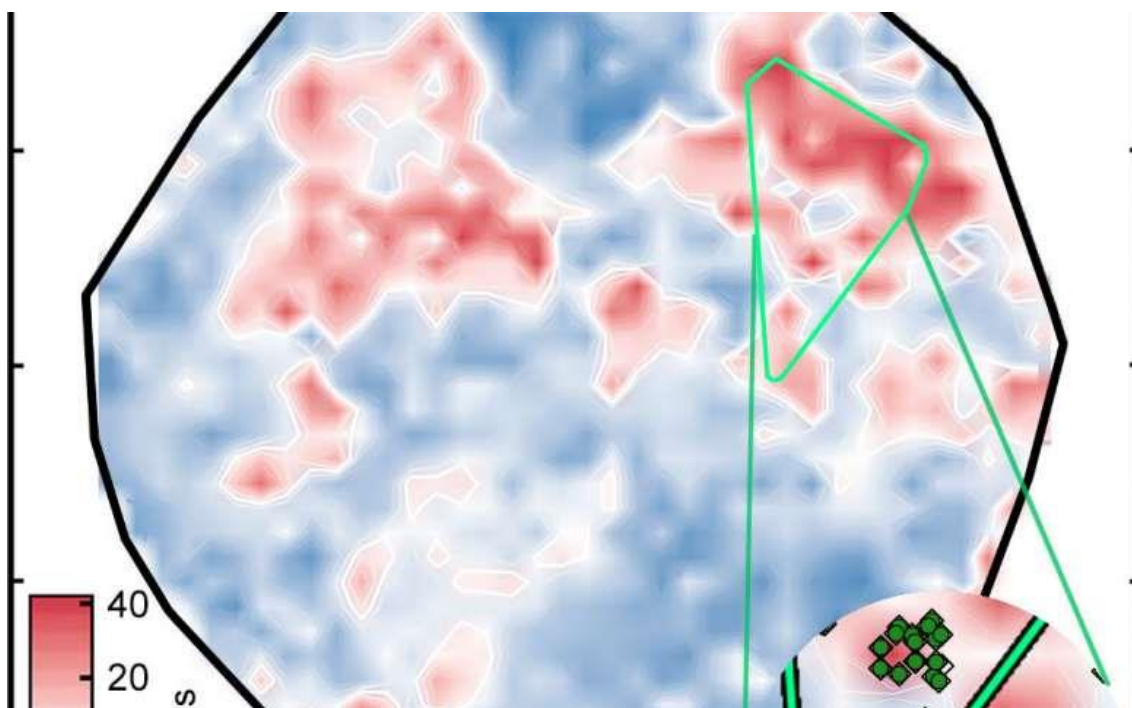
An artificial neural network previously trained on well-known compounds analyzed 5,600 transition metal complexes to identify potential spin-crossover complexes. The result was this plot, in which complexes are colored based on their spin-splitting energy in kilocalories per mole (kcal/mol). In promising candidates, that energy is within 5 kcal/mol of zero. The bright green diamonds in the inset are related complexes. Credit: Massachusetts Institute of Technology

To prescreen a data set, the genetic algorithm first randomly selects 20 samples from the full set of complexes. It then assigns a "fitness" score to each sample based on three measures. First, is its spin-crossover energy low enough for it to be a good SCO? To find out, the neural network evaluates each of the 20 complexes. Second, is the complex too far away from the training data? If so, the spin-crossover energy from the ANN may be inaccurate. And finally, is the complex too close to the training data? If so, the researchers have already run a DFT calculation on a similar molecule, so the candidate is not of interest in the quest for new options.

Based on its three-part evaluation of the first 20 candidates, the genetic algorithm throws out unfit options and saves the fittest for the next round. To ensure the diversity of the saved compounds, the algorithm calls for some of them to mutate a bit. One complex may be assigned a new, randomly selected ligand, or two promising complexes may swap ligands. After all, if a complex looks good, then something very similar could be even better—and the goal here is to find novel candidates. The genetic algorithm then adds some new, randomly chosen complexes to fill out the second group of 20 and performs its next analysis. By repeating this process a total of 21 times, it produces 21 generations of options. It thus proceeds through the search space, allowing the fittest candidates to survive and reproduce, and the unfit to die out.

