Computational Matter Physics of Life

Yehan Hathurusinghe

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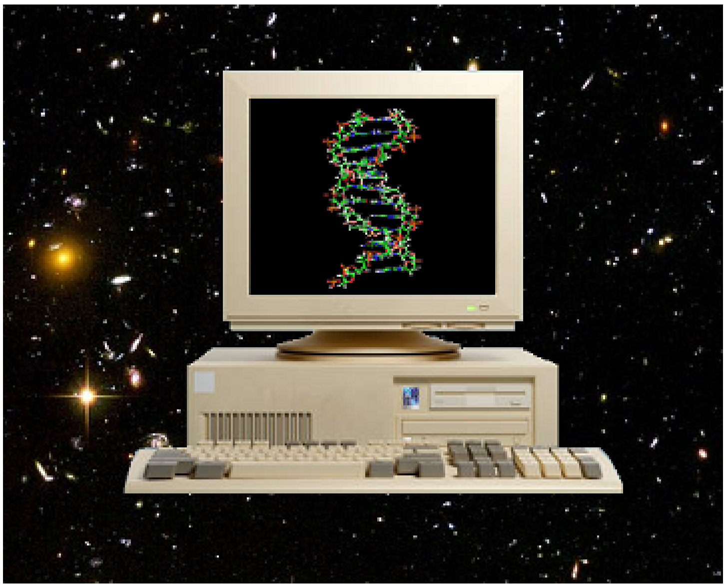

Abstract

The complexity of life, has long puzzled scientists and philosophers alike. This complexity has led some to question whether current scientific frameworks are inadequate for explaining life, suggesting that new concepts or theories might be necessary. Additionally, there has been speculation about whether life could fall into the realm of undecidability or uncomputability, similar to the Halting Problem in Turing Machines. However, this paper argues that life may not be as elusive as it appears. Instead, insights into the nature of life can be traced back to the work of John Von Neumann and his colleagues, such as Arthur Burks, who laid foundational ideas that can help demystify the complexities of living systems. The key lies in considering matter as having computational properties, leading to the emergence of a new genre of physics—*Computational Matter Physics*—which seeks to bridge computer science with traditional physics to better understand the computational nature of matter and its underlying principles that lead to complex phenomenon as life.

Contents

1 About the Author and his Work:

By 2020, Yehan found himself at a crossroads, uncertain of his next steps in life, though deeply focused on non-linear physics, complex systems, and non-equilibrium statistical mechanics. That year brought unprecedented global disruption as the world faced the COVID-19 pandemic, with alarming scenes of people collapsing unexpectedly. The fragility of life, so starkly apparent, ignited a deeper curiosity in Yehan—specifically about the Origin of Life, a subject likely already simmering in the background of his scientific pursuits.

Fortuitously, he encountered Professor Anton Zilman at the University of Toronto, who provided crucial guidance and support. Through a biophysics course, Yehan was assigned a final project, and he chose to deliver a 15-minute presentation on the Bacterial Flagellar Motor. That brief presentation spiraled into a three-year journey, during which he relentlessly explored the mystery of life's origins, voraciously consuming any material he could find on the subject.

At first, Yehan approached the problem naively, imagining molecules forming life through simple drawings and visual models. But soon, a profound realization struck him: life resembled a computational system far more than it did a complex mineral. From that point, his focus shifted to the computational theory of life, culminating in what he now calls "Computational Matter Physics." After three years of work, Yehan formulated postulates that frame this theory, and here, in this work, he presents his insights in the same chronological order in which they evolved.

Some may find the absence of a grand, defining equation disappointing, but Yehan emphasizes that this is not due to any deficiency in mathematical ability. Rather, it reflects the inherently conceptual nature of the problem at hand. In fact, Yehan's research required rigorous engagement with equations from non-equilibrium statistical mechanics and open quantum systems, which allowed him to approach these topics with a level of confidence necessary for addressing the deeper, conceptual challenges. Yehan believes he has developed a compelling explanation for the origin and nature of life, a fundamental physics problem that he contends is at the root of much of the scientific and conceptual confusion in the world today. Yehan avoids excessive rigor and formality, considering them unnecessary and time-consuming. He believes what he has presented is sufficient to convey his ideas clearly, without overwhelming the reader with complex symbols or convoluted definitions. Yehan has provided a comprehensive section on the reference material, ensuring that all relevant sources and works consulted during his research are properly documented for further reading and verification. Yehan has made use of ChatGPT to refine and enhance the clarity of his writing.

Yehan extends his gratitude to his teachers and friends, especially Professor Zilman and Mr. Prikolab, for their invaluable support and encouragement. He dedicates this work to the memory of his father and Professor Zilman, who sadly did not live to see its completion, and expresses deep appreciation to his mother for her unwavering support throughout the three years of research. He also recalls a childhood gift from a girl, a Meccano set, the parts have got missing in time. The work on the computational theory of life, in many ways, reminded him of that cherished Meccano set. Yehan would like to invite the respected audience to **assist in the peer review and publication of his work**, as he seeks valuable feedback and support for its advancement.

2 The Puzzle of Life

2.1 Life: Beyond Ordinary Matter

Among the mineral forms, life appears strikingly alien. The contrast is stark: between the inert simplicity of rocks and the extraordinary complexity of even the simplest life forms, such as bacteria, lies an immense chasm. Life, with its intricate cellular machinery and dynamic processes, seems profoundly more complex than the most elaborate minerals. This raises intriguing questions about the origins of life. Why has life evolved to be so vastly different from inanimate matter? Could it be that life originated from another world, existing in a universe of its own? Perhaps life was introduced by a superior agent, deliberately placed within the natural world? Could life have emerged from simple molecules?

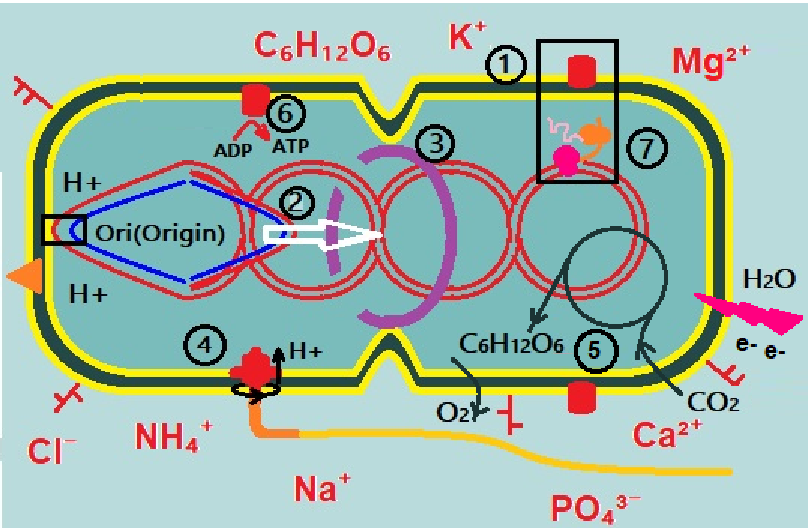

Figure 1: The intricate nature of the gram-negative bacterium is highlighted by its several complex systems: (1) The cell envelope, consisting of two membranes composed of proteins, lipids, sugars, and peptides, maintains the bacterium's shape and includes an intermediate space rich in positive ions. Membrane proteins function as pumps and sensors, regulating nutrient intake and cellular signals. (2) DNA replication is complex, with the new chromosome actively transported across the cell via protein interactions and a chemical gradient. (3) The Z-ring forms in coordination with DNA replication, constricting to divide the cell into daughter cells. (4) The flagellar motor, powered by the proton motive force, resembles a man-made electric motor, rotating the flagellum to enable bacterial motility. Its assembly is also complex. (5) Metabolism efficiently converts CO_2 and essential minerals into the cellular components required for growth, a remarkable phenomenon. (6) ATP synthase generates ATP from ADP using the proton motive force, providing the cell with its primary energy currency. (7) The translation and transcription processes, guided by codons that correspond to specific amino acids, ensure protein synthesis. Interestingly, in daughter cells, DNA in chromosomes, often align spatially identically to their parent, with respect to membrane proteins.

Panspermia is the hypothesis that life exists throughout the Universe and can be distributed by interstellar bodies such as meteoroids, comets, or dust, potentially seeding life on planets like Earth. The Greek philosopher Anaxagoras, who lived in the 5th century BCE, is considered the father of Panspermia. He believed that the Universe contained seeds of life, and that life on Earth began from the descent of these extraterrestrial seeds. Today, panspermia continues to intrigue as a theory suggesting that life might have been transported to Earth from extraterrestrial sources. Despite its appeal, panspermia does not fully address the ultimate origins of life, whether on Earth or elsewhere in the universe. Panspermia theories such as Thomas Gold's, which proposed that life on Earth originated from extraterrestrial waste left by aliens, provide amusing possibilities but fail to address the core mystery of life's origins.

Vitalism, is the belief that living organisms are fundamentally different from non-living entities due to the presence of a non-material force or principle, often referred to as the "vital spark" or "élan vital".

Early biologists, exploring embryonic development, were often perplexed by their observations. Caspar Friedrich Wolff, known as the father of epigenesis, introduced the concept of vis essentialis in his work Theoria Generationis, proposing an organizing force behind embryonic development. Wolff detailed plant development, illustrating how leaves differentiate from blossoms, and also studied the development of animal embryos. He proposed the existence of a "vis essentialis corporis," or essential formative force, which he believed, created order necessary for life.

Vitalism is no longer widely accepted by the scientific community, which now holds that life operates according to the same physical and chemical principles as non-living matter. However, many scientists quietly acknowledge that there are still aspects of life's complexity that remain elusive and not fully understood. While life may not be seen as extraordinary in a supernatural sense, the intricate processes that sustain it continue to puzzle researchers.

It must have been a relief when complexity of life was reduced to a single cell, simplifying the vast complexity of living organisms into a more manageable unit. This breakthrough came with the development of cell theory in 1838-1839, pioneered by Matthias Schleiden and Theodor Schwann. According to this theory, cells were identified as the fundamental building blocks of all living organisms, providing a unified framework for understanding biological processes. However, the complexity was not reduced but rather shifted to the intricate mechanisms within the cell itself. The true complexity of cellular structures remained elusive until the advent of electron microscopes in the 1930s. Emerging around 1931, these advanced microscopes allowed scientists to view internal components of cells and microbes with unprecedented clarity. This technological leap revealed a stunningly intricate system of molecular machines within cells. For instance, the flagellar motor, a microscopic rotary structure, operates similarly to a man-made electric motor, while kinesin proteins facilitate cellular transport with a walking mechanism akin to a tiny robotic motor. The sophisticated chemistry of enzymes like chymotrypsin further showcased the highly organized and intricate processes that sustain life. These discoveries challenged scientists to rethink their understanding of biology, unveiling the mechanical and complex nature of life at the molecular level.

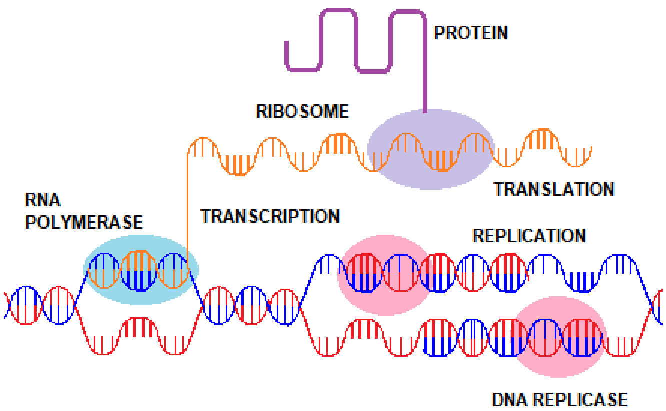

Figure 2: Diagram illustrating the processes of Transcription, Translation, and DNA Replication in a cell. During Transcription, the enzyme RNA polymerase unwinds the DNA double helix and synthesizes a complementary mRNA strand from the DNA template. Translation occurs when ribosomes, which are molecular machines, read the mRNA sequence and facilitate the assembly of amino acids into proteins with the help of transfer RNA (tRNA). DNA Replication involves the enzyme helicase unwinding the DNA double helix, followed by DNA polymerase synthesizing new complementary strands to produce two identical DNA molecules.

Even the simplest cells, like bacteria, are remarkably complex. Despite their simplicity compared to multicellular organisms, bacteria have intricate structures and functions that make them highly sophisticated. There is nothing found between life and minerals—these are distinctly separate categories. This stark difference between living organisms and non-living matter continues to challenge and intrigue scientists, highlighting the profound complexity of even the most basic forms of life.

Life is sustained by nano machines that enable cells to harness energy and nutrients from sources like sunlight, minerals, and turn CO_2 into essential building blocks—sugars, fatty acids, amino acids, and nucleic acids. These molecules, in turn, form the structural components of cells or contribute to the creation of new nano machines. These machines can also propel the cell toward energy and nutrient sources, maintaining its survival.

These nano machines are made of proteins and RNA, while DNA stores the necessary information for creating and regulating them in the form of a nucleotide base sequence. Within all cells, the processes of transcription and translation constitute the genetic machinery responsible for producing the nano machines that, in turn, form the structural components and carry out the functions of the cell. DNA replication, on the other hand, ensures that this genetic information is accurately copied and passed on during cell division, preserving the instructions for life.

2.2 Life: From No Extraordinary Matter

Despite the immense complexity of life, which often seems so alien compared to everything else in the natural world, philosophers and scientists since ancient times have embraced it as an intellectual challenge to be understood. The ancients must have also noticed the stark difference between inanimate minerals and the complexity of living organisms, prompting deep reflection on the nature of life. Records from ancient Greece illuminate how early philosophers grappled with the origins of life.

Thales of Miletus, widely regarded as the first Greek philosopher, rejected traditional mythological explanations of the world, and attempted to find rational reasons. His proposal for the origin of life was that it had formed out of water. His reasoning stemmed from the observation that all living organisms rely on water, and he believed that its apparent ability to move autonomously suggested it contained the principle of motion, which could give rise to motion in life itself. Although, the argument is incorrect by today's knowledge of physics, this had marked a significant shift toward naturalistic explanations, laying the foundation for scientific inquiry into the nature of the cosmos.

Building on Thales' observations, Anaximander, a Greek philosopher of the 6th century BCE, sought to provide a more detailed account of the development of life. Anaximander is credited with proposing one of the earliest evolutionary theories. He suggested that the fundamental principle of the universe, or archê, was not a specific element like water, as Thales had claimed, but the apeiron, meaning the "boundless" or "infinite." This eternal, indeterminate substance was the source from which all things emerged and into which they would eventually return. Anaximander theorized that from the combination of heated water and earth, fish or fish-like creatures were formed. Within these creatures, human beings developed as embryos, remaining enclosed until reaching maturity. Only after these animals split open were men and women released, fully formed and capable of sustaining themselves. Anaximenes, a student of Anaximander, further expanded on these ideas by proposing that the seeds of life existed in the air.

Spontaneous generation is the historical concept that living organisms can arise from non-living matter without any biological intervention. This theory was widely accepted until the 17th century and suggested that life could spontaneously emerge from inanimate objects or decaying organic material. For example, it was believed that maggots could develop from rotting meat or that mice could arise from piles of straw. This idea stemmed from observations of the natural world, where people noticed the sudden appearance of life in various environments, leading to the conclusion that such occurrences were due to spontaneous processes. However, experiments by scientists like Francesco Redi and Louis Pasteur disproved spontaneous generation, demonstrating that life comes from pre-existing life.

In contrast, abiogenesis refers to the natural process by which life arises from non-living chemical compounds, positing a gradual transition from simple organic molecules to complex life forms over time. This concept is supported by modern scientific research, which explores the conditions under which life could have originated on Earth. Abiogenesis is the scientific hypothesis that life originated naturally from non-living matter through a series of chemical processes. It posits that life emerged from simple organic compounds in prebiotic conditions without the involvement of living organisms.

The 1952 Miller-Urey experiment, conducted by Stanley Miller and Harold Urey, was a groundbreaking study in the field of abiogenesis. Aimed at simulating early Earth conditions, the experiment used a mixture of gases thought to be present in the primordial atmosphere—methane, ammonia, hydrogen, and water vapor—and subjected it to electrical sparks to mimic lightning. The results were striking: the experiment produced several organic compounds, including amino acids, which are fundamental building blocks of life. This experiment provided compelling evidence that organic molecules necessary for life could form under prebiotic conditions, supporting the hypothesis that life could have originated from simple chemical processes on early Earth. Those who underestimate the results of the Urey-Miller experiment may not fully grasp its significance. The production of such an essential building block of life from a simple prebiotic experiment stands as one of the most significant scientific findings in the history of human civilization, despite its simplicity.

The Murchison meteorite, which fell in Murchison, Victoria, Australia, in 1969, initially garnered significant scientific interest when it was confirmed to contain organic compounds. Subsequent analyses have revealed that this extraterrestrial rock harbors a diverse array of complex prebiotic molecules, including amino acids and nucleobases, crucial for life's building blocks. Remarkably, the meteorite also contains amphiphilic molecules that can form membranous vesicles when exposed to dilute aqueous solutions, providing insight into potential early prebiotic processes. However, despite these intriguing findings, nucleotides—the fundamental components of RNA and DNA—have not been detected in the Murchison meteorite.

