

First Congress

*International Society of
Diamagnetic Therapy*

**“The science of numbers
in the knowledge”**



13th – 14th September 2024
Magna Graecia University - Catanzaro

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What does mathematics have to do with medicine?

Let us ask to ChatGpt.

Mathematics plays a crucial role in medicine in various ways, from diagnosis and treatment planning to research and the development of new medical technologies. Here are several key areas where mathematics is integral to medicine:

1. Medical Imaging:

CT Scans and MRIs: Mathematical algorithms are used to reconstruct images from the raw data collected by these machines. Techniques like Fourier transforms and differential equations help convert the collected signals into clear, detailed images of the body's internal structures.

Image Analysis: Mathematics is used to enhance and interpret medical images, aiding in the detection and diagnosis of diseases such as tumors and fractures.



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2. Epidemiology:

Disease Modeling: Mathematical models help predict the spread of infectious diseases, understand their dynamics, and evaluate the potential impact of interventions like vaccinations and social distancing measures.

Statistical Analysis: Biostatistics is crucial for analyzing epidemiological data, identifying risk factors, and determining the effectiveness of treatments or public health interventions.

3. Pharmacokinetics and Pharmacodynamics:

Drug Dosage Calculations: Mathematics is used to determine the appropriate dosage of medications based on factors such as patient weight, age, and organ function, ensuring efficacy while minimizing side effects.

Modeling Drug Behavior: Differential equations model how drugs are absorbed, distributed, metabolized, and excreted by the body, optimizing drug design and delivery.

4. Genetics and Genomics:

Gene Sequencing: Algorithms and statistical methods are essential for analyzing DNA sequences, identifying genetic variations, and understanding their implications for health and disease.

Population Genetics: Mathematical models help study the genetic composition of populations and how it changes over time due to factors like natural selection and genetic drift.



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5. Biostatistics:

Clinical Trials: Statistical methods are used to design and analyze clinical trials, ensuring that results are valid, reliable, and can inform medical practice.

Outcome Prediction: Predictive models can estimate patient outcomes based on various clinical parameters, aiding in treatment planning and decision-making

6. Biomedical Engineering:

Medical Devices: Mathematics is fundamental in the design and optimization of medical devices such as pacemakers, prosthetics, and diagnostic equipment.

Biomechanics: Mathematical models simulate the mechanical behavior of biological tissues and systems, improving the design of implants and surgical techniques.

7. Personalised Medicine:

Data Analysis: Advanced mathematical techniques are used to analyze large datasets from electronic health records, genomic studies, and other sources, tailoring treatments to individual patients based on their unique characteristics.

8. Population Health and Public Health:

Resource Allocation: Optimization models help allocate limited medical resources effectively, ensuring that healthcare systems can respond efficiently to patient needs and public health crises.

Health Economics: Mathematical models evaluate the cost-effectiveness of different healthcare interventions, guiding policy decisions and resource allocation.



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In the past

The first applications of mathematics to medicine concerned epidemics. Faced with the raging plague and epidemics that ravaged populations, men did not know whether to turn to the gods or blame other men. The plague of Athens in 430 BC was attributed by Thucydides (460-399 BC) to the poisons thrown by the Spartans into the cisterns of Piraeus. The same opinion on the origin of epidemics was shared by Seneca (4 BC- 65 AD) who was convinced of the existence of "manufactured pestilence", and this was the dominant line of thought both in the Middle Ages and, also, for part of the modern era. The plague or cholera were due to the "presumed apparition of angelic beings, ministers of death and instruments of divine vengeance or the scapegoats were identified in certain social groups". The scapegoats were generally witches and Jews. In Central Europe, disastrous plague epidemics that decimated the population were accompanied by lynching and the plundering of property at the expense of Jews.



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Calls for moderation were equally frequent and almost always unheard. Pope Clement VI (1291-1352) issued a series of bulls calling on the clergy to protect them and to reject the accusations as unfounded: if they were truly the spreaders, why did they perish like the others from the epidemic? In January 1349, in Basel, when the authorities took severe measures against those who practiced violence against the Jews, the citizens rose up, unleashing an unprecedented manhunt. The captured Jews were locked in a building and burned alive. In Strasbourg, the Jewish population of the city was almost halved, in Worms, Frankfurt and Mainz, the Jews preferred to kill themselves rather than fall into the hands of the enraged mob. What happened to the Jews, also happened to witches. Women often on the margins of society were accused of everything: poisoning wells, causing livestock deaths and, obviously, spreading the infection. They ended up either lynched or burned at the stake. In Italy the behavior was not very different from the rest of Europe: as told by Alessandro Manzoni (1785-1873) for the plague of 1630, the belief was widespread that the plague was caused by "untori", who used greasy materials, powders and other poisonous preparations to spread the disease. This belief remained alive until the "Spanish flu". In fact, this epidemic was attributed, both in Italy and in the allied countries, to the Germans' bacteriological warfare: in the United States there were cases of health officials and nurses shot because they were accused of having inoculated the disease in the troops who were preparing to leave for Europe.^{13th – 14th September 2024}

We should not be surprised by this because we must take into account that popular superstition was often fueled by those who took advantage of it for their own interests, attributing the plague to a foreign power, a social class or a religious sect, which would have used the spreaders to spread the contagion. The people were terrorized by the alleged evil action of the spreaders and, inevitably, reacted by massacring and persecuting groups accused of being the architects or propagators of the epidemic. In the category of scapegoats, together with witches and Jews, also alchemists, foreigners, heretics and vagabonds fell. All categories that expressed diversity. During the Risorgimento, the reactionaries pointed out liberals and patriots to the common people as spreaders. The patriots of the Risorgimento did the same by inciting the plebs against the Bourbons, indicating them as promoters of the contagions that were raging in Italy. During a cholera epidemic in 1910-1911, the population of Southern Italy rebelled against administrators, doctors, and even King Victor Emmanuel III (1869-1947), accusing him of spreading the cholera disease with a “powder” in order to enslave the South by exterminating the southerners. Appeals to the use of reasoning appeared in vain in the newspapers. Conspiracy theory has always exercised a great fascination on the uncultured plebs and has always been used as a political weapon by populist political movements.

The history of mathematics in biomedical sciences can be traced back to 1760 when Daniel Bernoulli (1700-1782) published a study on the benefits of universal vaccination against smallpox. Bernoulli demonstrated, through the use of probability, that inoculating the entire population with a small dose of infected matter brought more benefits (immunity to the disease) than risks (the vaccination could have led to the death of the individual to whom it was administered). Bernoulli also calculated how much the average life of the population would be extended if smallpox were completely eradicated and found that mass vaccination would have extended life by an average of three years and two months. A very convincing fact even for the anti-vax of his time. This study on the dynamics of epidemics was a singular, although important, point in Bernoulli's scientific activity.

It took almost a century to see mathematical methods applied in the medical field again. In fact, in 1854, John Snow (1813-1858) used statistical tables to demonstrate that cholera was transmitted through contaminated water sources. He also used statistical methods to identify the water sources responsible for the cholera epidemic, including the infamous Broad Street pump. It should be noted that John Snow was a doctor. Curiously, the foundations of epidemiology based on mathematical models were laid from 1900 to 1935 not by mathematicians but by doctors.



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The first was W. H. Hamer (1862-1935) who suggested a law for the rate of new infections based only on the number of susceptible individuals (that is, those who can be infected) and the number of infectious individuals (who can infect). The second important contribution was made by Sir Ronald. A. Ross (1857-1932) who won the Nobel Prize for Medicine in 1902 for his demonstration of the dynamics of transmission of malaria between mosquitoes and humans. He discovered that the Anopheles mosquito carried the malaria parasite and this allowed the fight against the disease. Ross had a fierce dispute with the parasitologist Giovanni Battista Grassi (1854-1925) for priority in the discovery of malaria. Both had carried out the same studies and had arrived at the same conclusions at the same time. Basically, from what we can understand, Ross had discovered the passage of malaria from mosquitoes to birds and Grassi that from mosquitoes to humans. It would have been more fair to have awarded the Nobel Prize to both, but, according to an anecdote, Grassi paid dearly for the hostility he had developed with Heinrich Hermann Robert Koch (1843-1910), having criticized what he considered risky and deadly vaccination mechanisms proposed by Koch for tuberculosis, something that Koch considered very offensive. Whatever the reason why Ross was preferred to Grassi, what is certain is that this rivalry became even more intense when Ross won the Nobel Prize. Grassi always defended his independence and priority in the discovery. An article of his in Nature (January 1924) received a strong and indignant response from Ross in the same newspaper (March 8) to which Grassi replied, again in Nature, with a letter dated March 29.