Performing the 21-generation analysis on the full 5,600-complex data set required just over five minutes on a standard desktop computer, and it yielded 372 leads with a good combination of high diversity and acceptable confidence. The researchers then used DFT to examine 56 complexes

randomly chosen from among those leads, and the results confirmed that two-thirds of them could be good SCOs.

While a success rate of two-thirds may not sound great, the researchers make two points. First, their definition of what might make a good SCO was very restrictive: For a complex to survive, its spin-splitting energy had to be extremely small. And second, given a space of 5,600 complexes and nothing to go on, how many DFT analyses would be required to find 37 leads? As Janet notes, "It doesn't matter how many we evaluated with the neural network because it's so cheap. It's the DFT calculations that take time."

Best of all, using their approach enabled the researchers to find some unconventional SCO candidates that wouldn't have been thought of based on what's been studied in the past. "There are rules that people have—heuristics in their heads—for how they would build a spin-crossover complex," says Kulik. "We showed that you can find unexpected combinations of metals and ligands that aren't normally studied but can be promising as spin-crossover candidates."

### Sharing the new tools

To support the worldwide search for new materials, the researchers have incorporated the genetic algorithm and ANN into "molSimplify," the group's online, open-source software toolkit that anyone can download and use to build and simulate transition metal complexes. To help potential users, the site provides tutorials that demonstrate how to use key features of the open-source software codes. Development of molSimplify began with funding from the MIT Energy Initiative in 2014, and all the students in Kulik's group have contributed to it since then.

The researchers continue to improve their neural network for investigating potential SCOs and to post updated versions of molSimplify. Meanwhile, others in Kulik's lab are developing tools that can identify promising compounds for other applications. For example, one important area of focus is catalyst design. Graduate student in chemistry Aditya Nandy is focusing on finding a better catalyst for converting methane gas to an easier-to-handle liquid fuel such as methanol—a particularly challenging problem. "Now we have an outside molecule coming in, and our complex—the catalyst—has to act on that molecule to perform a chemical transformation that takes place in a whole series of steps," says Nandy. "Machine learning will be super-useful in figuring out the important design parameters for a transition metal complex that will make each step in that process energetically favorable." [26]

### Machine learning reveals rapid material classification

A research team at The University of Tokyo has developed a powerful machine learning algorithm that predicts the properties and structures of unknown samples from an electron spectrum. This process may rapidly accelerate the process of discovering and testing novel nanomachines, solar cells, and other electronic devices.

Tricorders are fictional devices first seen on the original Star Trek television show. In this science fiction setting, scientists could instantly learn about the rocks on alien planets with a quick scan.

Researchers at The University of Tokyo have taken a step towards making this concept a reality. They used data from core-loss electron spectroscopy, a set of standard laboratory tests that send electrons at a sample to determine the atomic elements in it and their bonding structure. However, the results from these instruments are difficult to interpret. To overcome this problem, they turned to machine learning. In contrast with conventional computer programs, machine learning algorithms do not need to be told what patterns to look for. Instead, the algorithms are trained by inputting many examples, and over time the program learns how to classify new unknown samples.

Here, the researchers chose a neural network that mimics the organization of the human brain. Data from known materials are sent as input, and the connections between neurons are adjusted to optimize the model's predictions. According to first author Shin Kiyohara, "with the increasing demand for nanoscale devices, tools for understanding molecular structures are becoming more and more valuable."

Although still a long way from a tricorder that can instantly identify alien rock formations, lead author Teruyasu Mizoguchi believes that "this method has enormous potential for use in quickly testing the properties of new materials." [25]