Organic molecules and minerals, fundamental to life, are widespread throughout the solar system and beyond. In the solar system, metallic compositions are typically found closer to the Sun, while organic materials are more common in the colder, outer regions. Venus, for instance, is rich in iron and sulfur with some trace phosphates, but lacks significant organic molecules and experiences extreme temperatures exceeding 450°C. Mars, on the other hand, contains phosphates, suggesting some potential for prebiotic chemistry. Titan, Saturn's largest moon, harbors an organic-rich environment at -179°C, with water present in the form of hard rock, methane clouds, and lakes of methane. The solar system exhibits a spectrum of organic compositions, with metallic worlds closer to the Sun and organic-rich environments farther out. Earth appears to fit between these extremes, balancing the characteristics of both metallic and organic worlds. Earth, uniquely positioned with its magnetic field shielding it from harmful radiation and its gravity retaining essential gases, occupies a favorable zone that supports and sustains life.

Since the original Miller-Urey experiment in 1952, a series of experiments have explored variations in prebiotic conditions to better understand the origins of life. One significant early development involved using hydrogen sulfide , which led to the production of amino acids containing sulfur. Although these experiments produced some amino acids, they did not account for all essential types, and some amino acids generated were not found in living organisms. Additionally, researchers lacked a clear understanding of which prebiotic molecules were crucial for life's origin. The formation of nucleosides remained particularly elusive. In 2015, a breakthrough came when researchers irradiated formamide ice at extremely low temperatures with proton radiation in the presence of meteoritic powder [Life and its Complexity, 3]. This approach yielded a wide variety of essential life-building blocks, including nucleosides and sugars, which had been challenging to produce in earlier experiments. More recently, in 2023, another team modified the Miller-Urey experiment by incorporating mineral-rich water with calcium phosphate and magnesium sulfate and running the experiment over several weeks. They successfully synthesized a broad range of life's building blocks, including nucleosides and nucleotides, with a notable production of ATP [Additional Topics, 51].

The extraordinary structure of RNA and DNA, with their neatly fitting double-strand configurations, might initially seem out of place or even alien. However, over the years, scientists have discovered many molecules that exhibit behaviors parallel to those of these canonical nucleic acids. Notably, synthetic nucleic acids (XNA) with modified bases and ribose skeletons have been identified, demonstrating similar structural and functional properties. Additionally, various nucleobase analogs have been found, displaying diverse base-pairing characteristics that expand our understanding of molecular biology and its potential alternatives. There is no reason to suggest that nucleic acids are inherently special; rather, they emerged from a broad pool of prebiotic polymers that were selected due to their exceptional advantages. Their distinctive properties likely provided them with significant evolutionary benefits, leading to their dominance in the molecular machinery of life [Additional Topics, 54] [Prebiotic Chemistry, 31,33,34].

There is no denying the overwhelming evidence supporting abiogenesis, which makes it impossible to approach with a hostile mindset. While life undeniably exhibits extraordinary behavior, it likely originated from the same fundamental elements that constitute ordinary matter. The remarkable difference arises from the unique properties and potential of organo-metallic compounds, which may have contained the necessary potential for the emergence of life.

3 Computers and Life

3.1 Computation Theories of the 20th Century

Modern computers may seem straightforward, with their clear-cut structure of inputs, outputs, a processing unit that performs computations, and primary memory where code and data are stored as files. These programs are loaded into secondary memory when needed to run, and everything is managed by an operating system that coordinates how other programs should execute. This simplicity might lead one to naively assume that computers were always as they are now. However, this perception is far from the truth. The earliest designs for computers were conceived by mathematicians who had both practical and theoretical considerations in mind. Notably, Alan Turing, often regarded as the father of modern computing, proposed a model for a computer, called the Turing Machine in 1936, that is quite different from the commercial systems used today.

A Turing Machine is a theoretical computational model defined by several core components: a finite set of states, including a designated initial state and one or more terminal (or halting) states. The machine operates on an infinite tape divided into discrete cells, each capable of holding a symbol from a finite alphabet. It is equipped with a read-write head that can move left or right along the tape and perform read and write operations on the tape's current cell. The machine's behavior is governed by a transition function, or transition table, which specifies the next state to transition to, the symbol to write on the tape, and the direction in which to move the read-write head based on the current state and the symbol read from the tape. The computation starts with an input tape containing initial symbols and concludes when the machine reaches a terminal state. The final output is the content of the tape, and the state of the machine, at the end of the computation.

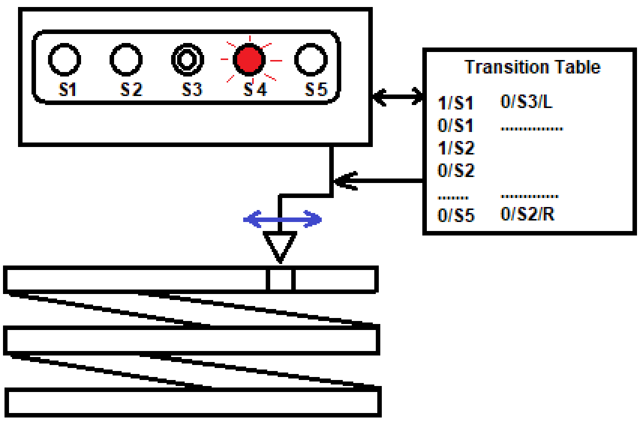

Figure 3: The Turing Machine: Consists of a finite set of states, including an initial and one or more halting states. It operates on an infinite tape divided into cells, each containing a symbol from a finite alphabet. A read-write head moves left or right across the tape, reading and writing symbols based on the machine's transition function. The transition table determines the next state, what symbol to write, and which direction to move the read-write head, all based on the current state and the symbol read from the tape.

As evident from the description, it became apparent that a Turing Machine might not always reach a terminal state, leading to cases where the computation does not terminate. This scenario, where the machine fails to halt on a given input, is associated with the Halting Problem. The Halting Problem seeks to determine whether a Turing Machine will halt or run indefinitely for a particular input. It was theoretically proven that no algorithm can solve the Halting Problem for all possible Turing Machines and inputs, establishing that it is undecidable. This proof highlighted the fundamental limits of computation and algorithmic predictability: that, not all problems can be solved by computations.

Computers are machines designed to perform computations, and the Turing Machine serves as a foundational model for understanding such machines. What is remarkable about the Turing Machine is its ability to abstract away the human element from the process of computation, enabling the study of computation as a purely mathematical and theoretical concept. This abstraction paved the way for the development of the Church-Turing Thesis, which posits that any computation that can be performed by a human using a mechanical process can also be performed by a Turing Machine. This thesis underscores the Turing Machine's significance, as it represents a simple yet comprehensive model of computation capable of executing any function that is computable.

While a particular Turing Machine can be designed to perform a specific function or a narrow range of functions, it is also possible to construct a Universal Turing Machine, which has the capability to simulate any other Turing Machine given its description. The construction of a Universal Turing Machine involves implementing a mechanism to handle and simulate the transition table of any Turing Machine, which is a computable problem. According to the Church-Turing Thesis, since handling transition tables is a computable problem, a Universal Turing Machine must exist capable of performing this task.

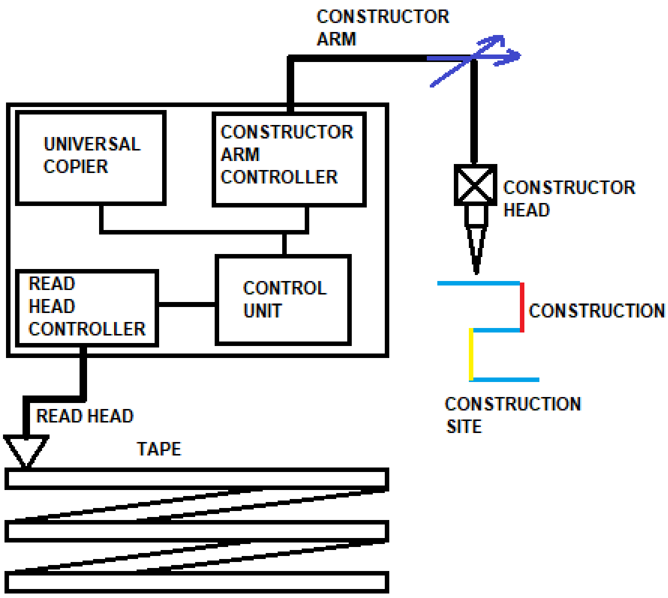

Figure 4: The Von Neumann's Universal Constructor: The Constructor Arm accurately places each building block as directed by the Constructor Arm Controller. The Read Head scans the tape and relays information to the Tape Head, which guides the Read Head's movement along the tape. The Control Unit coordinates the Constructor Arm and Read Head based on the tape's encoded instructions. The tape contains both the detailed description of the machine being built and the instructions for its assembly.

John von Neumann was a pioneering mathematician whose contributions to computational theory extended beyond traditional boundaries, delving into the realms of life and artificial intelligence. One of his notable innovations was the development of Cellular Automata, a computational model that simulates complex phenomena observed in nature through simple, discrete cells operating in a grid. Von Neumann's fascination with life led him to explore the possibility of implementing a complex, self-replicating artificial organism within this framework, known as the Universal Constructor. The Universal Constructor was designed as a theoretical machine capable of constructing other machines based on a given description.

It comprised several key components: a tape containing the machine's description and construction instructions, a reading head for interpreting the tape, a constructor arm for assembling components, a universal copier for replicating the tape, and a control unit for coordinating the entire process. The control unit translated the instructions from the tape into actions for the constructor arm, ensuring precise placement of each building block.

Self-replication was a critical aspect of this model, achieved by providing the Universal Constructor with a tape that encoded information for its own construction process. The universal copier played a crucial role in this mechanism, as it itself required only a finite amount of information to construct, was capable of reconstructing or copying a tape of any arbitrary length.

Two well-known examples of Cellular Automata are Langton's Loops and Conway's Game of Life [Computational Life, 30,32]. Langton's Loops are self-replicating structures that demonstrate how simple local rules can lead to complex behaviors, such as self-replication, which has implications for understanding artificial life and biological processes. Conway's Game of Life, on the other hand, illustrates how basic rules can give rise to a wide range of dynamic patterns, from stable structures to chaotic evolution. What makes the Game of Life particularly remarkable is its universal computational power; it has been proven to simulate a Turing machine, meaning it can, in theory, compute anything that is computable. This makes the Game of Life not only a fascinating example of emergent complexity but also a model of universal computation, demonstrating that even simple systems can perform complex, general-purpose computations. Both examples highlight the potential of Cellular Automata to model real-world phenomena and explore fundamental principles of life and computation.

John Von Neumann created the Von Neumann Cellular Automata model as part of his exploration into self-replicating systems and artificial life. His goal was to implement a Universal Constructor within this framework. This concept was groundbreaking as it sought to demonstrate how complex, self-replicating machines could emerge from simple rules in a discrete, computational space. Unfortunately, Von Neumann passed away in 1957 before fully realizing this vision. His work, however, was completed by Arthur Burks, who compiled and expanded Von Neumann's ideas into a comprehensive form in the book Von Neumann's *Theory of Self-Reproducing Automata*, published in 1969 [Computational Theory, 18]. This work provided the first formal framework for understanding self-replicating machines and laid the foundation for further research in artificial life and cellular automata. Over the years, as computers gained more processing power, researchers and enthusiasts have developed real, working implementations of Von Neumann's Universal Constructor [Computational Life, 31].

3.2 Von Neumann's Universal Constructor

One can't help but notice the striking parallels between the processes of life and Von Neumann's Universal Constructor. Initially, it is the tape, reminiscent of DNA, that draws attention. Upon closer examination, the resemblance becomes undeniable. The ribosome, which constructs proteins, mirrors the function of the constructor arm. The RNA polymerase operates like the read head, and DNA clearly represents the tape. Perhaps most notably, the universal copier aligns with the DNA replication machinery. What makes this connection even more remarkable is that Von Neumann passed away before much of the genetic machinery was uncovered in the 1960s.

Arthur Burks' book offers further insights into the Von Neumann Universal Constructor model by detailing its control unit, which contains a bank of hardwired universal functions. These functions, when combined in specific sequences, enable the universal constructor to perform any complex operation it is designed to execute. Notably, in the context of self-replication, there is a particular sequence of universal functions that, when executed in the prescribed order, results in the creation of an entirely new machine. The instructions for these operations are encoded on the tape as a sequence of symbols, guiding the constructor through the required steps to achieve either the construction of new machines or self-replication.

One can't help but wonder if proteins operate in a manner analogous to the universal functions described in Von Neumann's model. If proteins are indeed composed of universal functions, their sequence of application would be determined by the specific order of amino acids. In this sense, proteins could be viewed as complex functions that interact with their environment.

Von Neumann's Universal Constructor	Biological Life
Machines: Constructs created from basic building blocks. The Universal Constructor facilitates self-replication.	**Proteins and RNA:** Components formed from the building blocks of life, such as amino acids and ribonucleosides, polymerizing into peptides and RNA.
Tape: Contains instructions for constructing machines.	**DNA:** Provides genetic information required for synthesizing proteins, RNA, and other biomolecular nanoscale machines.
Tape Reader: Used to interpret the encoded information on the tape.	**RNA Polymerase:** Enzyme responsible for synthesizing RNA from a DNA template in a process known as transcription.
Universal Copier: Produces a copy of the tape during self-replication. Utilizes finite information from the tape for construction but can replicate the tape regardless of length or content.	**DNA Replicase:** A nanoscale machine composed of proteins that executes DNA replication. It uses a finite portion of the DNA sequence for construction but can replicate the entire DNA molecule, which may consist of millions of bits.
Constructor Arm: Employed to physically assemble machines by positioning building blocks.	**Ribosome:** Molecular machinery that constructs proteins from RNA sequences by assembling amino acids into a growing peptide chain.
Control Unit: Coordinates the construction arm's activities by processing information received from the tape.	**Gene Regulation Mechanisms:** Systems regulating protein production through repression and promotion processes that modify the state of the operon.

Figure 5: Comparison between Von Neumann's Universal Constructor and Biological Life

Another intriguing observation is the parallel between human hands and the concept of a universal constructor. Hands, in conjunction with the brain, function as a versatile tool capable of constructing a wide variety of machines and tools. Although hands cannot reproduce themselves due to the complexity of biological processes, one can imagine a mechanical hand potentially achieving such a feat. Similarly, proteins exhibit a form of versatility by folding into various shapes to facilitate metabolic reactions, akin to how hands manipulate objects to perform complex tasks, such as assembling molecular models using stick and ball sets. Over centuries, hands have evolved to create and refine tools, building civilization. In parallel, proteins use coenzymes—tools selected from a pool of prebiotic molecules during early evolutionary processes—to assemble the components of life. This analogy between hands and proteins is most intriguing.

If the theory of universal functions applied to proteins holds true, it could resolve much of the mystery surrounding life. Proteins possess the remarkable ability to fold into diverse shapes and adjust their structures to perform specific biological functions. This adaptability suggests that the chemical reactions and motor processes within biological systems are, in essence, computational tasks executed by proteins as their "executing machines". Consequently, the entire system of life may exhibit a form of universal computational power, where proteins for example, function as the programs carrying out complex biochemical operations.

The computational structure of life relies heavily on both motion and deformation. Motion refers to the relative displacement between two objects, while deformation involves the relative displacement of parts within the same object. Although motion is a fundamental and ubiquitous phenomenon in the natural world, it is not as directly implemented in computational models like Cellular Automata. In digital simulations, digital computations are more straightforward to implement than continuous motion, which is not naturally represented in these models. Cellular Automata simulate motion through digital computations, but in biological systems, motion itself is used to facilitate computations. This fundamental difference highlights that, in artificial life simulations, motion is an outcome of computational processes, whereas in real life, computations are carried out through the physical processes of motion and deformations.

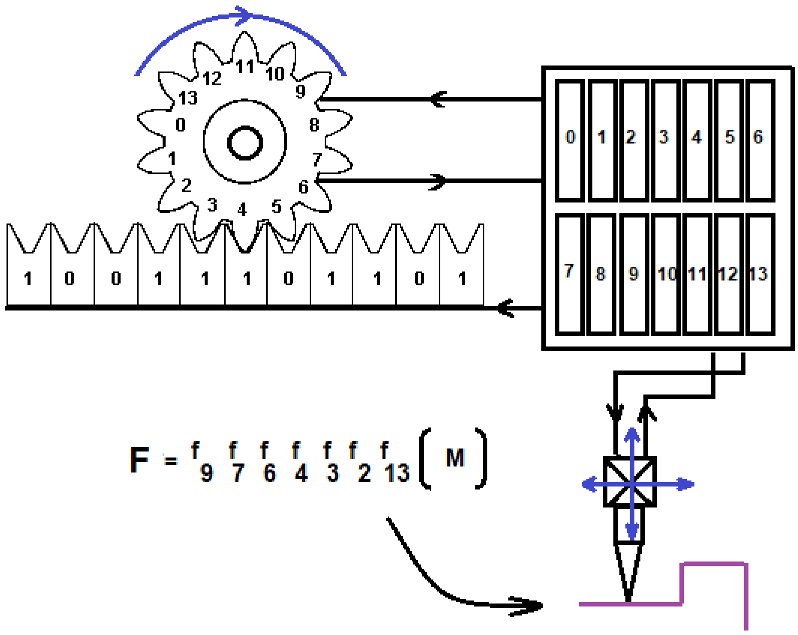

Figure 6: A schematic implementation for the Von Neumann's Universal Constructor, based on the book by Arthur Burks. [Computational Theory, 18]

3.3 Beyond Turing Machines

One of the significant challenges associated with Turing machines is determining whether a given input string on a particular Turing machine will eventually reach a terminal state, that is, an accept or reject state, and halt, or continue to run indefinitely. This challenge led to the formulation of one of the most important theorems in computational theory: the halting problem. It was proven that there is no single Turing machine or, equivalently, an algorithm that can determine whether any given Turing machine will halt for an arbitrary input string. Therefore, there are computational problems that even the most powerful computational model, the Universal Turing machine, cannot solve. This result parallels Gödel's incompleteness theorem in logic, which shows that there are statements in formal systems that cannot be proved or disproved within the system itself. Furthermore, since there are countably infinite Turing programs but beyond countably infinite mathematical functions, it follows that not every function can be computed by a Turing machine. This implies that there are far more functions that exist compared to those that can be represented and evaluated by any algorithmic process, further highlighting the inherent limitations of Universal Turing Machines: the most powerful computational machines plausible.