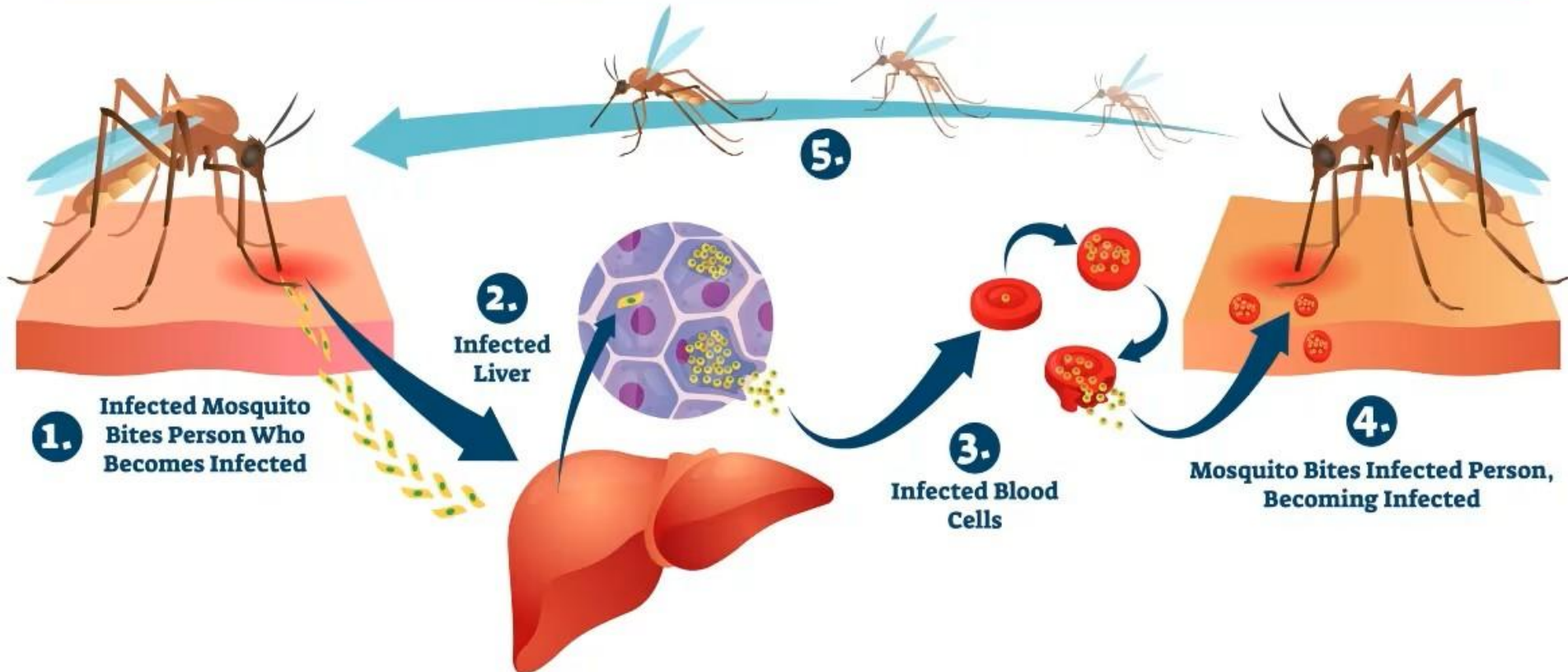


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MALARIA

MALARIA is a Mosquito-Borne Infectious Disease that Affects Humans and Other Animals. It is Caused by Single-Celled Microorganisms of the **PLASMODIUM** group.



The fact that malaria was carried by mosquitoes led to the belief that as long as mosquitoes were present in an area, malaria could not be eradicated. In 1911, Ross instead provided a simple mathematical model that showed that, to stop the spread of the disease, it would be sufficient to reduce the mosquito population below a critical level. This was the first introduction of the concept of the basic reproduction number, which has been a central idea in mathematical epidemiology ever since. Field trials supported this conclusion and led to sometimes brilliant successes in controlling malaria.

William Ogilvy Kermack (1898-1970) and Anderson Gray Mc Kendrick (1876-1943) were the authors of three papers published in 1927, 1932 and 1933 in which they described a model of the spread of communicable diseases that is still the basis of current models. The mathematics used to predict the spread of Covid19 had, in fact, its foundations laid a hundred years ago. Their model is now classified as the SIR model (Susceptible, Infected and Removed). This model divides a population P into three distinct populations:

S, those susceptible to being infected;

I, the infected who can infect the susceptible,

R, the removed, i.e. those who are not infected but who cannot be infected either because they have been vaccinated or because they are immune to the disease or because, having already been infected and then recovered, they have developed antibodies to the disease.

The Kermack and McKendrick model is based on a very intuitive property: we indicate with r how many people an infected person infects on average. If r is greater than 1, the infection spreads. If it is less than 1, the infection dies out. Let's take an example: if each infected person infects 2, the population of infected people will double each time until it reaches its peak in a short time. If we assume that r is equal to half, then for every two infected people, on average, there will be only one infection and therefore the population of infected people will halve until it dies out. The epidemic loses its virulence when r becomes less than one. This happens when the number of susceptible people S decreases or when it is more difficult for an infected person to find a susceptible person to infect. This situation is achieved in three ways:

- by vaccinating the population (thus increasing R and reducing S)
- when the epidemic has reached its peak and therefore the number of recovered people who have become Removed has increased (much)
- making contagion difficult by quarantining the infected.

This last method is easily implementable when an infected person becomes contagious after showing symptoms (symptomatic epidemic). If an infected person becomes contagious before showing any symptoms (asymptomatic epidemic) the containment measures become extremely heavy: isolation not only for those who show symptoms but also for their relatives and people they have come into contact with, accompanied by cancellation of public events, closure of schools and universities, etc etc). Exactly what happened to contain Covid19.

To prevent COVID-19 it is
safest to avoid physical
contact when greeting.
Safe greetings include a
wave, a nod, or a bow.

How should I greet
another person to avoid
catching the new
coronavirus?



#Coronavirus #COVID19

1 March 2020



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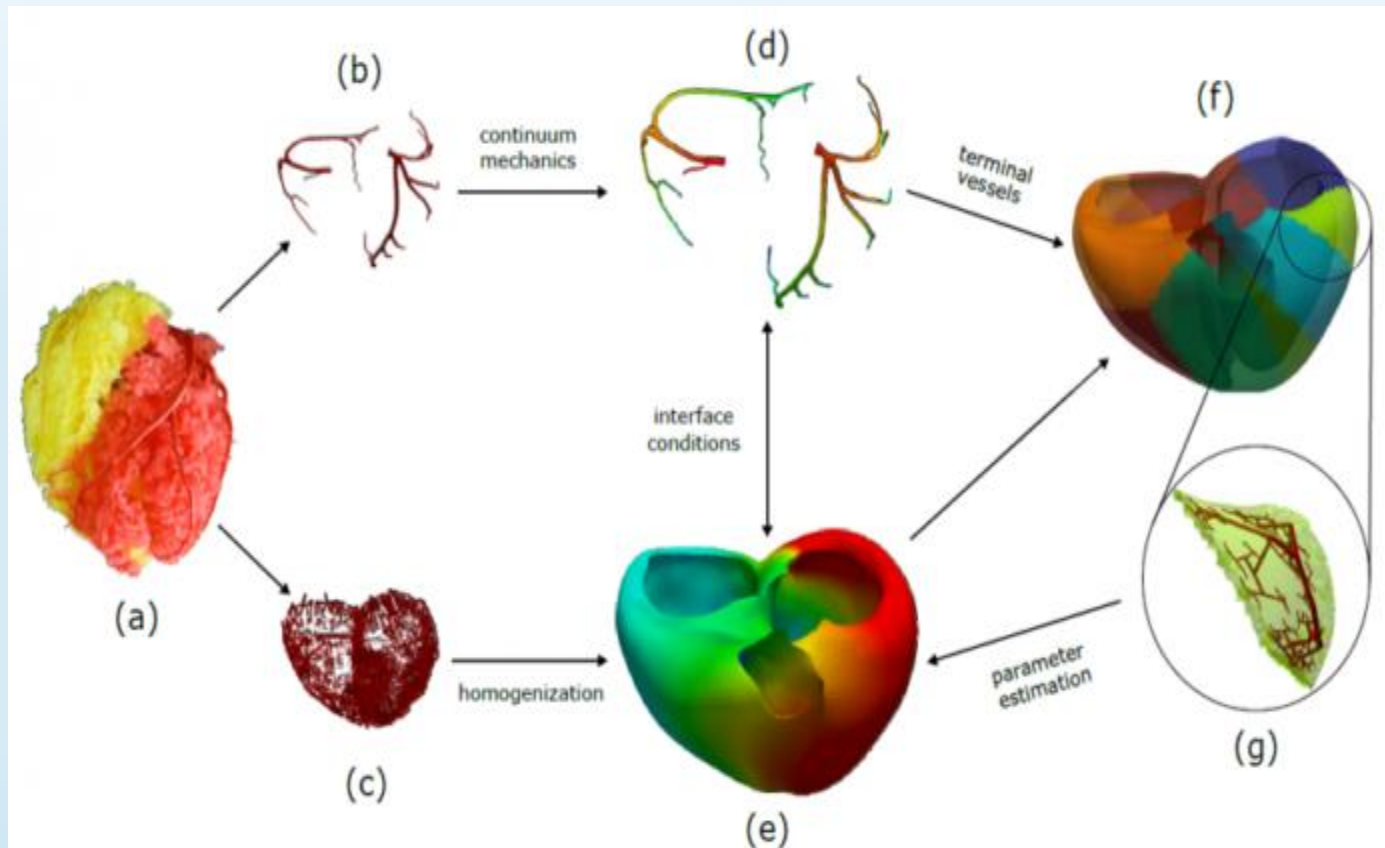
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Among the best-known applications of mathematics, the Hodgkin-Huxley model certainly stands out, which is a mathematical model that describes how action potentials in neurons are initiated and propagated. It is a set of nonlinear differential equations that approximate the electrical characteristics of excitable cells such as neurons and muscle cells. Alan Hodgkin (1914-1998) and Andrew Huxley (1917-2012) described the model in 1952 to explain the ionic mechanisms underlying the initiation and propagation of action potentials in the giant axon of the squid. They were awarded the Nobel Prize in Medicine in 1963 for this important work that marked the beginning of computational neuroscience.