## Synopsis: A Classical Machine Learning Algorithm Goes Quantum

Researchers have mathematically proven that a powerful classical machine learning algorithm should work on quantum computers.
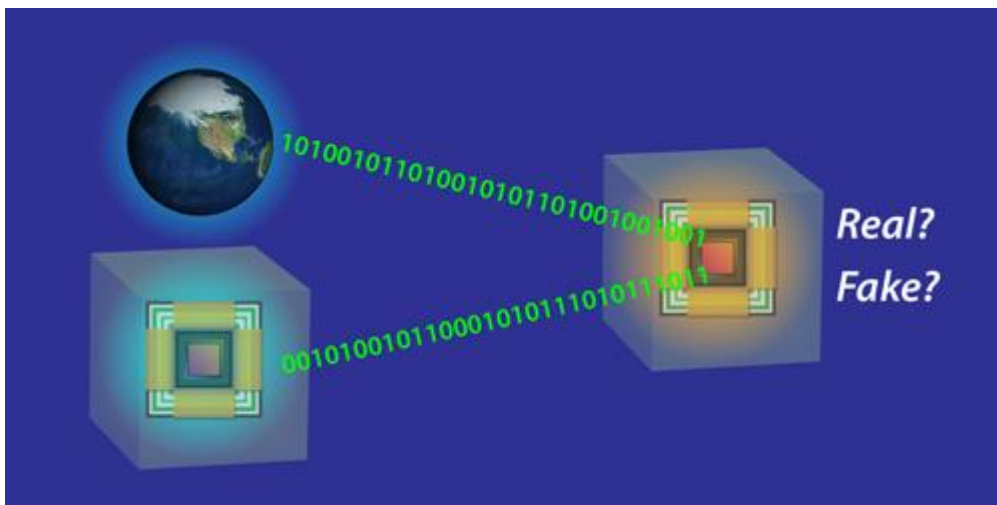


APS/**Alan Stonebraker**

In recent years, computer scientists have used machine learning algorithms known as generative adversarial networks (GANs) to manipulate data to startling effect. Applied to graphics, GANs can open closed eyes in photos and create forged videos of politicians speaking. Now, Seth Lloyd of the Massachusetts Institute of Technology, Cambridge, and Christian Weedbrook of the Canadian startup Xanadu have theoretically proven that the algorithm can be applied to quantum data sets. Similar to

classical GANs, quantum GANs, or QGANs, could be used to generate realistic-looking quantum data on quantum computers.

To identify and replicate patterns in data, GANs employ two competing components—a "generator" and a "discriminator"—that compete in a kind of game. Fed with real data, the generator tries to produce numbers whose statistical distribution mimics that of the real data. The discriminator then looks at the generator's data and guesses whether the numbers are real or fake. Using the discriminator's feedback, the generator progressively produces more realistic-looking numbers. The game eventually ends when the discriminator can no longer tell the fake numbers from the real ones—the generator has completely replicated the statistics of the real data. The game works because the discriminator fails exactly when the generator achieves its goal.

Lloyd and Weedbrook mathematically proved that a QGAN should operate in a similar fashion: Just like the classical case, the quantum discriminator fails when the quantum generator reproduces the statistics of real data. In the near future, the duo says that QGANs could be used to perform quantum simulations of molecules faster than classical computers and could help improve other applications including drug discovery, algorithmic trading, and fraud detection.

This research is published in ***Physical Review Letters***. [24]


## Deep learning cracks the code of messenger RNAs and protein-coding potential

Researchers at Oregon State University have used deep learning to decipher which ribonucleic acids have the potential to encode proteins.

The gated recurrent neural network developed in the College of Science and College of Engineering is an important step toward better understanding RNA, one of life's fundamental, essential molecules.

Unlocking the mysteries of RNA means knowing its connections to human health and disease.

Deep learning, a type of machine-learning not based on task-specific algorithms, is a powerful tool for solving the puzzle.

"Deep learning may seem scary to some people, but at the end of the day, it's just crunching numbers," said David Hendrix, the study's lead author. "It's a tool just like calculus or linear algebra, one that we can use to learn biological patterns. The amount of sequencing data we have now is huge, and deep learning is well suited to face the challenges associated with the vast amount of data and to learn new biological rules that characterize the function of these molecules."

RNA is transcribed from DNA, the other nucleic acid—so named because they were first discovered in the cell nuclei of living things—to produce the proteins needed throughout the body.

DNA contains a person's hereditary information, and RNA acts as the messenger that delivers the information's coded instructions to the protein-manufacturing sites within the cells.

Some RNAs are functional molecules transcribed from DNA that aren't translated into proteins. These are known as non-coding RNAs.

Every day, new RNAs are discovered, and gene sequencing technology has advanced to the point that molecular biologists are facing a "torrent" of new transcript annotations to glean information from, Hendrix said.

These vast datasets require new approaches, said the researcher, an assistant professor with joint appointments in biochemistry/biophysics and computer science.

Hendrix and colleagues gave a gated neural network training on both noncoding and messenger RNA sequences, then turned it loose on the data to "learn the defining characteristics of protein-coding transcripts on its own."

It did, with remarkable improvement over existing state-of-the-art methods for predicting protein-coding potential.