The inherent limitations of Turing machines led to the conceptualization of Oracles. An Oracle was envisioned as an abstract "black box" that could instantly determine a particular function, given that, it had access to an infinite lookup table for the function, and could produce an output effortlessly for any given input. Since not all functions are computable, and there are functions for which no Turing machine can be constructed, equipping a Turing machine with such an Oracle endows it with greater computational power than that of a purely computational Turing machine.

Another significant limitation of Turing machines is their inability to effectively handle real numbers and continuous data. Although Turing machines can asymptotically simulate continuous behavior, they cannot achieve perfect representation or computation of such behavior within a finite amount of time.

The analog computer model utilizes mechanical and electrical devices to perform continuous operations, such as integration and differentiation, on input continuous signals. In addition to these operations, it can also handle addition, multiplication (mixing), and phase changes, making it well-suited for processing real-world phenomena that require continuous data representation.

Quantum computers offer the ultimate computational power by representing a form of analog computing that operates in the quantum regime. Quantum Turing machines behave as a quantum wave, allowing their read/write head to exist in a superposition of multiple locations, enabling the machine to be in a superposition of states while the tape can have a superposition of configurations. This quantum wave characteristic, facilitates faster computations through parallel processing. However, quantum computers require quantum gates to implement the necessary quantum behavior, a capability that neither classical Turing machines nor traditional analog computers can achieve.

Together with single qubit gates, such as the Pauli gates (X, Y, Z), Hadamard gate (H), phase gates (S), and rotation gates (R_x, R_y, R_z), and Controlled Not (CNOT) gate enables the construction of any unitary operation on a quantum state of any size. By combining these gates in various sequences, it is possible to approximate any unitary transformation, as they form a universal set of quantum gates.

3.4 Quantum Biology

Researchers have been working diligently to build sophisticated quantum devices that barely perform simple computations, so they were surprised and even shocked when news emerged that biological processes like photosynthesis may be utilizing quantum mechanics. This also meant that further advances in biology would increasingly depend on the collaboration between biologists and physicists.

Initially, it was believed that exciton transport in the FMO (Fenna-Matthews-Olson photosynthetic complex) might be performing quantum computations, particularly employing Grover's algorithm to search for the reaction center. However, Seth Lloyd, a prominent researcher in quantum information theory, and his team found this proposal to be exaggerated and unfounded. They demonstrated that the remarkable efficiency (approximately 98%) of exciton transport through the FMO complex could be attributed to a phenomenon they termed environment-assisted quantum walks, where a delicate balance between decoherence due to the environment, and coherence enables efficient transport of quantum particles [Quantum Biology, 6].

The coherent model for the FMO complex acts as a random structure, resulting in the Anderson localization phenomenon, where energy eigenstates manifest as localized waves with extremely high localization at certain sites and minimal localization at others. Furthermore, coherent unitary evolution in quantum mechanics leads to bidirectionality. However, when non-unitary effects from the environment are introduced, unitarity is compromised, causing the evolution of the system to become unidirectional. Additionally, the environment distorts the energy structure of the original Hamiltonian, enabling transport across sites that were previously inaccessible due to large energy gaps.

Seth Lloyd's work revealed that the FMO complex is tuned to a specific temperature that corresponds to the environment in which the bacteria reside. At zero temperature, Anderson localization occurs, while at very high temperatures, the quantum Zeno effect manifests, causing the particle to behave as a classical particle. However, at the optimal temperature to which the FMO complex is tuned, the exciton behaves as a complex quantum wave, flowing toward the reaction center with a high probability. Effectively, the unidirectionality introduced by environmental effects enables the FMO complex to capture portions of the wave that constitute the exciton and funnel them toward the reaction center.

Other quantum phenomena have also been observed in biological systems. For instance, the process of avian navigation in certain bird species, such as European robins, is believed to involve quantum entanglement and the manipulation of spin states in cryptochrome proteins, allowing these birds to sense Earth's magnetic field. In some studies, researchers have demonstrated that quantum effects, such as tunneling, play a role in enzymatic reactions, enabling particles to bypass energy barriers that would be insurmountable in classical physics. Furthermore, recent investigations into the olfactory senses of mammals suggest that quantum tunneling may assist in the detection of odorant molecules, contributing to the sensitivity of the sense of smell.

As biological systems, such as proteins, operate at the nanoscale, it is no surprise that quantum effects play a significant role in their functionality. However, there is no evidence to suggest that proteins are executing complex quantum algorithms, such as Grover's algorithm, to solve problems. Nonetheless, these insights into the quantum nature of biological processes inspire quantum computer scientists to explore alternative methods of computing, particularly by leveraging environmental effects rather than attempting to mitigate them.

3.5 Computational Nature of Matter

Matter exhibits computational properties, and the computational distinction is what sets life apart from other forms of matter. While all matter can perform computations to some degree, the computational properties of life are far more complex and versatile. Living organisms, in particular, consist of matter that demonstrates a degree of universal computational power, enabling them to process information, adapt, and evolve in ways that non-living matter cannot. These special universal computational properties have arisen from the very matter that makes up life, allowing for the emergence of biological complexity and intelligence. For example, minerals, though capable of limited computations, are restricted to basic physical interactions, whereas life forms can process vast amounts of information, giving rise to behaviors and functions far beyond the capabilities of inert matter. This almost universal computational power of life, have emerged from the matter that constitutes life.

Viewing matter as computational devices is intriguing because it opens up compelling questions and provides valuable insights. For instance, can there be properties of matter that are fundamentally non-computable, akin to the halting problem in computer science, which presents limits to algorithmic processes? Could life itself be a phenomenon that defies complete deduction through algorithmic means, suggesting that certain aspects of biological complexity are beyond the reach of simple computational models? Additionally, how might the measurement problem and superposition in quantum mechanics, which reflect uncertainties and multiple potential states, manifest in the context of life? Alternatively, could it be that the universe behaves in a fundamentally computational manner, where all phenomena might be the result of underlying computational processes, and the measurement problem merely reflects a true sources of randomness?

Clearly, matter exhibits computational properties, as discussed in previous sections, particularly regarding the resemblance between universal constructors and living systems. Additionally, chemistry itself appears to function as a computational process, where bonds between molecules are formed and broken, leading to the creation of new compounds or changes in molecular conformation. Theoretical chemists often rely on the notion that chemistry operates in a computational manner, highlighting its algorithmic nature.

Some have wondered why equations work so effectively, questioning how humans can write down mathematical formulas that accurately predict the behavior of particles and other physical phenomena. This ability is rooted in the remarkable almost universal computational power of the human brain, which can simulate and model complex systems within its own neural networks. The brain's near-universal computational capacity allows it to process and understand intricate patterns and behaviors observed in the physical world, enabling humans to create equations that reflect these phenomena with precision. Essentially, the human mind acts as a powerful computational device, capable of mirroring the machines and systems it encounters, and thus producing mathematical representations that accurately capture the dynamics of the universe.

Investigating the computational nature of matter is a fascinating endeavor. Objects in the universe tend to follow well-defined computational trajectories, raising the question: who performs these computations? It seems that the fundamental particles or fields that constitute matter are responsible for carrying out these calculations. This is reminiscent of Cellular Automata, where individual cells determine their own fates through simple rules, yet collectively exhibit complex, long-range ordered behavior. Similarly, actual matter may exhibit exotic behaviors as a result of simple computations carried out by fundamental particles or their corresponding fields. This perspective suggests that the seemingly complex dynamics observed in the universe might emerge from basic computational processes intrinsic to the building blocks of matter.

Studying the computational nature of matter reveals a hierarchy, or more aptly, a nesting of computational structures. Commercial computers and robots are unquestionably computational as they perform explicit calculations. The computational entities that assembled them are human brains, which function as complex neural networks capable of universal computation. The eukaryotic cells that compose these human brains are also nearly computationally universal, containing genetic machinery analogous to Von Neumann's Universal Constructor, along with a cell membrane that acts as a computational interface. At a smaller scale, nanomachines, particularly proteins, perform the necessary computations for these individual biological cells. Further down, atoms and molecules carry out computations that dictate the behavior of these nanomachines, while subatomic particles are responsible for the computations governing atoms and molecules. Finally, the fundamental particles that make up these subatomic particles carry out their computations without relying on any deeper computational entity. Since nothing else computes the behavior of these fundamental particles, they can be considered physical manifestations of simple oracles. They lack internal structures to perform computations; instead, they are inherently the computation they represent.

Finally, spacetime itself exhibits computational power. Beyond the complex behavior of spacetime described by Einstein's general relativity, there are simpler computational properties intrinsic to space. For instance, spacetime allows for the addition of particle numbers and the superposition of wave and field amplitudes. These basic operations are fundamental to how physical processes unfold, suggesting that spacetime serves as a computational medium that facilitates the interactions and behaviors observed in the universe.

When the computational properties of space and matter combine, a unique form of computational behavior emerges: motion. It is the motion of subatomic particles that leads to the formation of atoms, and the movement of atoms and electrons that gives rise to molecules. The motion of molecules forms polymers, whose dynamics facilitate the creation of nano-machines such as proteins, flagella motors, and cells. The movement of individual cells eventually leads to the emergence of multicellular organisms, which, in turn, develop limbs to enable greater mobility. This suggests that motion is fundamental to enabling things to perform the computations they are capable of, making it an essential aspect of the computational nature of reality.

It is no wonder that motion plays such a critical role in building the computational capacity of matter. Even Turing machines require motion to operate, as the read/write head must move along the tape. Essentially, the computational behavior of the universe resembles a grand Turing machine, with multiple read/write heads composed of matter that move toward other matter in different locations to perform computations. Various natural machines, such as polymerases, flagellar motors, and the limbs of complex animals, facilitate self-directed motion through internal computations.

Complex matter appears to consist of building blocks that themselves are composed of simpler structures, forming a nested hierarchy. For example, a hand is composed of cells, which are made of macromolecules, which in turn consist of molecules, then atoms, and ultimately subatomic particles derived from fundamental particles. This hierarchical structure allows the behavior of higher-order objects to be mechanistically explained through their lower-order components. The fundamental particles and fields function as entities that cannot be further reduced, acting as the base level of this nested system of computational machines, with these base entities analogous to oracles.

The nature of matter is, of course, a subject of debate, and certain speculations lead to intriguing metaphysical ideas. One such notion is that the entire universe could be viewed as a vast mathematical function, with fundamental particles acting as oracles. Matter exhibits computational properties that manifest as physical reality, much like how mathematical functions such as the exponential function manifest behavior on a graph. The universe may exist in its current form simply because this is the only consistent manifestation of reality, where any deviation would lead to contradictions. Hypothetical fundamental particles could be conceived, but their existence would be impossible if they introduced unavoidable inconsistencies within the system. In this grand mathematical function, every sub-constituent is itself a sub-function, as in lambda calculus—functions acting on other functions to produce new functions. Under this perspective, even properties such as energy and momentum can be seen as computations in their own right, each contributing to the complex, interconnected structure of reality. This is an alternative theory to the multiverse, where only one universe exist, and it is a grand computation.

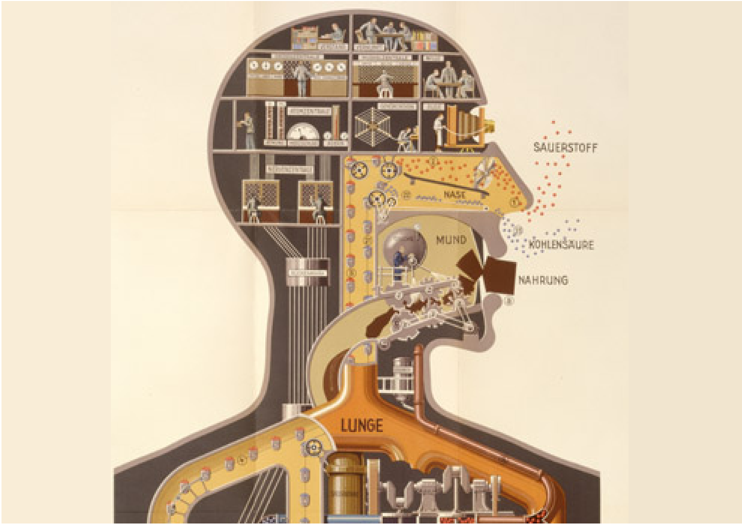

Figure 7: It is imaginitive to disposition that little men must be working inside men and perhaps even smaller men inside the little men, as this painting, *Man as Industrial Palace, Fritz Kahn, 1926* shows

Susskind emphasizes that the term "universe" refers to all that exists, and the idea of multiple universes is, in a strict sense, meaningless. He argues that the universe is a singular entity, and it may be the only noun in the English language that logically should not have a plural. According to Susskind, the laws governing the universe as a whole are fixed and cannot change. When discussing the "multiverse," however, Susskind is referring to different regions or "bubble sub-universes" within the larger framework of the universe, each potentially having distinct physical laws and constants due to variations in conditions like symmetry breaking and compactification of extra dimensions.

With respect to Susskind, the universe may be viewed as a special type of computational machine, within which numerous computations arise randomly, giving birth to different bubble sub-universes. In some of these sub-universes, certain computations evolve into universal constructors—systems capable of self-replication—that eventually give rise to life. In contrast, other computations may lead to dead ends or self-erasure, never forming any complex structures.

4 Susskind's Anthropic Principle

Leonard Susskind is a confident and vocal advocate of the Anthropic Principle, positioning it as a compelling solution to the fine-tuning problem in physics, particularly within the frameworks of String Theory, Inflationary Theory, and the Multiverse. He asserts that the universe's apparent fine-tuning is not a result of intelligent design or deliberate adjustment, but instead emerges naturally from the vast statistical possibilities offered by a multiverse. This argument is articulated with great confidence, as Susskind often emphasizes that the Anthropic Principle, combined with the structure of string theory, provides a reasonable explanation for the specific physical constants observed in the universe.

Susskind's work explores how String Theory postulates the existence of extra dimensions, beyond the familiar four-dimensional spacetime. These extra dimensions are often "compactified" or wrapped up into incredibly small spaces, rendering them undetectable at macroscopic scales. In string theory, these dimensions allow for strings—the fundamental building blocks of matter—to take on an enormous number of different configurations. Each configuration of the string vibrates in a specific way, leading to different physical laws and constants for each universe. The sheer number of possible configurations suggests that the multiverse contains a vast "landscape" of universes, each with its own unique physical laws.

This landscape of possible universes is a result of the different ways in which the extra dimensions can be compactified. Susskind explains that, due to these compactifications, universes can differ widely in their laws of physics, such as the values of particle masses, the strength of forces, and even the number of observable dimensions. This leads directly to the Anthropic Principle, where the existence of life in any given universe can only occur in regions of the multiverse that happen to have the right conditions for it, even though many universes may be hostile to life.

A crucial part of this framework involves spontaneous symmetry breaking. In the early stages of the universe, fundamental symmetries—such as gauge symmetries governing the forces of nature—could have been intact. However, as the universe evolved, these symmetries broke in different ways, depending on the local conditions in each bubble universe. As a result, different universes would exhibit different physical laws, based on how the symmetries were broken. For instance, one universe might have a different cosmological constant, or gravity could behave differently due to the way the symmetry was broken during its formation.

Susskind's argument relies on Inflationary Theory, which posits that the universe underwent a period of rapid expansion early in its history, causing regions of space to inflate and form bubble universes. Each of these bubbles could break symmetries differently and compactify extra dimensions in unique ways, leading to a multiverse where each universe has its own distinct set of physical laws. The mechanisms of symmetry breaking, combined with string theory's flexibility in allowing a vast array of configurations, explain how different laws of nature arise across the multiverse.

Susskind speaks confidently about these ideas, arguing that they offer a naturalistic explanation for the universe's properties without requiring fine-tuning or external intervention. He acknowledges that while these ideas are speculative and not directly testable at present, they align with the current understanding of string theory, extra dimensions, and inflation. Susskind's stance, while not universally accepted, represents a bold attempt to address one of the most profound mysteries in cosmology and fundamental physics [Cosmology, 1,2,3].

5 Computational Matter Physics: A new realm of physics

5.1 Postulates of Computational Matter Physics

Computational matter physics is to be founded on several core postulates, many of which are supported by the preceding discussions. These postulates provide a framework for understanding how computational principles are embedded within physical matter, from the behavior of fundamental particles to the complex processes in biological and engineered systems.

5.1.1 1st Postulate: Matter is Computational

In traditional physics, mathematics typically serves to describe the behavior of matter, but this postulate suggests something deeper: that matter itself is a computation. Matter is the optimal expression of the underlying computation that defines it, with the computation manifesting as the physical substance and structure of matter. This implies that the fundamental nature of matter is inseparable from the computational processes that give rise to it. Matter is the manifestation of a computation, inherently performing the computation that defines its existence. While mathematical equations on paper can simulate matter, the optimal mathematical representation of it, is it by itself. In this sense, matter is its own simulation, and the optimal simulation.

The first postulate explains why matter possesses computational characteristics and properties: because matter is a computation. Matter is composed of fundamental particles, whose collective behavior manifests through interactions of these particles and their associated fields. If these fundamental particles or fields lack internal structure, they can be considered as oracles within the computational model associated with matter. This perspective views the inherent properties of matter as emerging from the computational nature of its most basic components. A fundamental particle or a field, with no internal structure is its own computational representation. The computations that occur within fundamental particles or fields are referred to as **fundamental computations**, which give rise to computational properties of the matter they form. The computational behavior of more complex forms of matter is derived from these fundamental computations, serving as the building blocks for the emergent properties and behaviors observed at higher levels of organization.