Another application is that relating to the Radon transform, which was introduced in 1917 by Johann Radon (1887-1956) also providing a formula for the inverse transform. The Radon transform is widely applied in tomography to create an image from projection data associated with transverse scans of an object. This is because the Radon transform represents the projection data obtained as output from a tomographic scan and therefore the inverse of the Radon transform can be used to reconstruct the original density from the projection data allowing tomographic reconstruction.

A natural application to medicine is computational fluid dynamics, although highly non-trivial, The boundaries of vessels and cavities that convey and contain fluids in the human body are flexible (veins and arteries), time-varying (heart), porous (brain ventricles), or have complex geometry (lungs), which makes numerical modeling even more challenging.



See for instance <https://www.youtube.com/watch?v=ehL-YDc6-5w>

In the present

The discipline that is currently experiencing the greatest development is genetics: genome sequencing has the potential to transform medicine from a craft and statistical science to a hard science and can extend life and improve the human condition by defeating many diseases. This science studies the human hereditary material known as deoxyribonucleic acid, or DNA, which is a long self-replicating molecule containing the information that all living organisms need both to develop and to reproduce. DNA is found in every cell of the body and is passed down from parent to child. Every cell of a single individual has the same DNA. Although DNA was discovered in 1869 by the Swiss-born biochemist Fredrich Miescher (1844-1895), it took more than 80 years for its importance to be fully understood. Note that I used the word importance, not the word functioning because it still eludes us in its entirety.



 = Adenine

 = Thymine

 = Cytosine

 = Guanine

 = Phosphate
backbone

DNA



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The helix structure of DNA was first seen in 1951, through X-ray, by Rosalind Franklin (1920-1958) and interpreted in 1953 by James Dewey Watson (1928-) and Francis Crick (1916-2004) who gave a scientific explanation of the structure seen by Franklin. Watson and Crick, for their discovery, were awarded the Nobel Prize in 1962. It was a shame that Franklin's premature death prevented this important recognition from being shared with her. It would have been a nice sign of gender equality in a still very sexist era.

The human genome is composed of about 3.2 billion DNA bases, but other organisms have different genome sizes. The complexity of an organism is not directly proportional to the size of its genome. Some unicellular organisms have much more DNA than humans, for reasons that remain unclear. For example, the genome of an onion is five times larger than that of a human. Another strange thing is that the human genome contains about 20,000 genes, which are the stretches of DNA that code for proteins. But these genes only make up 1.2% of the total genome. The other 98.8% is known as non-coding DNA.

A very simplistic explanation, first developed in the 1970s by geneticist Susumu Ohno (1928-2000), holds that large genomes would inevitably harbor sequences, passively accumulated over many millennia, that did not code for any protein. For this reason, the size of an animal or plant's genome would have essentially no relation to its complexity, because the vast majority of its DNA would simply be junk.

DISCOVERY INSTITUTE PRESS

THE MYTH OF JUNK DNA



BY JONATHAN WELLS



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So much of our DNA would simply be a remnant of evolution, a bit like the cecum for us humans. The idea that 98.8% of our genome is useless is rapidly fading. Scientific progress in how DNA works is making us understand that even “junk” DNA has vital functions for our organism such as those studied by epigenetics, the science that studies heritable changes that cannot be explained by changes in the DNA sequence.

The first step in understanding how the human genome works was to sequence it. The first draft of the human genome was completed by the International Human Genome Consortium twenty years ago. It took them 3 years and the project cost a few billion dollars. As already written, the genome is a sequence of A, C, G and T approximately 3,200,000,000 digits long. Currently, sequencing techniques can only sequence DNA strands up to 1,000 bases long. So what you can do is break the DNA into smaller pieces, sequence them separately, and then try to put the lot back together. It's like a giant jigsaw puzzle with millions of pieces. With such large numbers, sequencing the entire genome of a complex organism is a mathematical nightmare. Algorithmics have made great strides, but whole-genome sequencing is still an inexact science. No sequencing technology is 100% accurate (although we've gotten to 99.99%) and highly repetitive strings in the genome remain very difficult to resolve.