"It's really exciting," Hendrix said. "With the competing programs, developers would tell the program what an open reading frame is, what a start codon is, what a stop codon is. We thought it would be better to have a more de novo approach where the neural network can learn independently."

A codon is a sequence of three nucleotides, the basic structural unit of nucleic acids. Codons act like a translator between the nucleotides in DNA and RNA and the 20 amino acids behind protein synthesis.

Compared to other approaches, the model that the OSU team developed, known as mRNN, was better by a statistically significant margin in nearly every available metric.

"It not only found stop codons, it distinguished real stop codons from other trinucleotides that match stop codons and recognized long-range dependencies in the sequences," Hendrix said. "It doesn't wait to see a stop codon—we found it makes its decision long before the stop codon, 200 nucleotides from the start codon. And it learned a subset of codons that were highly predictive of protein-coding potential when observed in a potential open reading frame."

Hendrix and colleagues dubbed these special codons "TICs—translation-indicating codons. [23]

## Finding the proteins that unpack DNA

A new method allows researchers to systematically identify specialized proteins that unpack DNA inside the nucleus of a cell, making the usually dense DNA more accessible for gene expression and other functions. The method, developed by a team of researchers at Penn State, and the shared characteristics of these proteins are described in a paper that appears online on July 12th in the journal *Molecular Cell*.

"Our genome is very compact, which means there is an accessibility issue," said Lu Bai, assistant professor of biochemistry and molecular biology and of physics at Penn State and senior author of the study. "A variety of proteins need to access DNA to copy its information into the RNA that will

eventually be used to make proteins, but DNA is tightly wrapped around proteins called histones that are then packed into bead-like structures called nucleosomes. These tightly packed nucleosomes make it hard for other proteins to bind.

"To solve this problem, cells use what we call 'nucleosome-displacing factors' to invade the condensed DNA and open it up. Until this study, we lacked a general method to screen for these factors and evaluate them."

Nucleosome-displacing factors are a special kind of transcription factor, proteins that bind to short, specific sequences of DNA called binding sites to control gene expression. They are also known as pioneer factors in animal cells. The researchers developed a fast, inexpensive "high-throughput" method to screen and categorize large numbers of transcription factors based on their ability to displace nucleosomes. The method artificially incorporates transcription factor binding sites into the nucleosomes and examines which factors are capable of reducing the presence of nucleosomes.

The researchers identified both new and previously known nucleosome-displacing factors. These factors, particularly those that strongly deplete nucleosomes, tend to be highly abundant in the nucleus and bind very tightly to DNA.

"We think some of these factors can physically compete with nucleosomes for locations on the DNA to bind," said Bai. "They may take advantage of the DNA replication process, when the nucleosome is temporarily disrupted and thus frees up some DNA. Because there are so many of these strong nucleosome-displacing factors in the cell, they immediately hop onto a binding site on the DNA and they refuse to dissociate. It's hard to assemble a nucleosome on top of that."

The researchers also identified some transcription factors that can displace nucleosomes without tapping into the DNA replication process.

"Even though we've known about some of these factors for decades, we still don't have the molecular details of how they work," said Bai. "In the future we hope to investigate, for example, which specific parts of these proteins may be important for nucleosome displacement."

In addition to identifying a suite of new nucleosome-displacing factors, this study provides a proof of concept of this screening method in the relatively simple system of yeast. The researchers plan to extend this method to more complex systems, such as mammals, and to different cell types and developmental stages.

"Pioneer factors are associated with the differentiation of cells into different, specialized cell types," said Bai. "If we can map out the key factors that are involved in cell type transitions, we may eventually be able to design a combination of transcription factors to artificially direct the fate of a cell. At least, that is the dream." [22]


## New technologies for producing medical therapeutic proteins

Bacterial systems are some of the simplest and most effective platforms for the expression of recombinant proteins. They are more cost-effective compared to other methods, and are therefore of great interest not only for Lobachevsky University researchers, but also for manufacturers of therapeutically important drugs.

However, in addition to the target recombinant proteins, cells also produce a large number of endogenous proteins, including SlyD. It is a small protein consisting of three domains. Its C-terminal region is rich in histidine residues, and SlyD therefore exhibits a high affinity for the 2-valent ions and is purified together with the target proteins in the course of metal-affinity chromatography. This results in the need for additional purification steps, and as a consequence, increases the cost of the technological process for obtaining therapeutic recombinant proteins.