Interactions between matter can be reduced to computations. Self-modifying code and meta programming are advanced programming techniques that enable programs to alter their own instructions or generate and manipulate code at runtime. Meta programming, supported by languages such as Python, Ruby, and Lisp, empowers developers to write code that can inspect and modify itself or other programs, facilitating flexibility and adaptability in software design. Notably, Turing machines and Cellular Automata serve as computational models that operate on their own code. In a similar vein, matter can be viewed as a program, or a computational machine, that acts on its own code. Essentially, matter functions as a computational machine that takes its surroundings as input and modifies its own code, thereby influencing its behavior. Matter can thus be viewed as a function that operates on itself by interacting with its surroundings, which are also functions. This dynamic behavior is analogous to lambda calculus function abstraction, where functions act on other functions to produce new functions.

In mathematics, the properties of functions can be analyzed through their graphical representation. However, when dealing with more complex functions, computer simulations are often employed to capture the multitude of possible behaviors, as simple graphs may be insufficient. When studying real-world systems, these are typically modeled as mathematical objects, and their behavior is examined through graphs or simulations. One might consider the physical world itself as a representation of a mathematical function. This perspective suggests that reality serves as the most accurate simulation of its own computational behavior, whereas computer simulations and graphs inevitably fall short of capturing its full complexity.

When one plots the exponential function on a graph, writes its algebraic form, and examines its properties, the significance of this special mathematical function becomes evident. Psychologically, computations are often thought of as processes that manipulate symbols on paper, but fundamentally, they are inseparable from matter, as eyes, hands, brains, pens, pencils, paper, and electronic components are all material objects. In truth, computations involving the exponential function are optimally represented using eyes, hands, brains, pens, pencils, paper, and electronic components. Similarly, when ribonucleotides and amino acids form polymers, they exhibit special computational properties that enable the complex behaviors observed in living systems. Like mathematical functions, these biological molecules have unique properties that correspond to their intricate behavior. However, unlike the exponential function, the complexity of their behavior is too great to be fully represented on paper or simulated by electronic computers; they are optimally simulated by themselves.

This realization has profound implications for understanding complex systems, such as life. From this perspective, life can be viewed as a computational object, akin to a mathematical function, with its observable phenomena serving as the representation of that function. The mathematical nature of life, cannot be fully expressed through any means other than its observed material manifestation. The mathematical object known as life is most effectively expressed through molecules. Essentially, some computational objects exist as matter.

5.1.2 1st Consequence: Physical properties of matter are derived quantities.

If matter is computational, and its collective behavior is computed by the fundamental particles and their associated fields, a natural question arises: what computes the physical properties of matter, such as position, momentum, and energy? The first postulate implies that these physical properties—position, velocity, momentum, and energy—are also derived from the inherent physical properties of the fundamental particles. In other words, while the fundamental computations manifest as the behavior of higher matter, their physical properties themselves arise as a byproduct of this process.

In this context, matter, as computing machines can be viewed as computational entities that essentially compute their own physical properties, such as energy. The operations they perform, governed by the fundamental rules of computation, inherently define characteristics such as state, energy consumption, and efficiency. Just as fundamental particles dictate the properties of matter through their interactions, machines determine their operational properties through the algorithms and processes they execute.

For example, a simple gas can be conceptualized as a computing machine, when provided with the initial configurations of the position and momentum of its constituent particles, this system computes the same quantities after a designated period of time. Similarly, a calculator, which is fundamentally composed of matter, demonstrates computational behavior when tasked with a specific calculation. When provided with a description of the calculation, the calculator not only executes the computation but also inherently determines the position and velocity of its constituent particles. Thus, this behavior continues to complex matter.

5.1.3 2nd Consequence: Matter are their own simulation

Recently, advances in technology have led to a growing belief among intellectuals that existence itself might be the result of a simulation. Elon Musk, CEO of Tesla and SpaceX, who associates intellectuals, even stated that the argument for simulation theory is "quite strong". However, defining what constitutes a simulation versus what is real becomes a complex issue. The distinction between simulation and reality can be illustrated by comparing a cellular automaton representing an organism and a "real" organism. In a cellular automaton, the behavior is derived from computations occurring within individual cells of the model. Similarly, a real organism's behavior emerges from the fundamental computations carried out by fundamental particles and fields. The key difference lies in the nature of these components: the cells of the cellular automaton organism are simulated by another, whereas the fundamental particles and fields of a real organism are inherent. These fundamental elements do not have internal structures; they simply manifest as oracles, embodying the properties of the computation they represent.

Matter, being computational in nature, computes their own behavior. Essentially, they simulate themselves. For instance, the average speed of a horse can be computed by creating a computer model of the horse and running a simulation. Alternatively, the horse itself can be made to run several laps to determine its average speed. In this sense, the horse acts as a computational machine, inherently simulating itself, and humans can utilize the horse's actions to compute its properties. The horse, through its physical existence and behavior, essentially embodies its own computational process, allowing for direct observation and measurement of its characteristics.

5.1.4 3rd Consequence: A measurement is a computation

In both quantum mechanics and thermodynamics, measuring a system results in a change to that system, indicating that observation is not a passive act but an active one. This act of measurement by an observer can be effectively described as a computation, as it involves the processing of information that influences the state of the system being observed. The computational machine that carries out this computation, of course, is the observer.

5.1.5 4th Consequence: Emergent behavior results from fundamental computations

Emergent behavior refers to complex patterns and properties that arise from the interactions of simpler components within a system, often leading to phenomena that cannot be easily predicted from the individual parts alone. Examples of emergent behavior range from vibrational modes in materials, known as phonons, to the intricate phenomenon of life itself. There are two possible pathways through which emergent behavior can arise. One possibility is that when these sub-constituents are combined, they create an oracle whose properties are independent of those of the individual components, resulting in a non-computational phenomenon. This notion is not far-fetched, as the collapse of the wave function serves as an example of a well observed un-computational phenomenon. Alternatively, emergent behavior may arise as a direct consequence of fundamental computations, as seen in Cellular Automata, which demonstrate how complex emergent phenomena can emerge from basic computational rules. This is also the accepted view within the field of computational matter physics: emergent behavior arises from fundamental computations. In this view, the interactions and computations performed by the simplest components of a system give rise to complex behaviors and properties that manifest at higher levels of organization.

Computational universality is a striking example of emergent behavior. The work of John Von Neumann demonstrated that a finite set of fundamental computations can lead to the formation of a Universal Constructor, a theoretical machine capable of constructing any other machine.

5.1.6 5th Consequence: Equivalence between Universal Constructors, and Universal Computers

Since matter is a computation and machines are composed of matter, machines are fundamentally equivalent to programs. Just as universal computers can simulate any other computation or program, universal constructors can construct a machine that can simulate a particular program. However, some programs are self-sufficient and require no additional computational framework to support their execution, as they are the machine itself—embodying both the computation and the mechanism for carrying it out. Universal Constructors are, therefore, fundamentally equivalent to Universal Computers.

It follows that, since Universal Computers are machines, a Universal Constructor can build a universal computer. Likewise, since universal constructors are programs, universal computers can simulate them. This establishes a reciprocal relationship between universal constructors and universal computers: one can physically construct the other, while the other can computationally simulate the first. This symmetry highlights the fundamental equivalence between construction and computation in this conceptual framework.

Universal constructors are said to be theoretical machines capable of building any other machine, including replicas of themselves, when provided with a set of instructions. These Universal constructors are computationally equivalent to that of a universal computer, which can perform any computation that can be algorithmically defined. The equivalence arises from the fact that a universal constructor can construct a universal computer, effectively enabling it to execute any computational task. Conversely, a universal computer can simulate the actions of a universal constructor, demonstrating the profound equivalence between these two computational machines. Importantly, this further highlights that matter itself is computational in nature.

5.1.7 6th Consequence: Independence from Space Time

It is peculiar that in nature there are instances where two separate entities, like the heme group and the iron cation, fit together perfectly despite originating from different places. Such a phenomenon might seem like a simple coincidence, or it could be dismissed as chemically unremarkable. However, the idea that two distinct things can fit so precisely raises deeper questions, especially if this fit arises from basic underlying laws that cannot predict in advance whether such a match will occur. This occurrence may be understood through the concept that computational properties exist independently of time and space. Two objects can align or match, regardless of where or when they were created, as this is a computational relationship. While this might seem obvious, it is a powerful and resourceful perspective for understanding how seemingly unrelated elements in nature can align or fit together through fundamental computational principles. Evidently, such rare occurrences happen at the nanoscale, where systems exhibit greater order, aside from humorous examples like trees shaped as various objects. Computational relationships are independent of space and time, and thus remain unaffected by the distance or time of their creation.

5.2 Theorizing Universal Constructors

While the concept of universal Turing machines or universal computers is well-defined and understood, there remains ambiguity in defining universal constructors. A universal constructor is a machine capable of constructing any physical object, including a copy of itself, given the appropriate instructions. Currently, there are only two known examples of universal constructors: biological life, which replicates itself through the processes of cell division and evolution, and Von Neumann's universal constructor, which was formulated as a conceptual model using cellular automata to demonstrate the principles of self-replication. This section aims to formalize the notion of universal constructors by developing theoretical frameworks that extend and refine the ideas behind these examples.

The sixth consequence states that universal constructors and universal computers are fundamentally equivalent. This equivalence can be easily demonstrated in Von Neumann's universal constructor within a cellular automata universe, where the constructor is capable of building a universal Turing machine, thereby embodying computational universality. However, when considering biological life, the scenario becomes significantly more complex. Biological life, hypothesized to have emerged from ordinary matter through natural processes, is strongly supported by empirical evidence, yet lacks a comprehensive mathematical explanation for its origins and the mechanisms behind its emergence.

Furthermore, life has evolved from the Last Universal Common Ancestor (LUCA) towards complex forms, such as eukaryotic intelligent multicellular life, capable of constructing advanced computers—including those built by institutions like IBM for classical computing, and companies like Google and DWAVE for quantum computing. Despite these advances, physical limitations restrict both biological systems and human-made commercial computers from being fully universal. One significant limitation is that life, in all its complexity, cannot be simulated entirely inside these commercial computers due to computational limits on memory, speed, and the complexity of biological interactions.

This reveals the need for a mathematical theory to handle such limitations in the equivalence between universal constructors and universal computers. Such a theory would have to consider the physical constraints—such as energy, resource limitations, and the sheer complexity of the systems involved—and develop a framework to express partial universality or degrees of universality in these contexts, accounting for the gaps in simulating complex, emergent phenomena like biological life within our current computational models.

5.3 Formal Definitions

An **oracle** is a computational machine or device that has no internal structure. It functions as an automatic look-up table, but it does not require an internal entity to perform the "looking". The oracle provides an immediate response to specific inputs, bypassing the need for internal computation or processes. The abstract form of a function, called the **abstract function**, is an oracle that corresponds to that function.

The **Fundamental Universal Computer** (FUC) is the Universal Computer upon which all computations are defined. It is constructed on operations that require oracles. For instance, in the assignment of a Universal Turing Machine as the FUC, the movement of its parts, is assumed to occur 'magically', as the machine relies on oracles to perform its steps without requiring a detailed internal mechanism of how the operations are physically carried out. A **machine** M is a program in the FUC, and it is its own **simulation**.

A computation over a space X, is a trajectory $x(t)$ defined on X, where both X and $x(t)$ can be continuous(as in Analog and Quantum Computing) or abstract(as in Turing Machines and Cellular Automata).

A **computational representation** of a function $f(x)$ in a space X is a set of trajectories $\{\Gamma(t)\}$ such that $\Gamma(0) = x$ and $\Gamma(T) = f(x)$ for each x. A program q in the Fundamental Universal Computer (FUC) that implements $\Gamma(t)$ is a simulation of f. If q has a description of the form $X \otimes D_q$ in the FUC, where X may represent a finite set of infinite tapes, but D_q is finite, then q is a **recursive** computational representation of f. Naturally, q is its own simulation. Moreover, trajectories can be viewed as functions with multiple outputs.

A **Universal Constructor** (UC) Ω is a specialized type of universal computer and a machine within the Fundamental Universal Computer (FUC). It features a distinct **construction function** that defines the concept of construction. Given any recursive function f, the UC has the capability to construct another machine q_f within the FUC that simulates f. Notably, the Universal Constructor Ω possesses the unique property that $q_\Omega = \Omega$. In other words, the machine constructed by UC Ω, that simulates the UC Ω is, in fact, Ω itself.

A **world** is a program in FUC where its attributes emerge from an initial condition where emergence is defined by a special **emergence rules** which defines what it means to emerge. A world can have a universal constructor as an emergent attribute.

5.3.1 Constructors

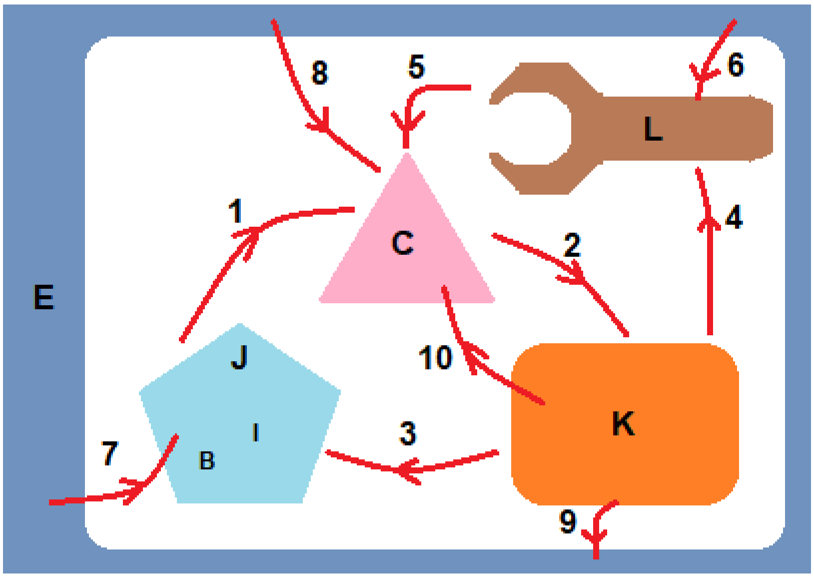

Figure 8: Universal Constructor System: Constructor C act on building blocks in J (1), utilizing tools L (5) and supported by environmental conditions E (8), to produce products K (2). Some of these products are released into the environment E (9), while others become part of the tools L (4) or contribute to forming new objects in J (3). The environment E supplies resources to both J (7) and L (6). C can also be a product in K (10).

A Constructor serves as an imperfect analog of a Universal Constructor (UC). The emergence of a UC can occur through a series of constructors, where new attributes contribute to incremental improvements, allowing the system to asymptotically approach the capabilities of the UC. The following discussion of a constructor is informed by insights gained from biological life and Von Neumann's work on his Universal Constructor.

This can be considered a definition of a Constructor and its associated system. A **Constructor System** is a structure $S = \langle E, J, C, K, L \rangle$, where E represents the environment, J denotes the building blocks, C is the constructor, K refers to the outputs, and L encompasses the tools. The constructor C employs the tools L to produce outputs K using the building blocks J, while the environment E provides resources to J, L, and assists C. Fundamentally, S, E, J, C, K, and L can all be viewed as programs. It is convenient to describe S as a function of E, and E as a function of S. That is, $S(E, S) \equiv S(E)$ and $E(S, E) \equiv E(S)$ respectively.

Interesting phenomena occur when constructors are able to produce themselves. This does not necessarily mean that they are universal constructors. For example, in chemical systems, particularly in autocatalytic systems, chemicals can participate in reactions that lead to their own production along with other products. Such constructors, which are capable of producing themselves but are not universal, can be referred to as **partial self constructors**.

A notion of complexity for self-constructors can be highly useful. For instance, a simple autocatalytic chemical system qualifies as a self-constructor, as does a bacterium capable of self-construction.

However, the bacterium is evidently more complex than the simple autocatalytic system. The complexity between two self-constructors can be characterized by their **Kolmogorov complexity**, providing a formal measure of their comparative intricacy. Thus, a self-constructor described by 100 bits is less complex than another constructor described by 10,000 bits, as measured by their respective **Kolmogorov complexity**.

Let C and C' be two constructors. The relation $C \leq_K C'$ holds when $|C| \leq |C'|$, where $|C|$ represents the **Kolmogorov complexity** of C with respect to the FUC. Additionally, the **Laws of Emergence** of the **World** can describe an evolutionary relationship between S and C' as $C \to C'$. When $C \to C'$, it may not necessarily follow that $C \leq_K C'$ in all special cases, but it is generally expected to hold. A series of the form $C_0 \to \cdots \to C_M$ represents an evolutionary progression of constructors, such that C_M asymptotically approaches the Universal Constructor.

There are countably infinite programs that a Universal Computer can run, and there are countably infinite corresponding machines that can be constructed by the Universal Constructor to simulate them. A subset of these programs constitutes the machines themselves, and this subset includes the Universal Constructor itself. While Universal Computers, such as digital Universal Computers, can implement any function using a single NAND gate, this requires the infinite possible configurations in which these gates can be connected. Generally, for a given recursive function f, a series circuit of the form $f = g_n'(\alpha_n) \circ \cdots \circ g_1'(\alpha_1)$ can be provided using a primary set of operations $G = \{g_1, g_2, \ldots, g_N\}$ in the Universal Computer such that $g_i' \in G$, and where α_i represents corresponding internal parameters for g_i. This continues to the Universal Constructor as it is computationally equivalent to a Universal Computer. This gives another way to compare two constructors, where $C <_G C'$ if $K \subset K'$ (where K denote the products of C). It does not necessarily mean however that $G \subset G'$.