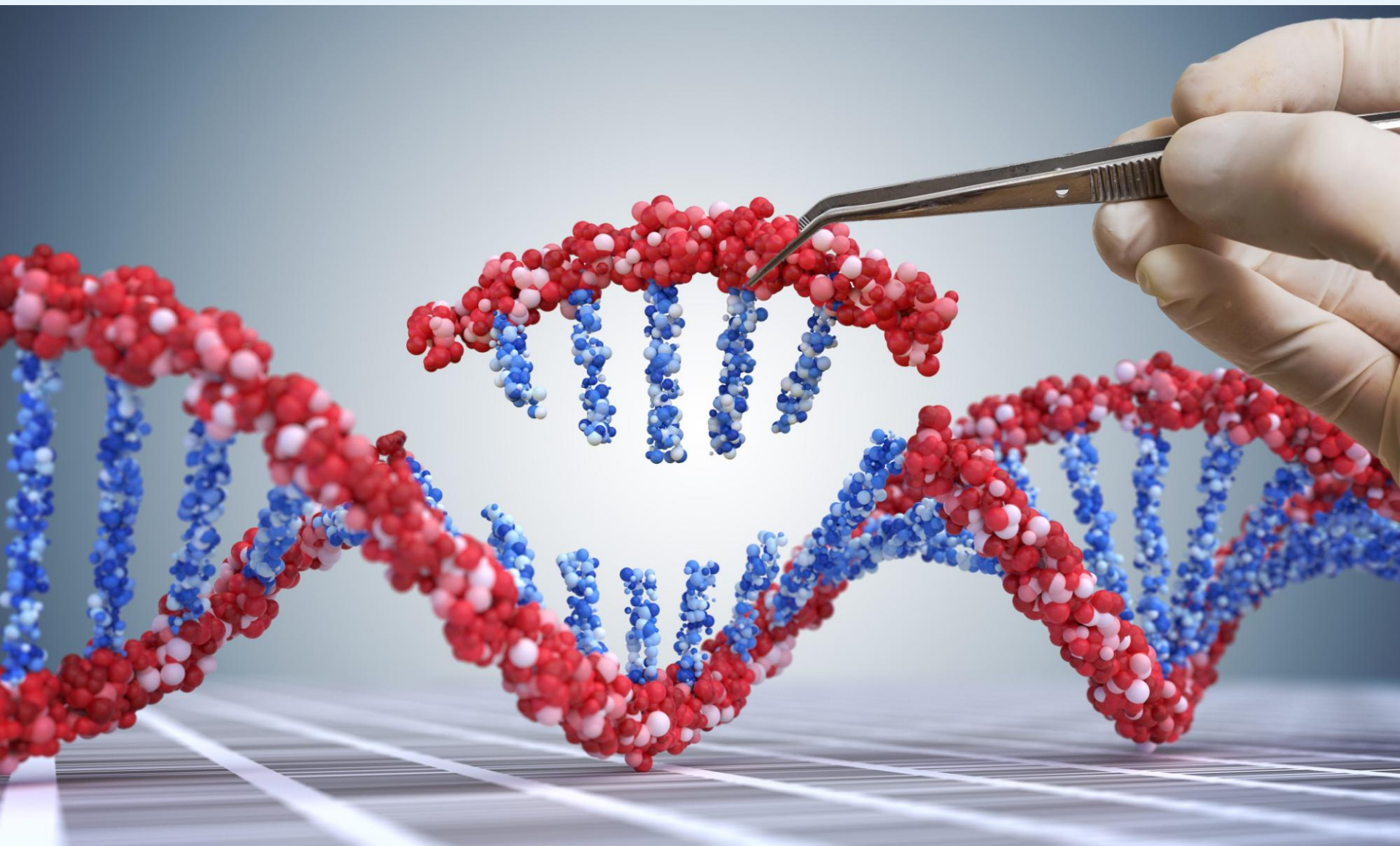


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Biological information, such as sequence comparisons for various individuals, obviously helps, but statistics also plays an important role because it can quantify levels of uncertainty. Statistical information about the probability and distribution of errors is in fact used by many algorithms to try to eliminate them. But until we are able to sequence an entire genome in one go, a lot of computing power and intelligent algorithms will be needed to put the pieces together, and combinatorial mathematics together with AI methodologies will remain the central tools to be used for genomic sequencing. The old combinatorial mathematics and the new mathematics based on deep learning will probably merge into a new discipline. Thanks to new algorithmic approaches, as early as 2013, the entire process of sequencing the human genome could have been performed in less than two weeks and at a cost of around a thousand dollars. Now it is offered commercially for around fifty dollars also accompanied by services such as genetic predisposition to diseases. This makes us understand the progress not only computational (which, although impressive, could not have explained the improvement in times and costs) but above all algorithmic. Currently, we can identify (and therefore, potentially cure) hereditary genetic diseases that derive from the "malfunctioning" of a single gene, but, unfortunately, many others depend on the combination of multiple genes. Now, finding the combination of genes that causes a specific disease has a mathematical and algorithmic difficulty that increases exponentially with the number of genes involved and is still not within the reach of modern science.



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While genomics is at the beginning of its journey as a discipline, proteomics (which concerns proteins and therefore also the study of RNA) is still in its infancy. Particularly interesting is the process of protein folding, which describes the phenomenon of a protein chain that folds on itself to become biologically active. The problem is extremely stimulating: it means finding the minimum of a functional that is very difficult (almost impossible) to treat mathematically and trying to simulate with the computer a phenomenon that occurs in nature in less than a thousandth of a second. It is very important to understand this phenomenon. When a protein folds badly, it seems that diseases characterized by degeneration of nervous tissue can originate. For example, the so-called "mad cow" (bovine spongiform encephalopathy) seems to have this cause. In 2020, AlphaFold, the AI system developed by DeepMind, managed to build the 3D structure of a protein starting from the information of the amino acid sequence that composes it, much more quickly and accurately than any method used so far. Understanding how proteins work in detail should significantly speed up drug discovery. Another challenge concerns so-called knotted proteins, which are proteins whose backbones get caught in a knot. To get a rough idea of what these are, if you were to imagine pulling a protein chain from both ends, as if you were pulling on a rope, instead of reverting to the original amino acid chain, it would get tangled in a knot.



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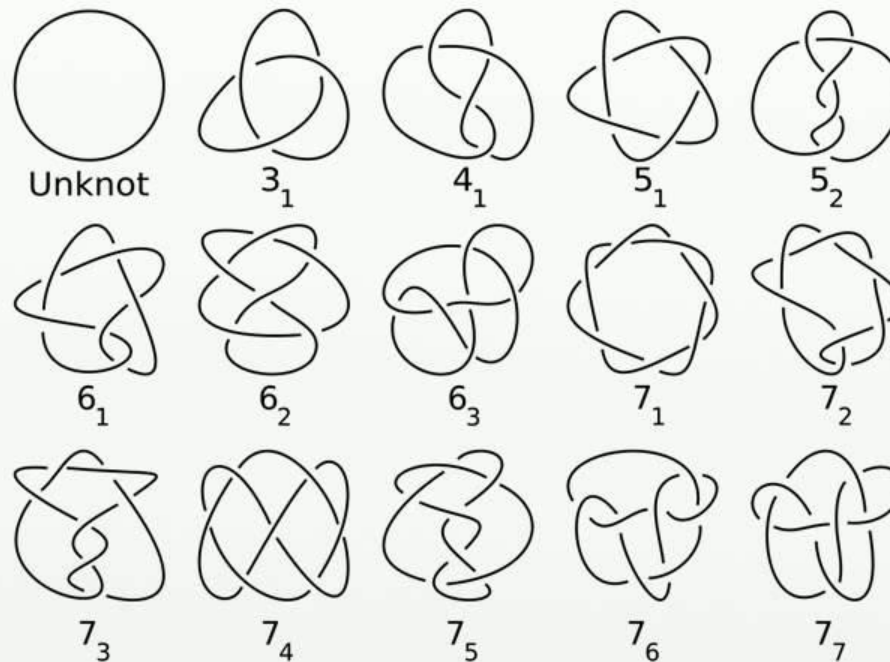


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Knotted proteins are very rare, making up only about one percent of the proteins in the protein database, and their folding mechanisms and function are not well understood. Although there are experimental and theoretical studies that suggest some answers, no systematic answers have yet been found to these questions. To understand the structure of these knots, the mathematical theory of knots, which was first developed in 1771 by Alexandre-Théophile Vandermonde (1735-1796), who explicitly noted the importance of topological features, is very useful. The actual mathematical studies on knots began with Carl Friedrich Gauss (1777-1855), who laid the mathematical foundations. In 1860, Lord Kelvin's (1824-1907) theory that atoms were knots in the ether led to Peter Guthrie Tait's (1831-1901) creation of the first mathematical classification of knots. This theory regained deep interest precisely when the chemist and biologist Marc L. Mansfield proposed, in 1994, that there could be knots in proteins.

An assumption that was proven to be true in 2000 by William R. Taylor. Note that knot theory could also be crucial in building quantum computers, if the topological quantum computing model proposed in 1997 by Russian physicist Alexei Kitaev (1963-) were to prevail. Clearly, important mathematical challenges await future generations.

Knot (mathematics)



https://en.wikipedia.org/wiki/File:Knot_table.svg

With researchers and scientists making incredible gains in understanding the complexities of DNA and the information it encodes, it is reasonable to imagine a world with fewer diseases and a longer lifespan. There is also hope that medicine will advance to be able to harness the power of our own cells to fight disease. For example, gene therapy is designed to introduce genetic material into cells to compensate for abnormal genes or to produce a therapeutically beneficial protein. Vaccines to contain the Covid19 outbreak used messenger RNA. Each new breakthrough in our understanding of DNA will lead to further advances in the idea of precision medicine where interventions will take into account the patient's unique biology and be individually tailored to each patient, rather than based on the response statistically predicted for all patients. Using genetics and a holistic view of individual genetics, lifestyle and environment, doctors will be able to not only accurately predict prevention strategies, but also suggest more effective treatment options.

Deciphering DNA and RNA has the potential to understand the human machine and intervene in an engineering way to cure genetic diseases that are currently impossible to cure. It is essentially like understanding the computer code that governs our existence and intervening to correct any errors. For the moment it is beyond our possibilities to think of improving it but this hypothesis is not excluded a priori.