A team of Lobachevsky University researchers under Professor Viktor Novikov, Director of the UNN Center for Molecular Biology and Biomedicine, has obtained a series of E. coli strains deficient in the SlyD/SlyX genes. The strains were engineered using λ-red mediated chromosomal deletion. (Figure 1.)

"The sequence of SlyD/SlyX in the E. coli genome was replaced by a gene responsible for resistance to the antibiotic kanamycin that was flanked on both sides by FRT sites, from where it was later removed by FLP recombinase," Viktor Novikov notes.

Using the example of recombinant bispecific protein MYSTI-2 consisting of two modules that are active centers of antibodies against mouse proteins F4/80 and TNF, the scientists compared the activity of proteins isolated from the original and mutant strains. As a result of the study, it was determined that the removal from the E. coli genome of the SlyD and SlyX genes, which presumably encode chaperones that support the spatial structure of Escherichia coli proteins, does not result in a disruption of recombinant proteins' functional activity.

By obtaining original E. coli strains, the researchers were able to solve the problem of contamination of recombinant proteins and to ensure their successful single-stage purification by metal-affinity chromatography.

"The obtained set of slyD/slyX-deficient strains of E. coli can be used to produce in a pure form a wide range of prokaryotic and eukaryotic proteins, including medical therapeutic proteins. This makes the development and production of new medicinal and preventive biological preparations easier, simpler and cheaper," concludes Viktor Novikov. [21]

## Mayo researchers find off/on switch for DNA repair protein

Damage to DNA is a daily occurrence but one that human cells have evolved to manage. Now, in a new paper published in *Nature Structural & Molecular Biology*, Mayo researchers have determined how one DNA repair protein gets to the site of DNA damage. The authors say they hope this discovery research will help identify new therapies for ovarian cancer.

While the human genome is constantly damaged, cells have proteins that detect and repair the damage. One of those proteins is called 53BP1. It is involved in the repair of DNA when both strands break. In the publication, Georges Mer, Ph.D., a Mayo Clinic structural biologist, and his team report on how 53BP1 relocates to chromosomes to do its job.

Dr. Mer explains that, in the absence of DNA damage, 53BP1 is inactive—blocked by a protein called "TIRR." Using a visualization technique called X-ray crystallography, the authors show that TIRR

obstructs an area on 53BP1 that 53BP1 uses to bind chromosomes. But what shifts TIRR away from 53BP1, so the repair protein can work?

The authors theorized that a type of nucleic acid called RNA was responsible for this shift. To test their theory, they engineered a protein that would bind to the 53BP1 repair protein and the RNA molecules released when DNA is damaged. This effort, plus other work detailed in the paper, provides evidence that their idea was sound. The authors report that when DNA damage occurs, RNA molecules produced at that time can bind to TIRR, displacing it from 53BP1 and allowing 53BP1 to swing into action.

"Our study provides a proof-of-principle mechanism for how RNA molecules can trigger the localization of 53BP1 to DNA damage sites," says Dr. Mer. "The TIRR/RNA pair can be seen as an off/on switch that blocks or triggers 53BP1 relocation to DNA damage sites."

Also in the paper, the authors report that displacing TIRR increases sensitivity of cells in cell culture to olaparib, a drug used to treat patients with ovarian cancer.

"Unfortunately, over time cancer cells develop resistance to drugs in this category, called 'PARP inhibitors.' Our work provides a new target, TIRR, for developing therapeutics that would help specifically kill ovarian cancer cells," Dr. Mer says.

Collaborators on this work include the Dana-Farber Cancer Institute and the Wellcome Trust Centre for Human Genetics at the University of Oxford in the U.K. In addition to Dr. Mer, other Mayo Clinic authors are Maria Victoria Botuyan, Ph.D., Gaofeng Cui, Ph.D., James R. Thompson, Ph.D., Benoît Bragantini, Ph.D., and Debiao Zhao, Ph.D.

The authors report no conflict of interest. Funding for this research was provided by the National Institutes of Health, including the Mayo Clinic Ovarian Cancer Specialized Program of Research Excellence, and the U.S. Department of Defense. Additional funding sources are listed in the publication. [20]


## Investigators say DNA database can be goldmine for old cases

A microscopic thread of DNA evidence in a public genealogy database led California authorities to declare this spring they had caught the Golden State Killer, the rapist and murderer who had eluded authorities for decades.