Thus, the internal **finite** structure of C may consist of some function bank G with an input with infinite possible configurations, such as a tape, describing α_i, the internal parameters of g_i, and the sequence $g_n(\alpha_n) \circ \cdots \circ g_1(\alpha_1)$ for simulating a given f.

Thus, a universal constructor can itself be characterized by a function bank $G = \{g_1, \ldots, g_N\}$, where a tape determines the arrangement of g_i in series and specifies the internal parameters α_i for each g_i. Interestingly, the Von Neumann Universal Constructor, as described in Arthur Burks' book, does not incorporate internal parameters. It is fascinating that in Von Neumann's model, the tape consists of a finite alphabet that prescribes the sequence of operations required for a complex task to be accomplished. For any function f, there exists a sequence represented as $f = g_n \circ \ldots \circ g_1$, which is corresponding to the input sequence $s_L \ldots s_1$. This similarity extends to biological systems, notably the DNA sequence, which encodes complex operations through a finite set of symbols.

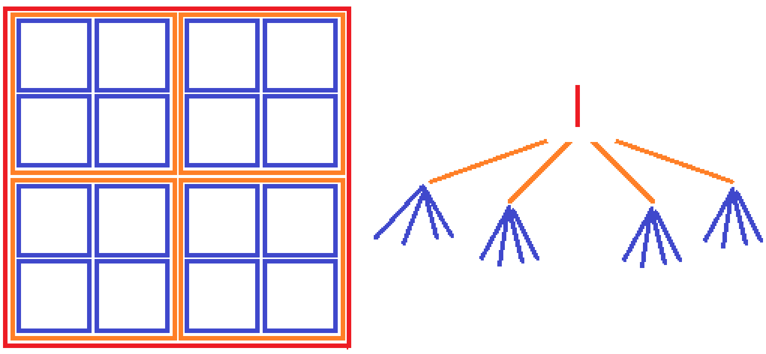

Figure 9: Nested Constructor System: The colors represent constructors, either copies or variations of the same type, which then form higher-order constructors.

There are two interesting models for the emergence of constructors. One is the **accretion model**, in which new parts are added to an existing constructor to enhance its functional capacity (add new characteristic functions to its bank) until it reaches a maximal configuration progressively. The second is the **nested model**, where constructors themselves form sets J, K, L such that they create a hierarchy of nested constructors, with one constructor made out of variations and copies of another.

There are empirical examples that serve as applications for the preceding definitions. Human hands are examples of constructors. Consider a student playing with a ball-and-stick chemistry modeling kit. The hands are constructors and have universality over the set of all possible ball-and-stick configurations. This is because the hands can bend, twist, and fold into several coordinated shapes, allowing them to maneuver through the assembly process of any of these configurations. However, the hands cannot make a copy of themselves, which suggests that they are not universal constructors in the strict sense and certainly not self-constructors. The hands are also free to use tools and make use of the environment, such as a table, to hold the work piece and to keep the parts within reach. Meccano sets are another example where human hands act as constructors to assemble complex structures from basic components, and tools such as screw drivers are used. Again,however, the hands cannot be made from a Mecanno set.

Von Neumann's universal constructor consisted of a function bank that contained its characteristic functions, which handled tape head and constructor arm head operations. The encoding for the set of operations was given by the tape.

As humans are able to build universal computers, and copies of themselves, life is a universal constructor, and the biological cells that make up the hands are also constructors. They represent a nested model for constructors. Cells are also individually capable of self-construction.

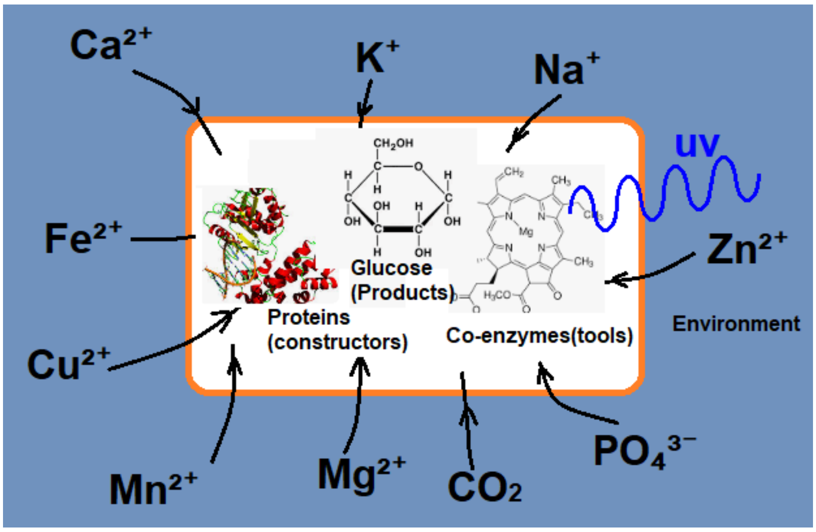

Figure 10: In the context of biological systems, a cell can be viewed as a constructor system (Refer to Figure 8) where proteins serve as the primary constructors, converting inputs such as carbon dioxide into essential products like glucose. These proteins utilize coenzymes as tools to facilitate these biochemical processes. The external environment is abundant with nutrients, Carbon Dioxide and energy sources like light, providing the necessary resources for cellular function. Together, proteins, RNA, and DNA enable the cell to operate as a self-constructing entity, orchestrating a complex interplay of molecular interactions that sustain life. The environment of a bacteria, is fascinating. Bacterial cells exhibit a fascinating characteristic with the presence of a slimy organic layer known as biofilm, which surrounds their cell envelope. This biofilm is composed of a complex mixture of polysaccharides, proteins, and nucleic acids, forming a protective and adhesive matrix. Its primary purpose is to enhance bacterial survival by providing a barrier against environmental stresses, such as desiccation and antimicrobial agents. Additionally, biofilms facilitate cell-to-cell communication and promote adherence to surfaces, allowing bacteria to thrive in various habitats and contributing to their resilience in both natural and clinical settings. Similarly, in animals, a protective layer known as the acid mantle exists, which is composed of fatty acids and lactic acid on the skin's surface. The acid mantle helps maintain the skin's pH balance, providing a defense against harmful microorganisms, supporting barrier functions, and preventing infections while also contributing to skin hydration. Together, these layers illustrate the intricate ways in which living organisms protect themselves and maintain their functionality. Thus, life is as a constructor system, consistently enveloped by a unique environment that sustains its functions.

5.4 Accretion Model for the Origin of Life

The origin of life has been a major topic of interest in the 21st century. Could something as remarkable as life have really emerged from a series of events starting from mere chemical building blocks? This is a question that continues to intrigue and challenge scientists of this era, as they seek to understand the complex processes that might have led from simple molecules to the self-sustaining, self-replicating systems recognized as life. The study of prebiotic chemistry, the formation of protocells, and the emergence of metabolic and genetic pathways all contribute to unraveling this profound mystery.

The accretion model for the origin of life suggests that life emerged from a self-constructor that progressively added parts until it reached the hypothesized **Last Universal Common Ancestor**(LUCA). LUCA is thought to be the most recent common ancestor of all currently living organisms on Earth. It likely had a cellular structure, a genetic code based on RNA or DNA, basic metabolic pathways, and the machinery for protein synthesis.

The **prebiotic matrix** is the hypothetical primordial layer on Earth's surface, preceding the emergence of life, where conditions were conducive to the formation of organic molecules and the development of early biochemical processes. The prebiotic matrix is the hypothetical region where abiogenesis events took place. The prebiotic matrix can be conceptualized as a uniform layer distributed across the Earth's surface, with a certain thickness. While it's plausible that atmospheric regions might have also contained prebiotic potential, and prebiotic matrix may not have been perfectly uniform and even discontinous across the earth, this is only a hypothetical assumption. If all matter in extant life originated from the prebiotic matrix, this hypothetical layer covering the Earth's surface would possess a thickness of a few centimeters.

The accretion model proposes that life may have emerged through a series of self-constructors, each stage progressively increasing in complexity by incorporating new information. In this model, successive generations of self-constructors build upon the previous ones, gradually accumulating functional capabilities and structural sophistication. The following exercise includes some numbers to provide perspective on the process, particularly concerning the time and space required for it.

Let the LUCA be a constructor system with an information size of approximately 2.5 million bits, which is comparable to the 9.2 million bits of the *Escherichia coli* genome. How could such a system have emerged in the prebiotic matrix? Could it have simply arisen from pure randomness? This cannot be the case, because if the physical size of a configuration is approximately 1 cubic micrometer, comparable to the size of a bacterium, then containing $2^{2.5 \text{ million}}$ configurations presents a formidable logistical challenge on Earth.

For the purpose of this exercise, consider the thickness of the prebiotic matrix to be approximately 1 meter, with physical size of a configuration approximately 1 cubic micrometer, ensuring sufficient space to contain 2^{100} configurations simultaneously. The algorithm for the emergence of LUCA constructor now constitutes a search process. If the LUCA constructor, with a size of approximately 2.5 million bits, is divided into 25 thousand sections, each 100 bits in size, and if the generation of configurations occurs exponentially over time, with a doubling period of 1 month, then it would take approximately 100 a 2^{100} sized space of configurations.

After 100 months, the entire prebiotic matrix will be populated by 2^{100} configurations, and the best 100-bit-long configuration will be able to out-compete the rest, which are erased. Initially, the first optimal replicator consists of a 100-bit code, which begins to accumulate additional 100-bit codes in progression, evolving into a larger and more efficient version that outcompetes others of similar complexity. This process can be repeated for all 25 thousand parts of the LUCA constructor, thus requiring a total time period of 2.5 million months, or approximately 0.2 million years.

A crucial insight is that even a system as intricate as a biological cell can be described by a finite quantity of information, even if that quantity reaches millions of bits. This finiteness implies that, under suitable conditions and processes, such complexity can, in principle, be systematically explored and ultimately realized. Thus, given the correct computational characteristics, a constructor system as complex as millions of bits, could emerge within a period of the order of a million years.

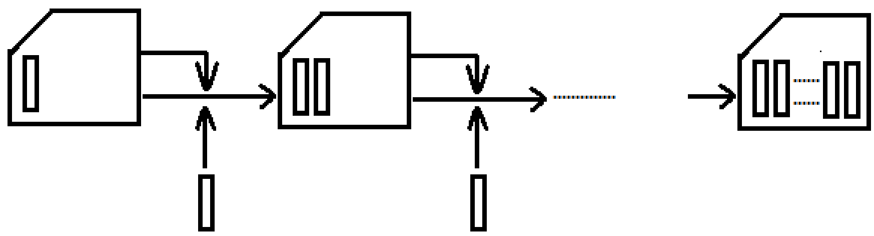

Figure 11: Accretion Model

In the context of the origin of life, RNA polymerase, a universal copier capable of complementary copying of any RNA template, may have played a pivotal role. This universal copier is particularly intriguing, as it can replicate any template of considerable length while requiring only a finite amount of information to be formed.

Consider a self-constructor, some proto-life form during the emergence of the Last Universal Common Ancestor (LUCA). This self-constructor would encompass a total amount of information denoted as I_T, with I_c representing the information required for the self-construction process, and I_m for metabolism and other essential processes. The advantage μ_c of the self-constructor can be quantified by the ratio:

$$\mu_c = \frac{I_T}{I_c}$$

indicating its ability to copy more information than that necessary for its own replication.

5.5 Nature's Perfect Fits

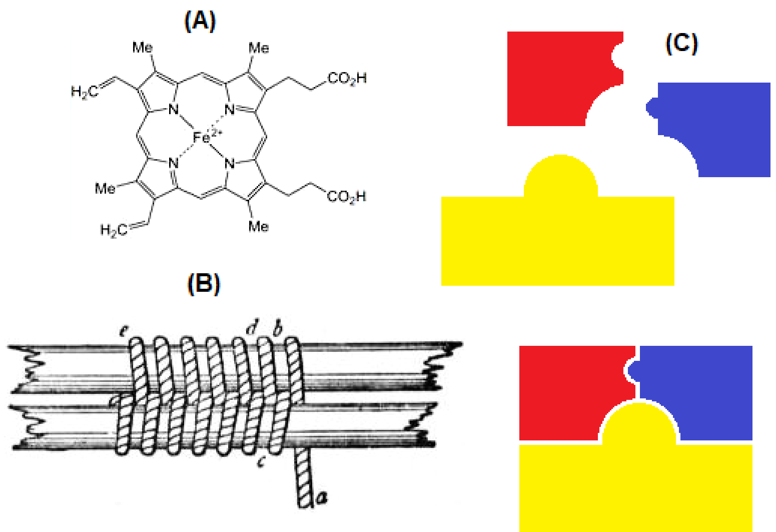

Figure 12: The unexpected harmony of natural components (A) The precise integration of the iron cation into the heme group. (B) The boundless possibilities that arise when a rope meets a stick. (C) Elements in nature, though originating from vastly different sources, often fit together like pieces of a jigsaw puzzle.

In nature, there are phenomena that seem remarkably strange, especially in biological systems. Consider how an iron cation fits perfectly into the hemoglobin heme, or how magnesium slots seamlessly into chlorophyll. These examples reflect a larger, almost magical complexity found when disparate elements come together. Just like a rope and stick—objects that could originate from different corners of the universe—yet when combined, they create an array of structures from knots to houses. This can be likened to a jigsaw puzzle, where each piece arrives from an unrelated source, yet fits together with precision. The reason for these coincidences lies in the computational nature of the universe. When A fits into B perfectly, this is not merely chance, but a reflection of a computational reality in the universe, as a result of 6th consequence. The origin or method of creation for A and B is irrelevant; their compatibility is determined solely by the underlying computational rules.

5.6 Observers

Observers play a central role in physics, as the description of reality depends on the perspective of the observer. In quantum mechanics, observation requires a measurement device that interacts with the system, which inherently changes the system's state due to the collapse of the wave function. This concept is highlighted by the measurement problem, where the observer's interaction fundamentally influences the outcome. In thermodynamics, the act of observation can be connected to the erasure of information. According to Landauer's principle, erasing one bit of information dissipates at least $k_B T ln(2)$ amount of energy as heat, where k_B is the Boltzmann constant and T is the temperature of the environment. This relationship signifies that observation, as a form of computation, as stated by the 4th postulate.

A simple model of an observer consists of three components: a sensorium, a device that performs the measurement of the system and relays the information, and a processor that interprets this information to produce an output description. The sensorium detects and interacts with the system, while the processor analyzes the gathered data to form a coherent representation of the observed phenomena.

An intriguing phenomenon in the context of observation is an observer making observations about itself, which is often associated with consciousness. This self-referential capability is considered a defining feature of consciousness by many scientists. Consciousness, as explored by prominent scientists, is often described as the state of being aware of and able to think about one's own experiences and environment.

If consciousness is defined as the ability of an observer to make observations about itself, then there are several analogous examples in the computational world. For instance, computer programs can read, analyze, and even modify their own code, a concept known as reflection or self-reference. A computer equipped with universal computational power is capable of performing any computable function on its own description, thanks to the foundational idea of Turing completeness. This capacity stems from the remarkable fact that a universal computational device, capable of running an infinite variety of programs, requires only a finite amount of information to describe itself. This property allows such systems to engage in self-reflection, akin to the concept of consciousness in biological entities, where introspective analysis becomes a part of its computational process.

Essentially, a conscious entity has the capacity to read a description of itself as well as its environment and to process both through its computational power. Even simple organisms like bacteria exhibit a basic form of this ability, as they can sense their environment and adjust their behavior accordingly, such as moving toward nutrients or away from harmful substances. Through evolution, more complex organisms have developed sophisticated mechanisms for self-awareness. The human brain, for instance, has evolved to create a detailed representation of itself while also accessing and processing information about the external environment. This evolutionary process has resulted in the ability to introspect, adapt, and make informed decisions, reflecting a deeper, more nuanced form of consciousness. The interplay between processing self-information and environmental information forms the basis for adaptive, intelligent behavior, akin to what is understood as consciousness.

Thus, consciousness might not be as mysterious or magical a phenomenon as it is often perceived to be. It could simply be the result of the brain's capacity for processing self-referential and environmental information, a capability that has gradually evolved over time. While it is true that the brain operates on a microscopic scale where quantum effects may play a role, these quantum processes do not imply anything beyond the scope of computation. Quantum computations, despite their potential complexity and the probabilistic nature of quantum mechanics, are still ultimately computations that can be described within the framework of computational theory.

5.7 Passive Organizational Power

One could conceptualize two distinct types of organizational powers. The first type is the most apparent, represented by a machine with organizational power, such as a brain, which actively participates in the process. This embodies an active process of organization and adaptation. The second type is a passive process, exemplified by an algorithm or program that exploits the rules of nature to yield a highly organized and complex product. A pertinent example of this is life itself, which primarily evolves through natural selection. Furthermore, primordial life, existing before the Last Universal Common Ancestor (LUCA), may have utilized mechanisms akin to the accretion model described earlier. Optimizing solutions to certain problems often necessitates a passive approach; for instance, when attempting to guess a password, the latter passive method frequently proves more effective. Similarly, problems like the traveling salesman problem and the training of neural networks showcase the efficacy of this passive method. An analogous example in life could be the way ecosystems develop and stabilize over time, where complex interactions and relationships emerge without a central directive, allowing for a self-organizing structure that results from passive processes over extended periods.