IF

GENETICALLY ENGINEERED PEOPLE



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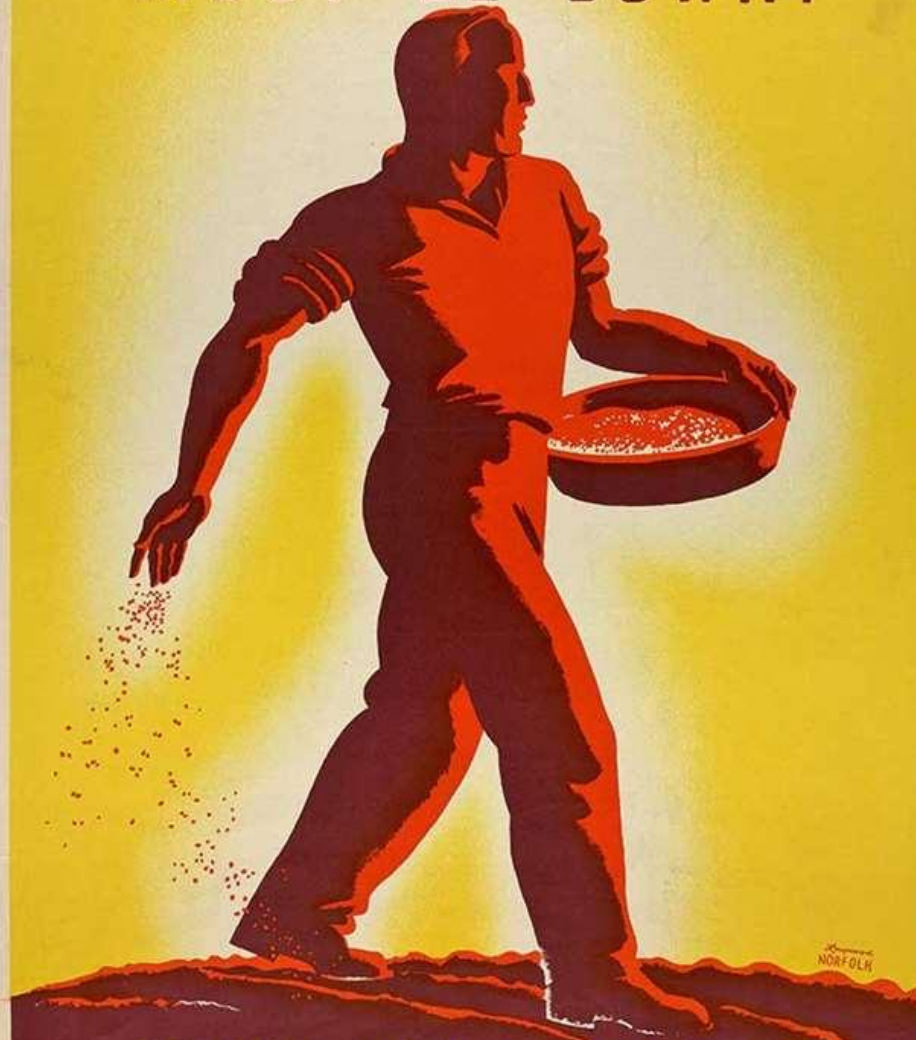


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Of course, these possibilities offered by technology raise a series of ethical problems because Humanity could, in a not too distant future, realize the crazy dream of Doctor Frankenstein by interfering with life. Will our great-grandchildren all be beautiful, very intelligent, tall, long-lived and, why not, blond? Is it right to interfere and play with the genetic dynamics that produced, after billions of years of evolution, the human race?

These are not easy problems to solve. If, on the one hand, it is very humane to intervene to prevent an unborn child from suffering from serious physical problems, what is, however, the ethical limit to be set? Is it legitimate to ask that the unborn child be beautiful and intelligent as well as healthy? What is the difference with eugenics if not that, with genomics, we intervene before birth and not after as with eugenics? But, on the other hand, how can we allow human beings to be born who suffer from diseases that could be cured by simply modifying their genome, perhaps by selecting the right egg and sperm? How far can we go? We are faced, once again, with the ethical neutrality of science. Science and technology are providing us with increasingly sophisticated tools. It is up to us to use them well or badly. It is not easy to make the right choice but it is a choice that we must start making now because the technological future has already arrived.

**ONLY *HEALTHY* SEED
MUST BE SOWN!**



**CHECK THE SEEDS OF
HEREDITARY DISEASE AND
UNFITNESS BY EUGENICS**

ISSUED BY THE EUGENICS SOCIETY, 69, ECCLESTON SQUARE, LONDON, SW1



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In the future? AI and Quantum?

The future is by its nature unknown so we can only make predictions. The scientific disciplines that have the greatest potential to impact medicine are AI and quantum technology.

Quantum Physics:

Some of the concepts that quantum physics introduces are much more difficult to accept because they conflict with beliefs that seemed more like indisputable certainties than mere scientific hypotheses. In fact, the following sentence has been attributed to the great physicist Richard Feynmann (1918-1988), which I believe could have been substantially shared until the middle of the last century: I think I can safely say that nobody understands quantum mechanics. When physicists began to understand the atomic structure and to imagine the atom as a small solar system with the nucleus, made of protons and neutrons, representing the sun and the electrons representing the planets that revolved around it (this model was proposed by Niels Bohr (they began to understand that nature was more complicated than they expected.

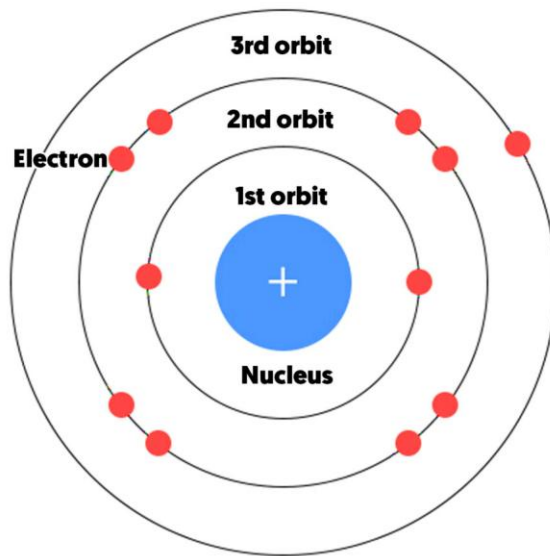


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BOHR'S ATOMIC MODEL



Niels Bohr proposed the **Bohr Model** of the Atom in 1915. The **Bohr Model** states the negatively charged electrons orbit a small, positively charged nucleus.

Main **characteristics of the Bohr's Atomic Model:**

- Electrons orbit the nucleus in orbits that have a set size and energy.
- The energy of the orbit is related to its size. The lowest energy is found in the smallest orbit.
- Radiation is absorbed or emitted when an electron moves from one orbit to another.

Furthermore, as the investigation progressed, new and unexpected phenomena appeared, such as the quantum nature of the universe. In fact:

- The quantum structure of energy was discovered by Max Karl Ernst Ludwig Planck (1858-1947): energy is structured as discrete packets that he called energy quanta.

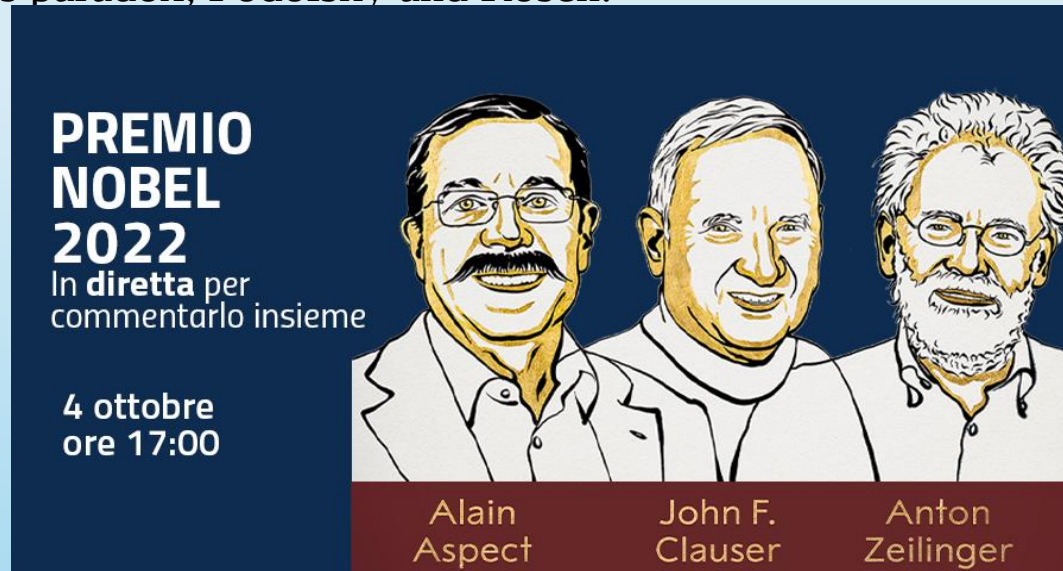
This point, although revolutionary, was not the stumbling block. It was the subsequent discoveries that were absolutely shocking: intuitively, the universe in which the laws of relativity and electromagnetism apply should be the same as the one that is divided into subatomic particles, but the physics of the infinitely small seems to be very different not only from that of relativity but also shows us a world that is absolutely different from the one we are used to living in. First of all, it is not deterministic but is intrinsically based on probability. Einstein himself did not accept this hypothesis at first and exclaimed: "God does not play dice in the universe!". In reality, the rules that govern the atomic world are much further from what we thought were immutable certainties. For example, the phenomenon of entanglement (hypothesized by Einstein, Podolsky and Rosen) says that there are events that determine instantaneous changes throughout the universe while relativity states that no information can be transmitted faster than the speed of light.