Emboldened by that breakthrough, a number of private investigators are spearheading a call for amateur genealogists to help solve other cold cases by contributing their own genetic information to the same public database. They say a larger array of genetic information would widen the pool to find criminals who have eluded capture.

The idea is to get people to transfer profiles compiled by commercial genealogy sites such as Ancestry.com and 23andMe onto the smaller, public open-source database created in 2010, called

GEDmatch. The commercial sites require authorities to obtain search warrants for the information; the public site does not.

But the push is running up against privacy concerns.

"When these things start getting used by law enforcement, it's very important that we ensure that to get all of the benefit of that technology we don't end up giving up our rights," said American Civil Liberties Union legal fellow Vera Eidelman.

She argues that when someone uploads their own DNA profile they aren't just adding themselves— they're adding everyone in their family, including dead relatives and those who haven't been born yet. She also said DNA mining could lead to someone's predisposition to mental and health issues being revealed.

"That one click between Ancestry and 23andMe and GEDmatch is actually a huge step in terms of who has access to your information," Eidelman said.

This month, DNA testing service MyHeritage announced that a security breach revealed details about over 92 million accounts. The information did not include genetic data but nonetheless reinforced anxieties.

Nevertheless, the effort is gaining steam with some genetic genealogy experts and investigators.

The shared DNA profiles "could end up being the key to solving one of these cold cases and getting the family closure and getting someone really dangerous off the streets," said CeCe Moore, the head of the genetic genealogy unit at the DNA company Parabon NanoLabs.

She's uploaded her personal genetic information to the public database and wants it to become a larger repository of information for genealogy hobbyists and investigators alike. Separately, Parabon NanoLabs has also uploaded DNA data from 100 unsolved crime scenes in hopes of finding suspects.

Private investigator Jason Jensen holds a Phenotype Report at his office Friday, June 15, 2018, in Salt Lake City. Groups of private investigators in Utah and California have been emboldened by the arrest of the suspected Golden State …more

Genetic genealogy has traditionally been used to map family histories. Labs analyze hundreds of thousands of genetic markers in an individual's DNA, compare them with others and link up families based on similarities. The public database was created to compare family trees and genetic profiles between the commercial sites, which don't cross-reference information.

Its potential as a police tool wasn't broadly known until the April arrest of Golden State Killer suspect Joseph DeAngelo in northern California. Prosecutors allege DeAngelo, a former police officer, is responsible for at least a dozen murders and about 50 rapes in the 1970s and '80s.

But the DNA-assisted hunt that led to his arrest wasn't flawless. It initially led authorities to the wrong man whose relative shared a rare genetic marker with crime-scene evidence. A similar thing happened when authorities used a different public DNA database to investigate a nearly two-decade-old Idaho murder in 2014.

In May, Moore used the public database to help police arrest a 55-year-old Washington man linked to the 1987 killing of a young Canadian couple. She suspects the method will lead to dozens of arrests in similar cold cases.

Courts haven't fully explored legal questions around the technique but are likely to allow it based on current law, said attorney and forensic consultant Bicka Barlow. The theory is that an individual's right to privacy does not extend to material they've abandoned, whether it's DNA or trash.

GEDmatch co-creator Curtis Rogers was initially unaware police used his site to find the suspected Golden State Killer. He's glad it's led to solving crimes but is worried about privacy issues. The site's

policy was updated in May and says it can't guarantee how results will be used. Users are allowed to remove their information.

A California-based group of volunteers called the DNA Doe Project has also used the database to identify two bodies that stumped authorities for more than a decade. The group encourages its thousands of online supporters to contribute to the public database.

"It's free, it's like three or four clicks and a couple minutes of your time," said co-founder Margaret Press. "It's altruistic if you have no interest in your own family history; if you did, it's a win-win."

A volunteer group of investigators and attorneys called the Utah Cold Case Coalition has made a similar appeal.

The idea may be particularly appealing in Utah, co-founder Jason Jensen suspects. An interest in genealogy is especially strong in the state, because tenets of The Church of Jesus Christ of Latter-day Saints emphasize the importance of family relationships in the afterlife.