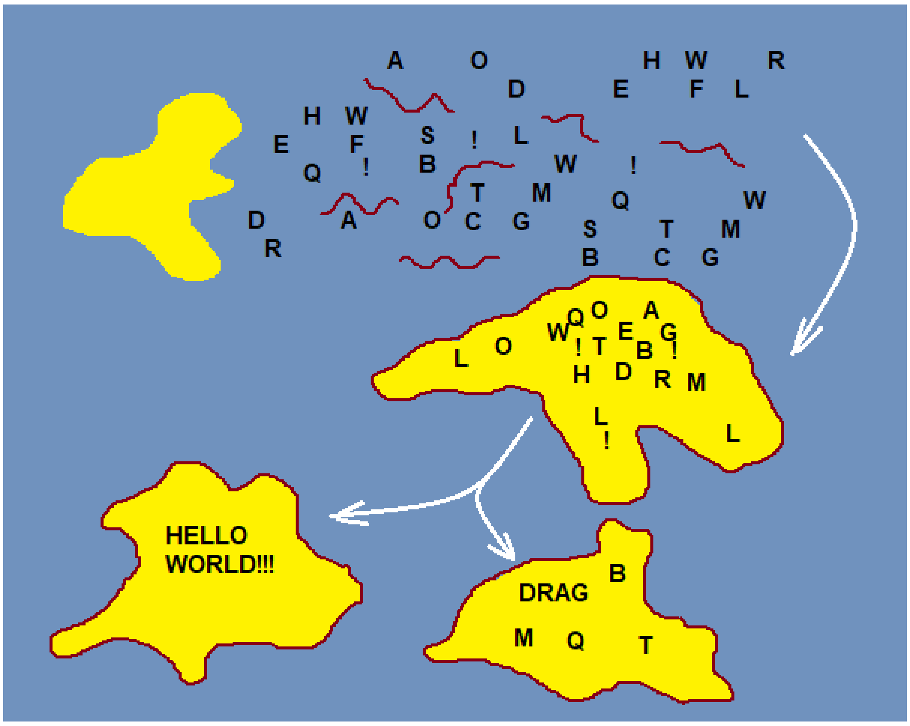

Figure 13: Finite Components and the Role of Organizational Fluid in Universal Computation: Even a device with universal computational power requires only a finite amount of information and can be constructed from a finite set of building blocks possessing the necessary computational attributes. An organizational fluid, capable of fission, fusion, and concentration of matter, can assist in the assembly of such a device.

However, whether it is the brain or nature, both possess universal computational power, at least asymptotically. The types of creations resulting from brain activity differ significantly from those arising in nature. Human brains have engineered artifacts characterized by precise order and intentionality, exemplified by complex machinery, sophisticated technology, and structured environments. In contrast, nature often produces outcomes that resemble Rube Goldberg machines—remarkably effective in their functionality yet seemingly chaotic in their organization.

A universal constructor requires a finite amount of information and, crucially, a finite quantity of building blocks. This raises the intriguing possibility of an organizational fluid that dynamically flows, collecting these components and assembling them into a universal constructor. Such a fluid could represent the underlying processes or principles that govern the arrangement and interaction of matter, effectively enabling the emergence of complex structures from simpler elements.

5.8 RNA, Proteins, and Nano-Machines

Life presents an exceptionally fascinating system for study, intersecting not only fields like quantum biology but also fundamental theories in physics, such as cosmology and string theory, as well as mathematical models that attempt to describe life itself. Structures like RNA, with its base-pairing properties, and protein-based nanomachines, such as the flagellar motor and polymerases, stand in stark contrast to ordinary matter like rocks, planets, and stars. These biological components provoke the question: what makes life so distinct? Life bears more resemblance to a computational system than to these inert objects. The previous discussion explored the behavior of life through the lens of computational theory, specifically through the principles of computational matter physics, which postulate that matter and its computational properties are inseparable and that matter itself is a form of computation. This leads into an examination of how these theories apply explicitly to the matter of life, including proteins, ribozymes, and nanomachines.

One of the first key distinctions to make when applying computational theories to biomolecular structures is the continuous nature of these biological systems, as opposed to the abstract, discrete systems typically discussed in computational models. Despite this apparent difference, the transition from abstract computation to the continuous dynamics of biomolecules is both elegant and intriguing.

The Cellular Automata implementation of Von Neumann's Universal Constructor (VNUC), as outlined in the previous section, involved a function bank $G = \{g_1, \ldots, g_N\}$ and a tape $X = x_M \ldots x_1$, where the operation $F = G(X) = g'_n \ldots g'_1$ with $g'_i \in G$ was executed by the VNUC. Although biological constructs such as hands or proteins appear to be continuous in nature, they exhibit strikingly modular behavior. For instance, the human hand, with its independently movable components—fingers, joints, a flexible palm, and a mobile wrist—can, when orchestrated by brain signals, create an array of complex objects, from clay pots to the machines that fabricate computers. Similarly, a protein's structure and function are wholly determined by its peptide sequence, implying that a modular computational architecture is deeply embedded in its seemingly continuous nature. This highlights an underlying modularity in biological systems that mirrors the discrete, modular framework seen in artificial constructors like the VNUC.

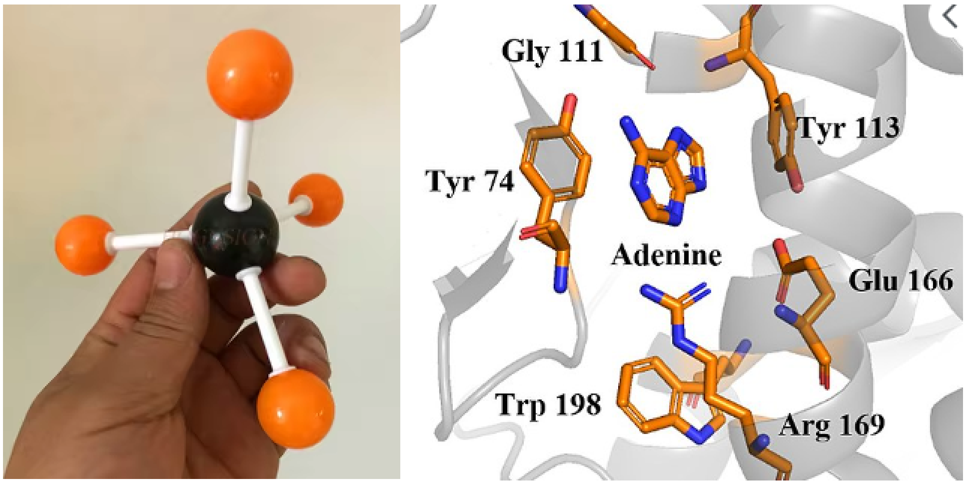

Figure 14: Hands, with their modular and flexible structure, can perform a wide variety of tasks, such as assembling molecular models out of ball-and-stick components, analogous to proteins that synthesize complex molecules with precision.

Protein folding is significantly influenced by electron delocalization, as explained through molecular orbital theory. In pi-stacking, for example, the delocalization of pi-electrons across aromatic rings allows for stabilizing interactions, which are crucial in maintaining the tertiary structure of proteins. Similarly, hydrogen bonding, a key force in protein folding, involves the delocalization of electrons between hydrogen atoms and electronegative atoms like oxygen or nitrogen. These forces, driven by electron delocalization, play an essential role in the overall stability and structural integrity of the protein.

Molecular synthesis can be understood as a transport phenomenon where molecular groups are transferred from one molecule to another. As molecules like ribonucleosides and amino acids form polymers, they introduce new degrees of freedom due to their folded structures. During chemical reactions, the transport of molecular groups is coupled to these higher-level degrees of freedom, which involve multiple molecular regions. This coupling leads to translocation and conformational changes in the molecules. Consequently, the transfer of molecular groups, as well as electrons and protons at the lower level, translates into the mechanical motion of nano machines, blurring the lines between chemistry and mechanics.

> *"Life is only a special and very complicated form of the motion of matter."*
> – Cyril Ponnamperuma

Motion is a fundamental aspect of computation theory, as evidenced by the operation of Turing Machines, which feature movable components essential for their functionality. Similarly, the Von Neumann Universal Constructor (VNUC) incorporates motion as a critical element in executing its functions. This incorporation of motion not only facilitates the carrying out of computational tasks but also simplifies the overall process, allowing for the dynamic manipulation of components that is crucial for constructing complex structures and performing intricate computations. Quantum mechanically, motion arises from the phenomenon of delocalization, where particles such as electrons exist in a superposition of states rather than being confined to a specific location. This delocalization allows for the exploration of multiple potential paths and interactions simultaneously, leading to observable changes in the position and behavior of particles.

Life can be viewed as a computational theory of motion, where molecular structures encode the mechanisms for self-driven motion. This encoding manifests through intricate interactions and dynamic processes, allowing molecules to undergo transformations that drive biological functions. The computational power inherent in these molecular motion systems is sufficient to facilitate the construction of a self constructing universal constructor.

Understanding how proteins and ribozymes work may seem difficult, but there are examples that help in grasping their function if studied properly. For instance, consider the versatile nature of hands—they can perform numerous tasks. Hands could theoretically replace proteins and ribozymes in a ball-and-stick model of life, where DNA and cell wall components are modeled as simple ball and stick versions of them. However, a significant limitation of this analogy is that hands would not be able to replicate themselves. It is conceivable, though, to imagine mechanical versions of hands that, using mechanical parts, could accomplish such replication. These mechanical hands would be capable of tasks like DNA replication and synthesizing new pairs of hands from their constituent building blocks. How is it that hands can perform such a wide range of functions? Hands possess a vast number of degrees of freedom, including the intricate movements of fingers, each finger operating independently within certain constraints. There exists a path through these degrees of freedom such that objects interacting with the hand are transformed into new objects.

An automated machine can be conceptualized as comprising four key components: a **controller**, the **actuated system** (the part being driven), a **feedback system**, and a **driver**. The controller directs the actuated system along a defined trajectory through its degrees of freedom, continuously adjusting its movement based on feedback to ensure accurate execution. The feedback system provides the controller with real-time signals about the output, and the driver supplies the controller with the necessary energy for its operation. The **workpiece** is the object that is acted upon by the automated system.

The mechanical hand can be viewed as such an automated system, where the driver supplies energy in the form of a square wave, and the controller directs this energy to the appropriate part of the actuator, which consists of the joints of the hand acting as pivots for the levers represented by the skeletal components. A feedback signal specifies the position of the actuated system. When the hand interacts with the workpiece, the system encounters a random, but possibly smooth, potential. The driver applies sufficient force to overcome this potential. The operation of this automated system is divided into micro-operations, each carried out by the driver in a modular manner. The potential of the actuated system features deep wells, where the system settles after each micro-operation during the inactivated phase of the square wave signal. The **driver** consists of predefined functions that execute the micro-operations from a function bank. An input tape describes a program based on this function bank, enabling the driver to carry out the operation.

Let the degrees of freedom of the mechanical hand be given by $\Theta = \{\theta_1, \ldots, \theta_n\}$. Then, the actuator component consists of its kinetic and potential energies, $K_a(\dot{\Theta})$ and $V_a(\Theta)$, respectively. The micro-operations are expressed through

$$G = \{\partial_{\theta_i} V_a(\Theta) \,|\, \theta_i \in \Theta\}$$

.

If the workpiece is described by a set of parameters $\Xi = \{\xi_1, \ldots, \xi_m\}$, which characterize its state and potential $V_w(\Xi)$, such that its definite states are represented by wells in $V_w(\Xi)$, then the universality of the mechanical hand, described by the parameter set Θ, with respect to the workpiece described by Ξ, lies in the ability to couple the Ξ system to the Θ system. This coupling enables the construction of a universal constructor using the Ξ system; in fact, another mechanical hand can be constructed through this process. The preceding discussion assumed a continuous system; however, similar considerations could be applied to discrete systems and hybrid systems as well.

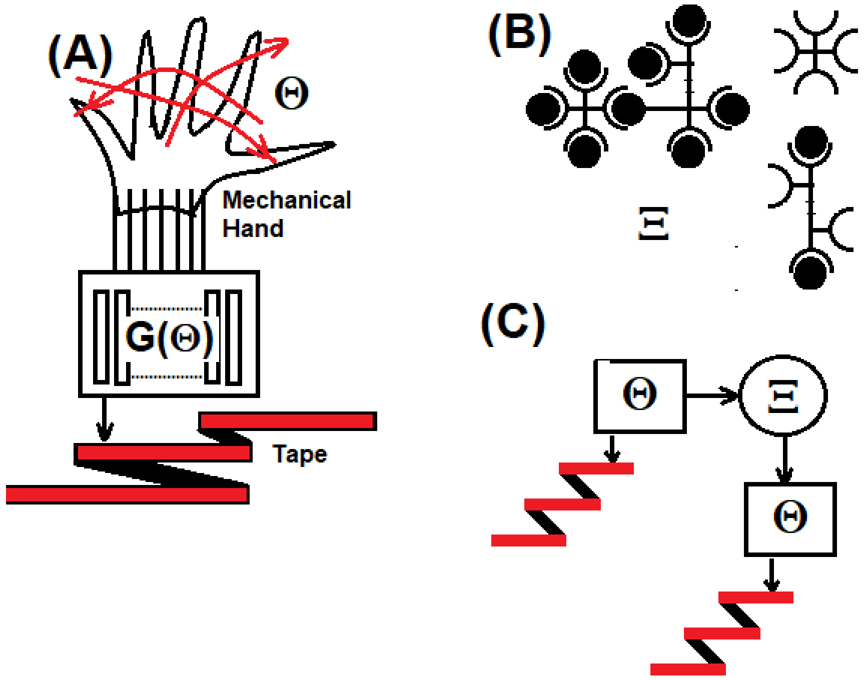

Figure 15: The diagram illustrates a model of the mechanical hand as a universal constructor with a function bank $G(\Theta)$ (A). The workpiece consists of the Ξ degrees of freedom (B). The Θ system couples to the Ξ system in such a way that a replica of the Θ system can be created, as it possesses universal computational power (C).

One must now consider how such a phenomenon could arise naturally: a universal constructor that can construct itself and can also emerge from a random pool of components, as is the case with the problem of the origin of life. Indeed, while a mechanical hand—characterized by independently movable fingers and comprehensible micro-operations—may be easy for the human brain to conceptualize, it poses a significant challenge for nature. This is likely the reason why, within living cells, there are no mechanical hand-like structures; instead, proteins exist. While proteins are extremely difficult for the human mind to grasp, they appear to pose no such challenge for nature. This discrepancy arises because while both the human brain and nature function as computational systems, albeit with different coding schemes. What is easy for the human mind may not be so for nature, what is easy for the nature may not be so for the human mind. A more mathematical way to express this is that Kolmogorov complexity is relative to the computational system in question. While there are theorems in information complexity stating that an optimized prefix coding machine exists, nature operates based on what has the simplest Kolmogorov complexity within the language it uses. In this context, peptides and RNA chains outperform a mechanical hand in terms of simplicity. Where the human hand requires billions of cells to form, nature's constructs, such as proteins and RNA, achieve complexity through far more efficient coding schemes.

What makes polymers, particularly peptides and RNA, so special? There must be something remarkable about the universe that led to the creation of these two essential polymers. Or most likely, it might be that there is something inherently unique about the shared properties of these polymers that contributed to their fundamental role in life's emergence. These polymers consist of numerous degrees of freedom, with individual units capable of forming hydrogen bonds and covalent bonds. This structure is somewhat analogous to a special cellular automata, where the units are arranged in a linear sequence but possess the capacity to fold into intricate three-dimensional structures through forming weak and string bonds through delocalization of protons(H^+ ions) and electrons.

In peptides, the degrees of freedom arise primarily from the backbone and side-chain rotations. The peptide backbone is composed of repeating units of amide bonds, which restrict rotation due to partial double-bond character. However, two main degrees of freedom are associated with each amino acid residue: the ϕ and ψ torsion angles around the α carbon. The side chains of the amino acids contribute additional rotational degrees of freedom, depending on the specific amino acid. These chains vary in rigidity, with bulkier or aromatic side chains introducing more constraints. The rigid parts of peptides involve the peptide bonds, limiting conformational flexibility, while the free parts are represented by the rotations around the ϕ and ψ angles and the side-chain orientations, which allow peptides to adopt different secondary structures such as α-helices and β-sheets.

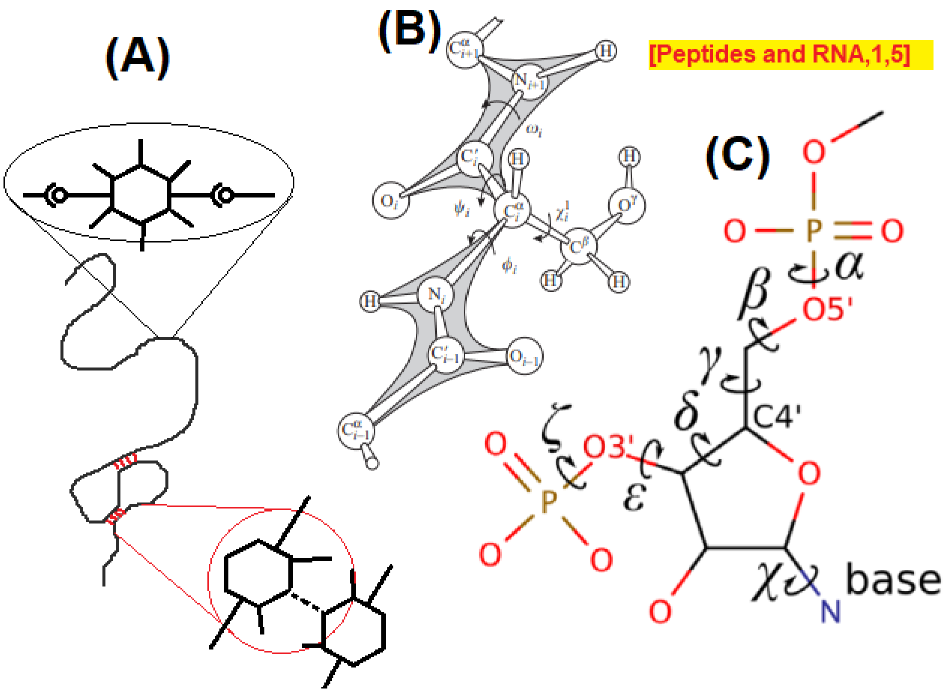

Figure 16: Both peptides and RNA share a common structural pattern: they consist of individual units—amino acids for peptides and nucleosides for RNA—connected by flexible joints, with each unit possessing the ability to interact with other molecules (A). The degrees of freedom in peptide chains (B) and RNA (C) play a crucial role in determining their structural flexibility and functional capabilities. This flexible polymer structure represents nature's alternative for a system that can potentially function collectively as a universal constructor. Like the mechanical hand, it can grasp, manipulate, and move objects, but unlike the mechanical hand, it possesses a far simpler form and has the likelyhood to emerge from a random pool of simple chemicals.