Finally, the very structure of the infinitely small makes us ask (or, to be more precise, doubt) what reality is. We summarize the main findings:

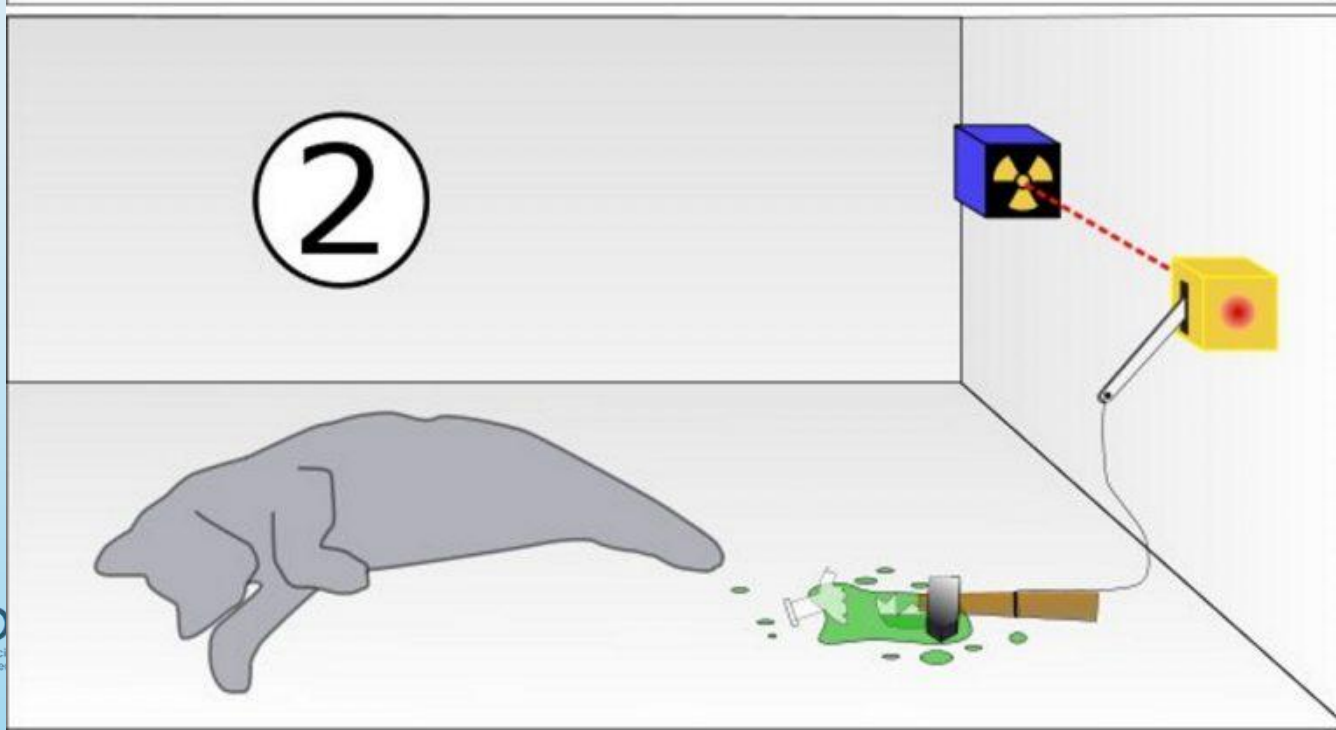
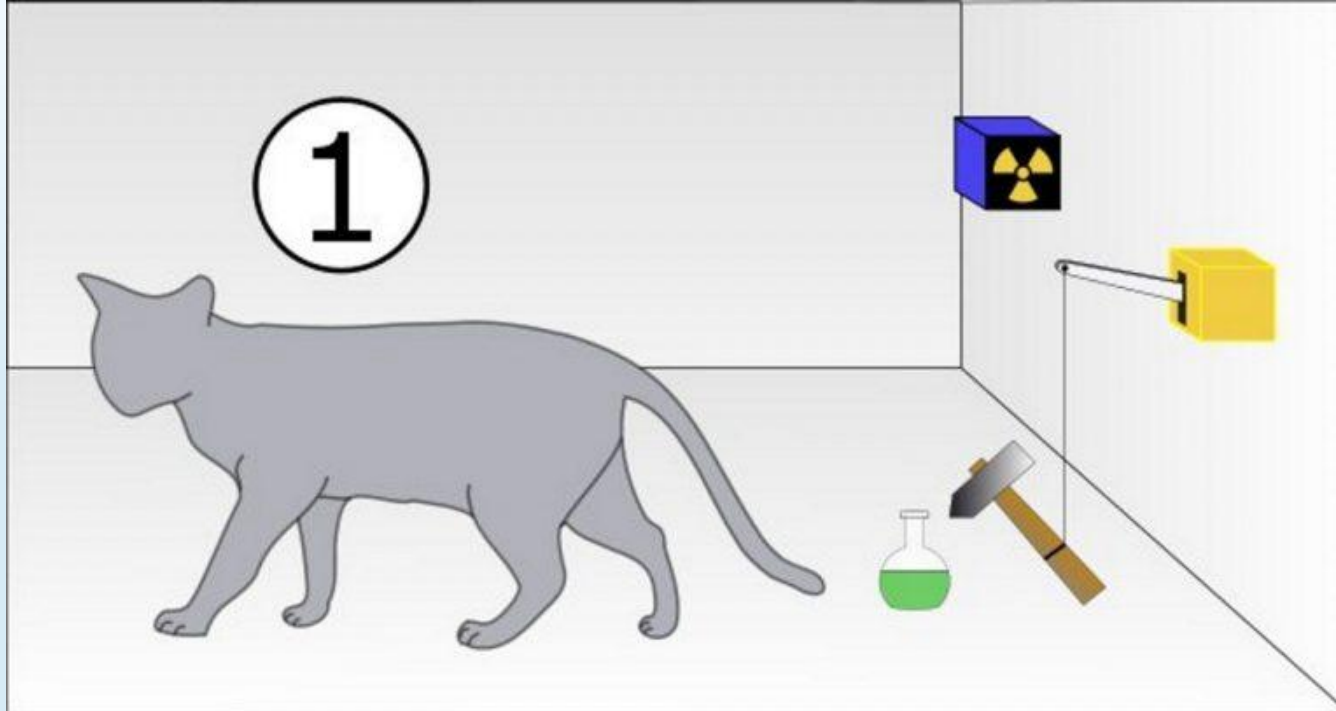
- Wave-particle dualism is characteristic of all matter at the atomic level: it was hypothesized by Born and Louis De Broglie.
- The uncertainty principle was introduced by Werner Karl Heisenberg: he says that it is not possible to measure the speed, for example, or the momentum of an electron without altering the position.

This fact is much deeper than what one might imagine at the beginning: it is not that we do not yet know how to measure these quantities but that, in the future, with better instruments and a better approach, we will be able to do so. No, we will never be able to do it because it is precisely the physics of the infinitely small that is intrinsically structured on this uncertainty. Heisenberg's uncertainty principle led to unexpected things: it was not possible to know the position and velocity of a particle at every instant, but only the probability that an electron was in a certain area. When Bohr and Heisenberg extended the probabilistic interpretation of the Born wave function, they considered meaningless questions about the values of the quantities of a physical system before it was measured, since the measurement process randomly extracted one of the values allowed by the wave function describing the quantum state of the system.