"Arguably that one person can post up their DNA and might potentially break a case that somebody back in Nantucket (Massachusetts) is trying to solve," Jensen said. [19]

## Researchers build DNA replication in a model synthetic cell

Researchers at Delft University of Technology, in collaboration with colleagues at the Autonomous University of Madrid, have created an artificial DNA blueprint for the replication of DNA in a cell-like structure. Creating such a complex biological module is an important step towards an even more ambitious goal: building a complete and functioning synthetic cell from the bottom up.

Copying DNA is an essential function of living cells. It allows for cell division and propagation of genetic information to the offspring. The mechanism underlying DNA replication consists of three important steps. First, DNA is transcribed into messenger RNA. Messenger RNA is then translated into proteins—the workhorses of the cell that carry out many of its vital functions. The job of some of these proteins, finally, is to perform the last step in the cycle: the replication (or copying) of DNA. After a cell has replicated its DNA, it can divide into two daughter cells, each containing a copy of the original genetic material.

### Closing the cycle

Researchers had already realized all of the separate steps mentioned above. Japanese scientists, for instance, created a minimal, stand-alone system for messenger RNA and protein synthesis by taking the relevant components from *E. coli* and tweaking them. But no one had yet been able to combine this system with autonomous DNA replication. "We wanted to close the cycle and be the first to reconstruct the entire flow of genetic information inside a cell-like structure called a liposome," said group leader Christophe Danelon.

Combining the Japanese system with a module for DNA replication proved difficult. "We tried a few approaches, but none seemed to work convincingly," said Danelon. Then, Ph.D. student Pauline van

Nies came up with the idea to use the DNA replication machinery of a virus called Φ29. "Viruses are very intriguing from a molecular biology point of view," said Van Nies. "They are extremely efficient in encoding proteins in a small genome and in robustly replicating their genetic information." In human cells, DNA replication is managed by hundreds of proteins. Φ29 only needs four.

### Composing DNA

Many years ago, researchers working at the Autonomous University of Madrid discovered the DNA replication mechanism of the Φ29 virus and managed to isolate it. Van Nies and Danelon worked with these researchers to combine the genes that encode for the replication mechanism with the genetic code that is necessary to operate the Japanese module for transcription and translation.

Van Nies composed a unique DNA blueprint that took into account a number of different factors related to the flow of genetic information, such as a suitable binding site for the ribosome, an element that is essential for the production of proteins.

### Combining machinery

A goal that now comes into view is combining the new module that regulates the flow of genetic information with other essential cellular functions such as growth and division. Last year, the Danelon group created a way to synthesize the phospholipids that make up liposomes, such as the ones the researchers used in this project. The yield of phospholipids was still too small to sustain growth, but Danelon is confident his group can optimize this process.

Cell division may be a tougher nut to crack. In modern cells, it requires a streamlined process in which copied DNA is neatly packed and then evenly distributed towards the poles of the cell. Concurrently, specialized proteins squeeze the mother cell into two daughter cells. Danelon thinks a simple 'budding' mechanism could also do the trick. "I think we can create liposomes that grow until they start budding. If enough DNA is being produced, hopefully enough of these primitive daughter cells will contain the new DNA to sustain a cell population." This may well be how the very first cells self-reproduced, before evolution equipped them with a more elegant and robust solution.

### Building a synthetic cell

The mission that ties together all of the fundamental research described above is the construction of a synthetic cell that can grow, divide and sustain itself. Scientists at Delft University of Technology play a leading role in this exciting new research direction that may ultimately lead to intimate understanding of the inner workings of a cell. Research supporting the initiative could lead to advances in biotechnology, health and energy. [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 squaraine and (1,4bis(N,Ndimethylamino)naphthalene) to the pFA molecule resulting in its cleavage. The new fatty acid joins the existing minimal cell thus increasing it in size. After reaching some critical size, the minimal cell should divide (i.e. self-replicate) into two separate smaller minimal cells. [7]

## Quantum Biology

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

## Quantum Consciousness

Extensive scientific investigation has found that a form of quantum coherence operates within living biological systems through what is known as biological excitations and biophoton emission. What this means is that metabolic energy is stored as a form of electromechanical and electromagnetic excitations. These coherent excitations are considered responsible for generating and maintaining long-range order via the transformation of energy and very weak electromagnetic signals. After nearly twenty years of experimental research, Fritz-Albert Popp put forward the hypothesis that biophotons are emitted from a coherent 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 $E = h\nu$ and $E = mc^2$, $m = h\nu /c^2$ that is the $m$ depends only on the $\nu$ 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.

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