In RNA, the degrees of freedom are more complex due to the additional sugar-phosphate backbone and the nitrogenous base attachments. Each nucleotide in RNA features several key torsional angles that define its conformational flexibility. The γ angle corresponds to the rotation around the $C4' - C5'$ bond of the ribose sugar, while the δ angle describes the rotation around the $C3' - C4'$ bond within the ribose ring itself. Moving into the phosphate backbone, the ϵ angle involves the rotation around the $C3' - O3'$ bond, and the β angle defines the rotation around the $C5' - O5'$ bond. Additionally, the angles η and α describe rotations around the $P - O3'$ and $P - O5'$ bonds, respectively, further contributing to the backbone's flexibility. The χ angle governs the rotation between the ribose and the nitrogenous base, providing another layer of freedom that influences the base pairing and stacking interactions. The backbone's flexibility, combined with these torsional degrees of freedom, allows RNA to fold into intricate three-dimensional structures crucial for its biological functions.

The generators of peptides and RNA, which perform micro-operations, are the 20 amino acids and the nucleosides for peptides and RNA, respectively. This system possesses the unique property that the tape itself is composed of the actual functional units, allowing the process to occur without the need for an external control unit. Which is an elegant way to implement a universal constructor in nature. This essentially enforces the postulate of computational matter physics, which asserts that matter is fundamentally computational. These polymer machines can couple their degrees of freedom with those of other molecules, as well as their own, enabling them to establish a universal constructor.

6 References

6.1 Life and its Complexity

[1] Zimmer, C. (2017, March 1). Scientists say Canadian bacteria fossils may be Earth's oldest. *The New York Times.* `https://www.nytimes.com/2017/03/01/science/earths-oldest-bacteria-fossils.html`

[2] Noffke, N., Christian, D., Wacey, D., Hazen, R. M. (2013). Microbially induced sedimentary structures recording an ancient ecosystem in theca.3.48 Billion-Year-Old Dresser Formation, Pilbara, Western Australia. *Astrobiology, 13*(12), 1103–1124.

[3] Saladino, R., Carota, E., Botta, G., Kapralov, M., , . ., Rozanov, A. Y., Krasavin, E. A., Di Mauro, E. (2015). Meteorite-catalyzed syntheses of nucleosides and of other prebiotic compounds from formamide under proton irradiation. *Proceedings of the National Academy of Sciences of the United States of America, 112*(21).

[4] Criado-Reyes, J., Bizzarri, B. M., Garcıa-Ruiz, J. M., Saladino, R., Di Mauro, E. (2021). The role of borosilicate glass in Miller–Urey experiment. *Scientific Reports, 11*(1). `https://doi.org/10.1038/s41598-021-00235-4`

[5] Han, T., Runnegar, B. (1992). Megascopic Eukaryotic Algae from the 2.1-Billion-Year-Old Negaunee Iron-Formation, Michigan. *Science, 257*(5067), 232–235.

[6] Rahman, I. (2016, December 6). PALAEONTOLOGY — Article: Fossil Focus ¿ Fossil Focus: Acritarchs. *PALAEONTOLOGY Online.* `https://www.palaeontologyonline.com/articles/2016/fossil-focus-acritarchs/`

[7] Barras, C. (2018, April 30). A fossil may rewrite the story of how plants first lived on land. *New Scientist.* `https://www.newscientist.com/article/2167645-a-fossil-may-rewrite-the-story-of-how-plants`

[8] Grens, K. (2020, February 25). Oldest green algae fossil discovered in China. *The Scientist Magazine®.* `https://www.the-scientist.com/news-opinion/oldest-green-algae-fossil-discovered-in-china`

[9] Cabeen, M. T., Jacobs-Wagner, C. (2007). Skin and bones: the bacterial cytoskeleton, cell wall, and cell morphogenesis. *Journal of Cell Biology, 179*(3), 381–387.

[10] Porter, S. L., Wadhams, G. H., Armitage, J. P. (2011). Signal processing in complex chemotaxis pathways. *Nature Reviews Microbiology, 9*(3), 153–165.

[11] Davies, J. A. (2005). *Mechanisms of Morphogenesis.* Elsevier Academic Press.

[12] Scholey, J. M., Brust-Mascher, I., Mogilne, A. *Cell division.* [Incomplete reference]

[13] Koppers, M., Özkan, N., FarıAs, G. G. (2020). Complex interactions between Membrane-Bound organelles, biomolecular condensates and the cytoskeleton. *Frontiers in Cell and Developmental Biology, 8.*

[14] Hillis, D. M., Price, M. V., Hill, R. W., Hall, D. W. (2022). *Principles of Life.* Macmillan Learning.

6.2 Peptides and RNA

[1] Fonseca, R., Pachov, D. V., Bernauer, J., Van Den Bedem, H. (2014). *Characterizing RNA ensembles from NMR data with kinematic models.* Nucleic Acids Research, 42(15), 9562–9572. https://doi.org/10.1093/nar/gku707

[2] Kriwacki, R. W., Hengst, L., Tennant, L., Reed, S. I., Wright, P. E., Dueber, J. E., Yeh, B. J., Bhattacharyya, R. P., Lim, W. A. (2009). *Protein dynamism and evolvability.* Science. https://www.indiana.edu/~lynchlab/PDF/evocellbio/wk10_Tokuriki_2009.pdf

[3] Yang, G., Miton, C. M., Tokuriki, N. (2020). *A mechanistic view of enzyme evolution.* Protein Science, 29(8), 1724–1747. https://doi.org/10.1002/pro.3901

[4] Jayaraman, V., Toledo-Patiño, S., Noda-García, L., Laurino, P. (2022). *Mechanisms of protein evolution.* Protein Science, 31(7), e4362. https://doi.org/10.1002/pro.4362

[5] Hansmann, U. (2003). *Protein physics—a course of lectures by Alexei V. Finkelstein and Oleg B. Ptitsyn, 2002.* Academic Press. , 354 pp., ISBN: 0122567811. Bulletin of Mathematical Biology, 65(5), 961–962. https://doi.org/10.1016/s0092-8240(03)00043-0

[6] Koshlan, T., Kulikov, K. (2018). *Mathematical modeling of protein complexes.* In *Biological and medical physics series.* https://doi.org/10.1007/978-3-319-98304-2

6.3 Origin of Life and Prebiotic Chemistry

[1] Bugg, T. D. H. *Bacterial Peptidoglycan Biosynthesis and its Inhibition.*

[2] Nobel Laureate Lecture: Dr. Venkatraman "Venki" Ramakrishnan. (2011, January 14). *YouTube.* Retrieved September 6, 2022, from https://www.youtube.com/watch?v=MktZsKh-zXQ

[3] Build-a-Cell seminar Loren Williams: The Origins and Evolution of the Ribosome. (2020, November 16). *YouTube.* Retrieved September 6, 2022, from https://www.youtube.com/watch?v=674Uxjmnyqs

[4] Osterman, I. A., Dikhtyar, Y. Y., Bogdanov, A. A., Dontsova, O. A., Sergiev, P. V. (2015). Regulation of Flagellar Gene Expression in Bacteria. *Biochemistry. Biokhimiia, 80*(11), 1447–1456. https://doi.org/10.1134/S000629791511005X

[5] Aldridge, P., Hughes, K. T. (2002). Regulation of flagellar assembly. *Current opinion in microbiology, 5*(2), 160–165. https://doi.org/10.1016/s1369-5274(02)00302-8

[6] Rohs, P., Bernhardt, T. G. (2021). Growth and Division of the Peptidoglycan Matrix. *Annual review of microbiology, 75,* 315–336. https://doi.org/10.1146/annurev-micro-020518-120056

[7] Dajkovic, A., Lutkenhaus, J. (2006). Z ring as executor of bacterial cell division. *Journal of molecular microbiology and biotechnology, 11*(3-5), 140–151. https://doi.org/10.1159/000094050

[8] Viollier, P. H., Thanbichler, M., McGrath, P. T., West, L., Meewan, M., McAdams, H. H., Shapiro, L. (2004). Rapid and sequential movement of individual chromosomal loci to specific subcellular locations during bacterial DNA replication. *Proceedings of the National Academy of Sciences of the United States of America, 101*(25), 9257–9262. https://doi.org/10.1073/pnas.0402606101

[9] Jalal, A., Le, T. (2020). Bacterial chromosome segregation by the ParABS system. *Open biology, 10*(6), 200097. https://doi.org/10.1098/rsob.200097

[10] Madigan, M. T., Martinko, J. M., Stahl, D. A., Clark, D. P. (2010, December 27). *Brock Biology of Microorganisms (13th Edition)* (13th ed.). Benjamin Cummings.

[11] Chemistry, O. P. R. S. B. (1999, October 19). *The Organic Chemistry of Enzyme-Catalyzed Reactions* (1st ed.). Academic Press.

[12] Lilley, D. M. J., Eckstein, F., Rodnina, M. V. (2008). *Ribozymes and RNA Catalysis.* Van Haren Publishing.

[13] *Michaelis-Menten Kinetics and Briggs-Haldane Kinetics.* (n.d.). https://depts.washington.edu/wmatkins/kinetics/michaelis-menten.html

[14] Brown, J. (2023, June 28). How NOT to think about cells. *SubAnima.* https://www.subanima.org/veritasium/

[15] SubAnima. (2022, October 14). How NOT to think about cells [Video]. *YouTube.* https://www.youtube.com/watch?v=jPhvic-eqbc

[16] Güttinger, S., Laurell, E., Kutay, U. (2009). Orchestrating nuclear envelope disassembly and reassembly during mitosis. *Nature Reviews Molecular Cell Biology, 10*(3), 178–191.

[17] Zhao, H., Pykäläinen, A., Lappalainen, P. (2011). I-BAR domain proteins: linking actin and plasma membrane dynamics. *Current Opinion in Cell Biology, 23*(1), 14–21.

[18] Barlowe, C. (2010). ER sheets get roughed up. *Cell, 143*(5), 665–666.

[19] Walczak, C., Heald, R. (2008). Mechanisms of mitotic spindle assembly and function. In *International review of cytology* (pp. 111–158).

[20] Alberts, B. (2002). *Molecular biology of the cell.*

[21] Leondaritis, G., Eickholt, B. J. (2015). Short Lives with Long-Lasting Effects: Filopodia Protrusions in Neuronal Branching Morphogenesis. *PLOS Biology, 13*(9), e1002241.

[22] The Royal Institution. (2019, December 19). What is Life? - with Paul Nurse [Video]. *YouTube.* https://www.youtube.com/watch?v=_z-SUo2wP4I

[23] Cartwright, J. H. E. (2024). 2500 years ago scientific theories of the origin of life arose in ancient Greece. *Received: 8 January 2024 / Accepted: 27 March 2024.*

[24] Augustin, M., Pellò, C. (2021). Life and lifeforms in early Greek atomism. *Apeiron.* https://doi.org/10.1515/apeiron-2021-0035. Published online July 12, 2021.

6.4 Prebiotic Chemistry

[1] Miller, S.L., Urey, H.C. Oró, J. Origin of organic compounds on the primitive earth and in meteorites. *J Mol Evol 9*, 59–72 (1976). https://doi.org/10.1007/BF01796123

[2] Criado-Reyes, J., Bizzarri, B.M., García-Ruiz, J.M. et al. The role of borosilicate glass in Miller–Urey experiment. *Sci Rep 11*, 21009 (2021). https://doi.org/10.1038/s41598-021-00235-4

[3] Parker, E. T., Cleaves, H. J., Dworkin, J. P., Glavin, D. P., Callahan, M., Aubrey, A., Lazcano, A., Bada, J. L. (2011). Primordial synthesis of amines and amino acids in a 1958 Miller H2S-rich spark discharge experiment. *Proceedings of the National Academy of Sciences of the United States of America, 108*(14), 5526–5531. https://doi.org/10.1073/pnas.1019191108

[4] Glindemann, D., De Graaf, R. M., Schwartz, A. W. (1999). Chemical reduction of phosphate on the primitive earth. *Origins of life and evolution of the biosphere: the journal of the International Society for the Study of the Origin of Life, 29*(6), 555–561.

[5] Schwartz A. W. (2006). Phosphorus in prebiotic chemistry. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences, 361*(1474), 1743–1749.

[6] Ferus, M., Knížek, A., Civiš, S. (2015). Meteorite-catalyzed synthesis of nucleosides and other prebiotic compounds. *Proceedings of the National Academy of Sciences of the United States of America, 112*(23), 7109–7110.

[7] Saladino, R., Botta, G., Delfino, M., Di Mauro, E. (2013). Meteorites as catalysts for prebiotic chemistry. *Chemistry (Weinheim an der Bergstrasse, Germany), 19*(50), 16916–16922.

[8] Powner, M., Gerland, B. Sutherland, J. Synthesis of activated pyrimidine ribonucleotides in prebiotically plausible conditions. *Nature 459*, 239–242 (2009).

[9] Wikipedia contributors. (2022, September 12). Transition metal carboxylate complex. *Wikipedia.* Retrieved September 22, 2022, from: `https://en.wikipedia.org/wiki/Transition_metal_carboxylate_complex`

[10] Frenkel-Pinter, M., Bouza, M., Fernández, F.M. et al. Thioesters provide a plausible prebiotic path to proto-peptides. *Nat Commun 13*, 2569 (2022).

[11] Huber, C., Eisenreich, W., Hecht, S., Wächtershäuser, G. (2003). A possible primordial peptide cycle. *Science (New York, N.Y.), 301*(5635), 938–940.

[12] Saladino, R., Botta, G., Bizzarri, B. M., Di Mauro, E., Garcia Ruiz, J. M. (2016). A Global Scale Scenario for Prebiotic Chemistry: Silica-Based Self-Assembled Mineral Structures and Formamide. *Biochemistry, 55*(19), 2806–2811.

[13] Adewuyi, Y.G., Cho, S.Y., Tsay, R., Carmichael, G.R. (1984). Importance of formaldehyde in cloud chemistry. *Atmospheric Environment, 18*, 2413-2420.

[14] Gerack, C. J., McElwee-White, L. (2014). Formylation of amines. *Molecules (Basel, Switzerland), 19*(6), 7689–7713.

[15] Costanzo, G., Saladino, R., Crestini, C., Ciciriello, F., Di Mauro, E. (2007). Nucleoside phosphorylation by phosphate minerals. *The Journal of biological chemistry, 282*(23), 16729–16735.

[16] Krasnopolsky, V. A. (1989). Vega mission results and chemical composition of Venusian clouds. *Icarus, 80*(1), 202–210.

[17] Milojevic, T., Treiman, A. H., Limaye, S. S. (2021). Phosphorus in the Clouds of Venus: Potential for Bioavailability. *Astrobiology, 21*(10), 1250–1263.

[18] *Apatite Leaching using H2SO4 Methanol.* (2018, September 24). Metallurgist Mineral Processing Engineer. Retrieved September 22, 2022, from `https://www.911metallurgist.com/apatite-leaching-h2so4-me`

[19] `https://courses.lumenlearning.com/suny-geneseo-astronomy/chapter/titan-and-triton/`

[20] Sleep N. H. (2010). The Hadean-Archaean environment. *Cold Spring Harbor perspectives in biology, 2*(6), a002527.

[21] Shaw, G. H. (2014). Evidence and arguments for methane and ammonia in Earth's earliest atmosphere and an organic compound–rich early ocean. *Earth's Early Atmosphere and Surface Environment.* `https://doi.org/10.1130/2014.2504(01)`

[22] Sleep N. H. (2010). The Hadean-Archaean environment. *Cold Spring Harbor perspectives in biology, 2*(6), a002527.

[23] Wächtershäuser, G. (1992). Groundworks for an evolutionary biochemistry: The iron-sulphur world. *Progress in Biophysics and Molecular Biology, 58*(2), 85–201.

[24] Brack, A. (1998, December 28). *The Molecular Origins of Life: Assembling Pieces of the Puzzle* (1st ed.). Cambridge University Press.

[25] Lee, J. K., Samanta, D., Nam, H. G., Zare, R. N. (2019). Micrometer-Sized Water Droplets Induce Spontaneous Reduction. *Journal of the American Chemical Society, 141*(27), 10585–10589. https://doi.org/10.1021/jacs.9b03227

[26] *Venus The atmosphere.* (n.d.). *Encyclopedia Britannica.* Retrieved September 22, 2022, from https://www.britannica.com/place/Venus-planet/The-atmospher

[27] Sivakova, S., Rowan, S. J. (2005). Nucleobases as supramolecular motifs. *Chemical Society Reviews, 34*(1), 9.