This view of quantum physics is called the “Copenhagen Interpretation”. But then what was reality if it materialized, at the atomic level, only when subjected to measurement? The answer given by Heisenberg to this question is very emblematic: "modern physics has decidedly decided in favor of Plato. In fact, the smallest units of matter are not physical objects in the ordinary sense, they are forms, ideas that can be expressed in a unique only in mathematical language". **In other words, reality does not exist (which only manifests itself when an experiment is carried out) but only the mathematical function that describes it exists.** This theory was demonstrated by Alain Aspect, John F. Clauser and Anton Zeilinger who won the Nobel Prize for Physics in 2022 for this. In a context like this, clearly, thought experiments were absolutely necessary. The two most famous are Schrödinger's cat and Einstein's paradox, Podolsky and Rosen.



We describe Schrödinger's gedankenexperiment using his words «You can also construct completely burlesque cases. A cat is locked in a steel box together with the following infernal machine (which must be protected from the possibility of being grabbed directly by the cat): in a Geiger counter there is a tiny portion of radioactive substance, so little that in the course of a 'now perhaps one of its atoms will disintegrate, but also, equally probably, none; if the event occurs the counter signals it and activates a relay of a hammer which breaks a vial with cyanide. After leaving this entire system undisturbed for an hour, one would say that the cat is still alive if in the meantime no atoms had disintegrated, whereas the first atomic disintegration would have poisoned it. The wave function of the entire system leads to the affirmation that in it the live cat and the dead cat are not pure states, but mixed with equal weight.» The paradox arises from the fact that in quantum mechanics a probabilistic representation is used: to show the fact that a particle can be placed in different positions, it is described as if it were simultaneously in all possible positions. And, by placing the cat in a closed box, it too ended up being in a "superposition of states" and therefore both alive and dead at the same time. Note that this paradox is still discussed and a source of new research today. According to some modern theories, this "macro" version of the superposition principle should not be considered valid: de coherence (in non-physical words, the choice of a specific state) for macro systems occurs immediately and is independent of the fact that there is a measurement that collapses the system into one of the possible states.



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The Einstein, Podolsky and Rosen paradox was proposed in the 1935 article "Can the quantum description of physical reality be considered complete?". Into this alleged paradox the three authors introduced what, however, will turn out to be an important characteristic of quantum systems, entanglement. According to quantum mechanics it is possible to create a set consisting of two particles linked together. This means that the measurement of one particle instantly influences the corresponding value of the other. This remains true even if the two particles are spaced apart, without any spatial limit. Therefore the laws that regulate the Universe are not local: the correlation that binds the two particles is transmitted from one to the other instantly, making the quantum theory structurally non-local and not fully responsive to the cause-effect principle. The current theory, however, also tells us that entanglement cannot be exploited to transmit information instantly and therefore the principle of relativity which says that the maximum speed is that of light is not violated.



AI:

Turing is considered the father of artificial intelligence. This is because he began a new era both by laying the foundations for the construction of electronic calculators and by naively asking questions relating to thinking machines that made human beings reflect on concepts mistakenly taken for granted. In this way he generated a new form of mathematics, computer science, which has the same logical rigor as mathematics, but uses different formal processes to better adapt to the reality of automatic calculation. Turing asked himself the question in 1950: «Can machines think?» in his 1950 article Computing machinery and intelligence.

Turing's genius consisted in giving, in his famous article, a definition of an intelligent machine, very operational and which made no reference either to the concept of intelligence or to the definition of machine. The test conceived by Turing was a variation of the "imitation game". In the original version of the game there are three participants: a man A, a woman B and an examiner C. Examiner C is in a room separate from the other participants. The aim of the game for the examiner is to determine which of the other two participants is the man and which is the woman. Turing imagined replacing A with a machine. So C had to identify who the machine was and who the human being was. Turing asked himself the question: "Will the questioner give an incorrect answer as often as when the game is played between a man and a woman?". This last question, therefore, replaced the original question: "Can machines think?".

TURING TEST



COMPUTER

Player A



HUMAN RESPONDER

Player B



INTERROGATOR / QUESTIONER

Player C



-  Answers to Question
-  Question to Respondents



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The first person who attempted to create a machine that could cope with the Turing test was Joseph Weizenbaum (1923-2008) who created the ELIZA program. This program, without claiming to understand language, was able to converse on limited topics. ELIZA played the role of "psychotherapist" and managed to deceive several people, making those who were conversing with this chatbot believe that they were in the presence of a real doctor capable of treating psychopathological disorders, so much so that some even felt relief after the sessions . In reality this program was far from satisfying the Turing test: simple programming "tricks" had in fact been used. The way the program worked was this: ELIZA looked for some key word in the patient's statement, at which point, if it found it, it elaborated a sentence according to some rule associated with that word; otherwise it produced an acontextual observation. ELIZA was a huge success, so much so that it amazed Weizenbaum himself. The psychiatrist Kenneth Colby (1920-2001), who argued that within a few years programs like ELIZA could be used in therapeutic practice, also created a similar program, PARRY which simulated the linguistic behavior of a paranoiac and this program also managed to deceive several psychiatrists. Subsequently, a psychiatric session was also organized between PARRY and ELIZA.

Network Working Group
Request for Comments: 439
NIC: 13771

V. Cerf
SU-ERL
21 January 1973

PARRY Encounters the DOCTOR

The session recorded below actually happened on 18 September 1972 and is herewith reproduced for your entertainment.

Good Evening.

Tell me your problems. Please terminate input with a period or a question mark.

*People get on my nerves sometimes.

I am not sure I understand you fully.

*You should pay more attention.

Suppose you should pay more attention.

*You're entitled to your own opinion.



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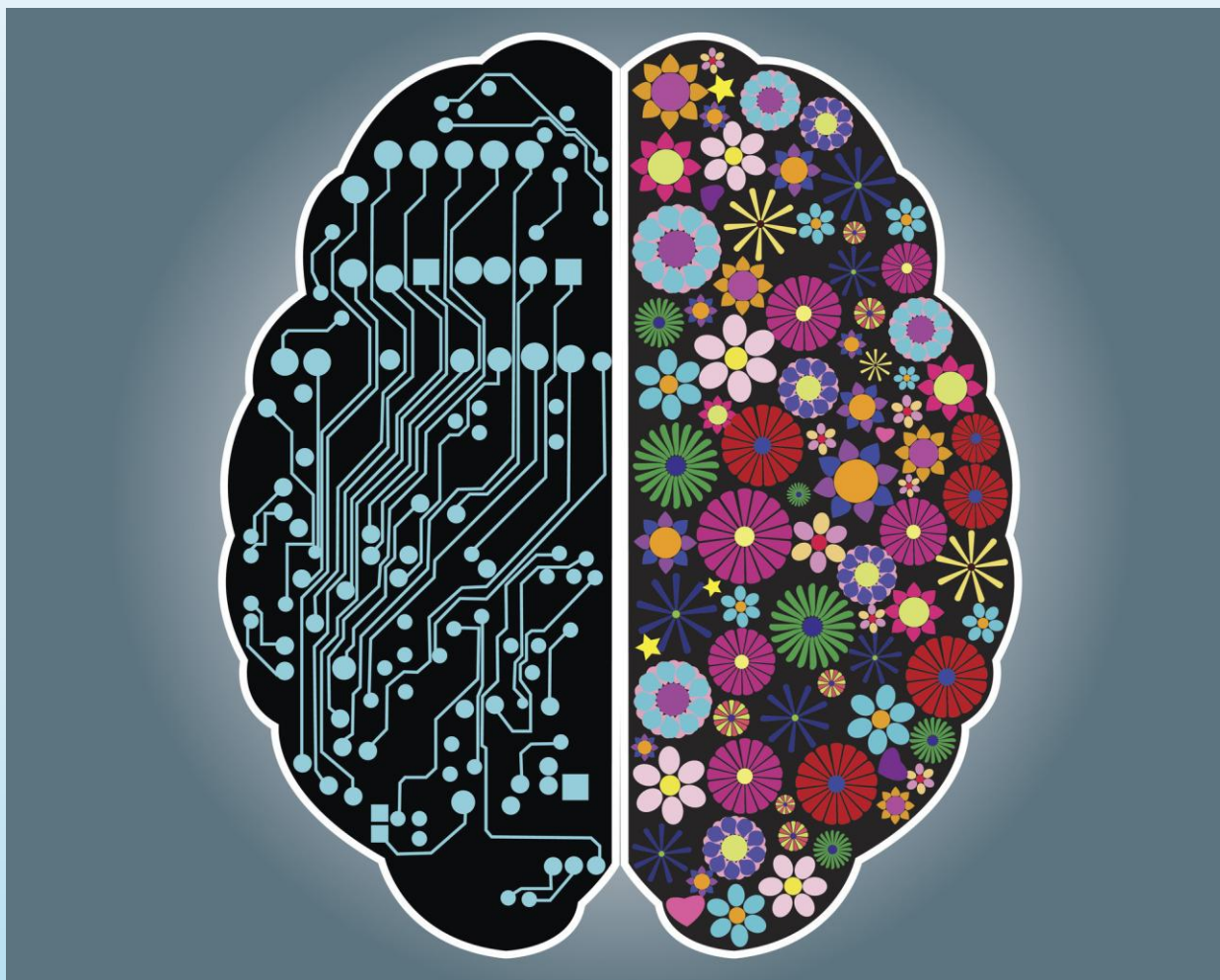
Currently, modern chatbots can easily pass the Turing test. But we don't consider them intelligent. Turing was right in considering the ability to speak to be intelligence. But it is a type of intelligence that, roughly speaking, is confined to the left hemisphere of the brain together with the ability to calculate and program. The most creative part is confined to the right hemisphere. According to Fagin, the current development of the AI will lead to C-3PO type droids. Capable of speaking six million languages but not much more.



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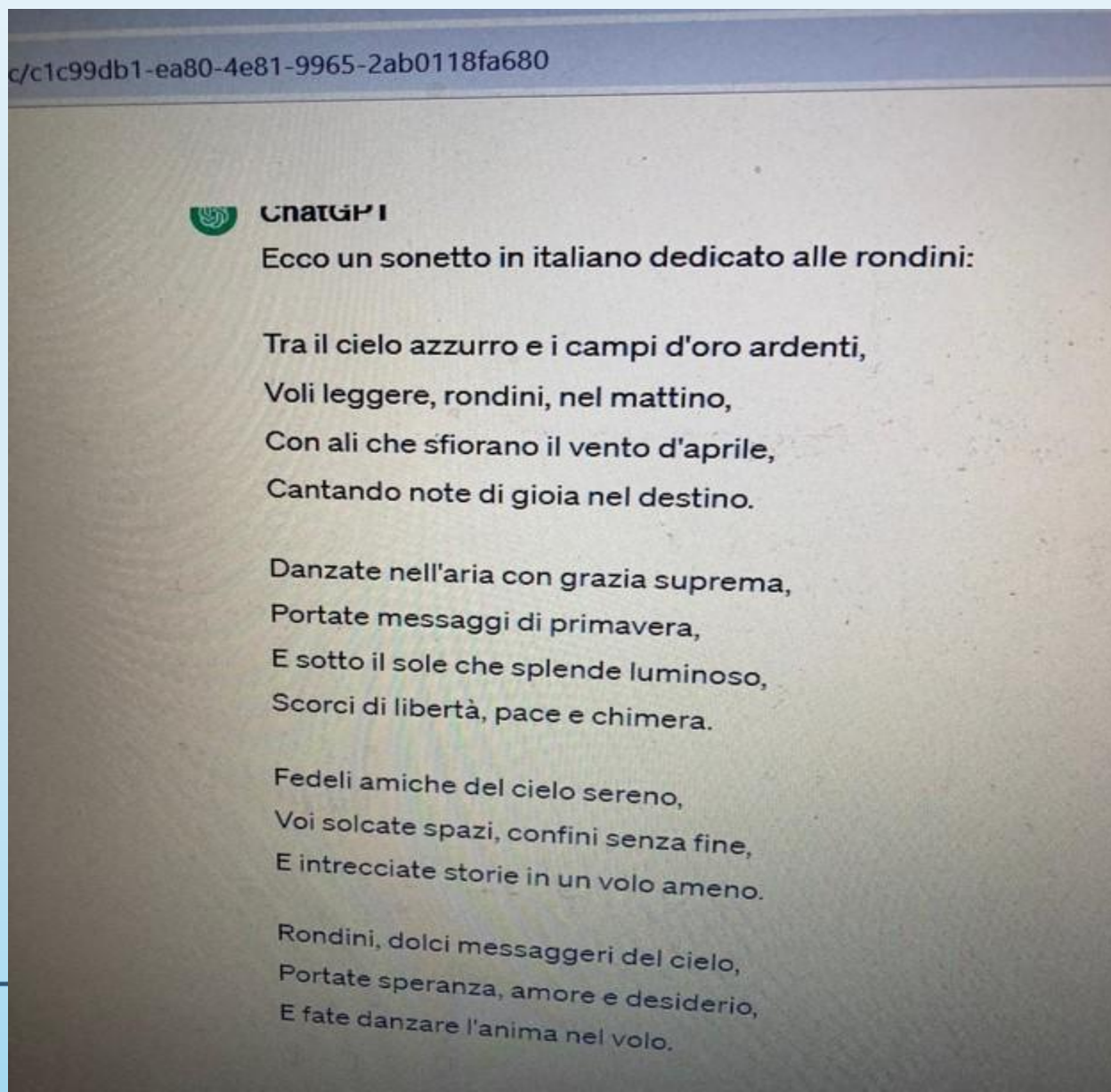
A possibility to replicate the functions of the right hemisphere is quantum technology.

The quantum mind or quantum consciousness is a group of hypotheses proposing that local physical laws and interactions from classical mechanics or connections between neurons alone cannot explain consciousness, positing instead that quantum-mechanical phenomena, such as entanglement and superposition that cause nonlocalized quantum effects, interacting in smaller features of the brain than cells, may play an important part in the brain's function and could explain critical aspects of consciousness. These scientific hypotheses are as yet unvalidated, and they can overlap with quantum mysticism.

The most successful theory is due to the theoretical physicist Roger Penrose and to the anaesthesiologist Stuart Hameroff collaborated to produce the theory known as "orchestrated objective reduction" (Orch-OR). Penrose and Hameroff initially developed their ideas separately and later collaborated to produce Orch-OR in the early 1990s. They reviewed and updated their theory in 2013.

The theory is not entirely convincing, but it manages to explain why the brain is so efficient in terms of energy consumption and why there are intuitions, which are real leaps in knowledge.

Meanwhile AI is moving forward. For example, AI would have won the silver medal in the mathematics olympics and can write more or less acceptable poetry.



In short, building intelligent droids, with a positronic brain like Asimov and increasingly similar to humans, is not only a question of mechanics and electronics, but also of psychology. Unlike humans and some animals, the machines created to date are not capable of having a perception of themselves: they do not know what shape they have, they cannot imagine themselves in the future or place themselves within a hypothetical scenario. The only way they can learn is to use models, simulations and sets of rules (the software) provided by humans, and spend a lot of time in repetitive and laborious cycles of trial and error. Robots are not currently capable of implementing autonomous learning processes that lead them, over time, to develop new skills. The digital revolution that began eighty years ago has not only had the technological repercussions that are before our eyes (smartphones, social networks, internet, virtual reality, e-commerce, cryptocurrencies, self-driving cars, robots, metaverse etc) but it had repercussions on the scientific method (putting it in front of a potential crisis) and on mathematics (processing languages follow rational logics but which are somehow different from mathematics). The tumultuous development of the digital world is making us reflect on concepts that we mistakenly took for granted such as intelligence and self-awareness and has also changed the paradigms of the economy: digital goods follow Moore's law (1929-) and therefore double their performance every 18 months and have exponential and non-linear growth unlike physical goods which grow linearly

For example, philosopher Nick Bostrom (1973-) in a 2003 article postulated the “Simulation Hypothesis” in which the world we live in was supposed to be just a very detailed computer simulation. Elon Musk (1971-) took up this idea by arguing it on the fact that on November 29, 1972 Atari had released Pong, the first video game to have a real commercial success: “50 years later, games are photorealistic 3D worlds. What does this trend imply for our reality?”. If Humanity survived for the next thousand years and Moore's empirical law remained valid, we would have more powerful computers than we have today. With that incredible computing power, computers of the future would allow future generations to recreate simulations of their ancestors and it would be impossible to distinguish physical reality from virtual reality. We could all be inside a simulated reality as represented in the film The Matrix without realizing it and, above all, without, however, the red pill that Morpheus offers in the film to Neo, the protagonist of the film. A statement which, among other things, cannot be logically contested in any way, because it is assumed that the two worlds (the real one and the digital one) are indistinguishable from each other. But is it true that we are faced with magnificent (informatics and mathematics) and progressive fortunes? Is it credible to hypothesize a thousand years of continuous progress? No one can answer this question, but the impression is that since Turing started talking about AI, just 80 years have passed in which progress has not only been continuous but also increasingly accelerated.



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