[28] Yang, H., Xi, W. (2017). Nucleobase-Containing Polymers: Structure, synthesis, and applications. *Polymers, 9*(12), 666.

[29] Root-Bernstein, R., Baker, A., Rhinesmith, T., Turke, M. J., Huber

[30] Downey, A. M., Richter, C., Pohl, R., Mahrwald, R., Hocek, M. (2024). Direct one-pot synthesis of nucleosides from unprotected or 5-O-monoprotected D-ribose. *[Journal Name].*

[31] Diafa, S., Hollenstein, M. (2015). Generation of aptamers with an expanded chemical repertoire. *[Journal Name].*

[32] Vorbrüggen, H. (1996). Some recent trends and progress in nucleoside synthesis. *Acta Biochimica Polonica, 43*(1), 25–36.

[33] Kato, Y., Minakawa, N., Komatsu, Y., Kamiya, H., Ogawa, N., Harashima, H., Matsuda, A. (2005). New NTP analogs: The synthesis of 4'-thioUTP and 4'-thioCTP and their utility for SELEX. *Journal Name, Volume*(Issue), Page range.

[34] Schmidt, M. (2009). Xenobiology: A new form of life as the ultimate biosafety tool. *BioEssays, 31*(11), 1190–1195. https://doi.org/10.1002/bies.200900147

6.5 RNA World

[1] Petrov, A. S., Gulen, B., Norris, A. M., Kovacs, N. A., Bernier, C. R., Lanier, K. A., Fox, G. E., Harvey, S. C., Wartell, R. M., Hud, N. V., Williams, L. D. (2015). History of the ribosome and the origin of translation. *Proceedings of the National Academy of Sciences of the United States of America, 112*(50), 15396–15401.

[2] Build-a-Cell seminar Loren Williams: The Origins and Evolution of the Ribosome [Video]. YouTube. Retrieved September 22, 2022, from https://www.youtube.com/watch?v=674Uxjmnyqs

[3] Tamura K. (2011). Ribosome evolution: emergence of peptide synthesis machinery. *Journal of biosciences, 36*(5), 921–928.

[4] Davidovich, C., Belousoff, M., Bashan, A., Yonath, A. (2009). The evolving ribosome: from non-coded peptide bond formation to sophisticated translation machinery. *Research in microbiology, 160*(7), 487–492.

[5] Farias, S. T., Rêgo, T. G., José, M. V. (2014). Origin and evolution of the Peptidyl Transferase Center from proto-tRNAs. *FEBS open bio, 4*, 175–178.

[6] Rivas, M., Tran, Q., Fox, G. E. (2013). Nanometer scale pores similar in size to the entrance of the ribosomal exit cavity are a common feature of large RNAs. *RNA (New York, N.Y.), 19*(10), 1349–1354.

[7] Petrov, A. S., Bernier, C. R., Hsiao, C., Norris, A. M., Kovacs, N. A., Waterbury, C. C., Stepanov, V. G., Harvey, S. C., Fox, G. E., Wartell, R. M., Hud, N. V., Williams, L. D. (2014). Evolution of the ribosome at atomic resolution. *Proceedings of the National Academy of Sciences of the United States of America, 111*(28), 10251–10256.

[8] Lilley, D. M. J., Eckstein, F., Rodnina, M. V. (2008). Ribozymes and RNA Catalysis. Van Haren Publishing.

[9] Mutschler, H., Wochner, A., Holliger, P. (2015). Freeze-thaw cycles as drivers of complex ribozyme assembly. *Nature chemistry, 7*(6), 502–508.

[10] Mutschler, H., Taylor, A. I., Porebski, B. T., Lightowlers, A., Houlihan, G., Abramov, M., Herdewijn, P., Holliger, P. (2018). Random-sequence genetic oligomer pools display an innate potential for ligation and recombination. *eLife, 7*, e43022.

[11] Olasagasti, F., Rajamani, S. (2019). Lipid-Assisted Polymerization of Nucleotides. *Life (Basel, Switzerland), 9*(4), 83.

[12] J., L. D. M., Eckstein, F. (2008). Ribozymes and RNA catalysis. RSC Publishing.

[13] Mizuuchi, R., Blokhuis, A., Vincent, L., Nghe, P., Lehman, N., Baum, D. (2019). Mineral surfaces select for longer RNA molecules. *Chemical communications (Cambridge, England), 55*(14), 2090–2093.

[14] The Ribonuclease P Family By THOMAS A. HALL and JAMES W. BROWN.

[15] YouTube. (2014, October 13). Anna Marie Pyle (Yale U./HHMI) part 1: RNA structure. YouTube. Retrieved October 1, 2022, from `https://www.youtube.com/watch?v=WCrlm18KQ48`

[16] YouTube. (2020, November 16). Build-a-cell seminar Loren Williams: The origins and evolution of the ribosome. YouTube. Retrieved October 1, 2022, from `https://www.youtube.com/watch?v=674Uxjmnyqs`

[17] Ekland, E. H., Szostak, J. W., Bartel, D. P. (1995). Structurally complex and highly active RNA ligases derived from random RNA sequences. *Science (New York, N.Y.), 269*(5222), 364–370.

[18] Johnston, W. K., Unrau, P. J., Lawrence, M. S., Glasner, M. E., Bartel, D. P. (2001). RNA-catalyzed RNA polymerization: accurate and general RNA-templated primer extension. *Science (New York, N.Y.), 292*(5520), 1319–1325.

[19] Shechner, D. M., Grant, R. A., Bagby, S. C., Koldobskaya, Y., Piccirilli, J. A., Bartel, D. P. (2009). Crystal structure of the catalytic core of an RNA-polymerase ribozyme. *Science (New York, N.Y.), 326*(5957), 1271–1275.

[20] RNAfold server: `http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi`

[21] Kudella, P. W., Tkachenko, A. V., Salditt, A., Maslov, S., Braun, D. (2021). Structured sequences emerge from random pool when replicated by templated ligation. *Proceedings of the National Academy of Sciences of the United States of America, 118*(8).

[22] Layzer, D. (1980). The Hypercycle: A Principle of Natural Self-Organization. *M. Eigen, P. Schuster. The Quarterly Review of Biology, 55*(4), 434.

6.6 Additional Topics

[1] Pirajno, F., & Cawood, P. (2019). *Hydrothermal Processes and Mineral Systems* (Softcover reprint of the original 1st ed. 2009). Springer.

[2] Rajamani, S., Vlassov, A., Benner, S., Coombs, A., Olasagasti, F., & Deamer, D. (2008). Lipid-assisted synthesis of RNA-like polymers from mononucleotides. *Origins of Life and Evolution of the Biosphere: The Journal of the International Society for the Study of the Origin of Life*, 38(1), 57–74.

[3] Mutschler, H., Wochner, A., & Holliger, P. (2015). Freeze-thaw cycles as drivers of complex ribozyme assembly. *Nature Chemistry*, 7(6), 502–508.

[4] Segré, D., Ben-Eli, D., Deamer, D. W., & Lancet, D. (2001). The lipid world. *Origins of Life and Evolution of the Biosphere: The Journal of the International Society for the Study of the Origin of Life*, 31(1-2), 119–145.

[5] Albertsen, A. N., Duffy, C. D., Sutherland, J. D., & Monnard, P. A. (2014). Self-assembly of phosphate amphiphiles in mixtures of prebiotically plausible surfactants. *Astrobiology*, 14(6), 462–472.

[6] Chen, I. A., & Walde, P. (2010). From self-assembled vesicles to protocells. *Cold Spring Harbor Perspectives in Biology*, 2(7), a002170.

[7] J., L. D. M., & Eckstein, F. (2008). *Ribozymes and RNA Catalysis.* RSC Publishing.

[8] Mutschler, H., Taylor, A. I., Porebski, B. T., Lightowlers, A., Houlihan, G., Abramov, M., Herdewijn, P., & Holliger, P. (2018). Random-sequence genetic oligomer pools display an innate potential for ligation and recombination. *eLife*, 7, e43022.

[9] Mizuuchi, R., Blokhuis, A., Vincent, L., Nghe, P., Lehman, N., & Baum, D. (2019). Mineral surfaces select for longer RNA molecules. *Chemical Communications (Cambridge, England)*, 55(14), 2090–2093.

[10] Hall, T. A., & Brown, J. W. (2021). The Ribonuclease P Family.

[11] YouTube. (2014, October 13). Anna Marie Pyle (Yale U./HHMI) part 1: RNA structure. Retrieved October 1, 2022, from `https://www.youtube.com/watch?v=WCrlm18KQ48`

[12] YouTube. (2020, November 16). Build-a-cell seminar Loren Williams: The origins and evolution of the ribosome. Retrieved October 1, 2022, from `https://www.youtube.com/watch?v=674Uxjmnyqs`

[13] Ekland, E. H., Szostak, J. W., & Bartel, D. P. (1995). Structurally complex and highly active RNA ligases derived from random RNA sequences. *Science (New York, N.Y.)*, 269(5222), 364–370.

[14] Johnston, W. K., Unrau, P. J., Lawrence, M. S., Glasner, M. E., & Bartel, D. P. (2001). RNA-catalyzed RNA polymerization: accurate and general RNA-templated primer extension. *Science (New York, N.Y.)*, 292(5520), 1319–1325.

[15] Shechner, D. M., Grant, R. A., Bagby, S. C., Koldobskaya, Y., Piccirilli, J. A., & Bartel, D. P. (2009). Crystal structure of the catalytic core of an RNA-polymerase ribozyme. *Science (New York, N.Y.)*, 326(5957), 1271–1275.

[16] RNAfold server: `http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi`

[17] Kudella, P. W., Tkachenko, A. V., Salditt, A., Maslov, S., & Braun, D. (2021). Structured sequences emerge from random pool when replicated by templated ligation. *Proceedings of the National Academy of Sciences of the United States of America*, 118(8).

[18] Prywes, N., Blain, J. C., Del Frate, F., & Szostak, J. W. (2016). Nonenzymatic copying of RNA templates containing all four letters is catalyzed by activated oligonucleotides. *eLife*, 5, e17756.

[19] He, C., Gállego, I., Laughlin, B., Grover, M. A., & Hud, N. V. (2017). A viscous solvent enables information transfer from gene-length nucleic acids in a model prebiotic replication cycle. *Nature Chemistry*, 9(4), 318–324.

[20] Mayer, C., Schreiber, U., Dávila, M. J., Schmitz, O. J., Bronja, A., Meyer, M., Klein, J., & Meckelmann, S. W. (2018). Molecular Evolution in a Peptide-Vesicle System.

[21] Tekin, E., Annalena Salditt, Philipp Schwintek, Sree Wunnava, Langlais, J., Saenz, J., Tang, D., Schwille, P., Mast, C. B., & Braun, D. (2022). Prebiotic Foam Environments to Oligomerize and Accumulate RNA. *ChemBioChem*, 23(24).

[22] Morasch, M., Liu, J., Dirscherl, C. F., Ianeselli, A., Kühnlein, A., Vay, K. L., Schwintek, P., Islam, S. A., Corpinot, M. K., Scheu, B., Dingwell, D. B., Schwille, P., Mutschler, H., Powner, M. W., Mast, C. B., & Braun, D. (2019). Heated gas bubbles enrich, crystallize, dry, phosphorylate and encapsulate prebiotic molecules. *Nature Chemistry*, 11(9), 779–788.

[23] Lerin-Morales, K. M., Olguín, L. F., Mateo-Martí, E., & Colín-García, M. (2022). Prebiotic chemistry experiments using microfluidic devices. *Life*, 12(10), 1665.

[24] Sharma, A., Czégel, D., Lachmann, M., Kempes, C. P., Walker, S. I., & Cronin, L. (2023). Assembly theory explains and quantifies selection and evolution. *Nature*, 622(7982), 321–328.

[28] Hoffmann, H., Payton, D. W. (2018). Optimization by Self-Organized Criticality. *Scientific Reports, 8*(1).

[29] Bak, P., Chen, K., Creutz, M. (1989). Self-organized criticality in the 'Game of Life". *Nature, 342*(6251), 780–782.

[30] Vattay, G., Salahub, D. R., Csabai, I., Nassimi, A., Kaufmann, S. A. (2015). Quantum criticality at the origin of life. *Journal of Physics: Conference Series, 626*, 012023.

[31] Langton, C. (1990). Computation at the edge of chaos: Phase transitions and emergent computation. *Physica D: Nonlinear Phenomena, 42*(1–3), 12–37.

[32] Douglas Ashton. (2011b, April 8). Scale invariance in the critical Ising model [Video]. YouTube. `https://www.youtube.com/watch?v=fi-g2ET97W8`

[33] Gershenson, C. (2004). Introduction to Random Boolean Networks.

[34] Kauffman, S. (1969). Metabolic Stability and Epigenesis in Randomly Constructed Genetic Nets.

[35] Irwin, L., Méndez, A., Fairén, A., Schulze-Makuch, D. (2014). Assessing the possibility of biological complexity on other worlds, with an estimate of the occurrence of complex life in the milky way galaxy. *Challenges, 5*(1), 159–174.

[36] Mayer, C., Schreiber, U., Dávila, M. J., Schmitz, O. J., Bronja, A., Meyer, M., Klein, J., Meckelmann, S. W. (2018). Molecular Evolution in a Peptide-Vesicle System.

[37] Xue, M., Black, R. A., Cornell, C. E., Drobny, G. P., Keller, S. L. (2020). A Step toward Molecular Evolution of RNA: Ribose Binds to Prebiotic Fatty Acid Membranes, and Nucleosides Bind Better than Individual Bases Do. *ChemBioChem, 21*(19), 2764–2767.

[38] Lai, Liu, A. Chen, Edited by Bartel. (2021). Encapsulation of ribozymes inside model protocells leads to faster evolutionary adaptation. Massachusetts Institute of Technology, Cambridge, MA.

[39] Czerniak, T., Sáenz, J. (2022). Lipid membranes modulate the activity of RNA through sequence-dependent interactions. *Proceedings of the National Academy of Sciences of the United States of America, 119*(4).

[40] Black, R. A., Cohen, Z. R., Todd, Z. R., Maibaum, L., Catling, D. C. (2023). Stabilization of prebiotic vesicles by peptides depends on sequence and chirality. *Research Square (Research Square).*

[41] DasGupta, S., Zhang, S., Szostak, J. W. (2023). Molecular crowding facilitates Ribozyme-Catalyzed RNA assembly. *ACS Central Science, 9*(8), 1670–1678.

[42] Black, R. A., Blosser, M. C., Stottrup, B. L., Tavakley, R., Deamer, D. W., Keller, S. L. (2013). Nucleobases bind to and stabilize aggregates of a prebiotic amphiphile, providing a viable mechanism for the emergence of protocells. *Proceedings of the National Academy of Sciences of the United States of America, 110*(33), 13272–13276.

[43] Kahana, A., Lancet, D. (2021). Self-reproducing catalytic micelles as nanoscopic protocell precursors. *Nat Rev Chem, 5*(12), 870-878. doi: 10.1038/s41570-021-00329-7.

[44] Deamer, D. W. (1985). Boundary structures are formed by organic components of the Murchison carbonaceous chondrite. *Nature, 317*(6040), 792–794.

[45] Society, P. (2023, December 18). How did Earth get its water? *The Planetary Society.* `https://www.planetary.org/articles/how-did-earth-get-its-water#:~:text=Around%204.0%20to%203.8%20billion,could%20have%20brought%20water%20here.`

[46] Deamer, D. W., Pashley, R. M. (1989). Amphiphilic components of the Murchison carbonaceous chondrite: Surface properties and membrane formation. *Origins of Life and Evolution of Biospheres, 19*(1), 21–38.

[47] Cuomo, F., Lopez, F., Angelico, R., Ambrosone, L., De Socio, P., Ceglie, A. (2015). Molecular interactions mediated by nucleo-base functionalized lipids. *Journal of Surface Science and Technology, 31*, 59–68.

[48] Yang, H., Yi, J. W., Bang, E., Jeon, E. M., Kim, B. H. (2011). Cationic nucleolipids as efficient siRNA carriers. *Organic and Biomolecular Chemistry, 9*(1), 291–296.

[49] Post, E. a. J., Fletcher, S. P. (2020). Dissipative self-assembly, competition and inhibition in a self-reproducing protocell model. *Chemical Science, 11*(35), 9434–9442.

[50] Mohseni, M., Rebentrost, P., Lloyd, S., Aspuru-Guzik, A. (2008). Environment-assisted quantum walks in photosynthetic energy transfer. *The Journal of Chemical Physics, 129*(17).

[51] Root-Bernstein, R., Baker, A., Rhinesmith, T., Turke, M. J., Huber, J., Brown, A. W. (2023). "Sea Water" Supplemented with Calcium Phosphate and Magnesium Sulfate in a Long-Term Miller-Type Experiment Yields Sugars, Nucleic Acids Bases, Nucleosides, Lipids, Amino Acids, and Oligopeptides. *Life, 13*(2), 265.

[52] Pellestor, F., Paulasova, P. (2004). The peptide nucleic acids (PNAs), powerful tools for molecular genetics and cytogenetics. *European Journal of Human Genetics, 12*(9), 694–700.

[53] Chandru, K., Jia, T. Z., Mamajanov, I., Bapat, N. V., Cleaves, H. J. (2020). Prebiotic oligomerization and self-assembly of structurally diverse xenobiological monomers. *Scientific Reports, 10*(1).

[54] Räuchle, M., Leveau, G., Richert, C. (2020). Synthesis of Peptido RNAs from Unprotected Peptides and Oligoribonucleotides via Coupling in Aqueous Solution. *European Journal of Organic Chemistry, 2020*(45), 6966–6975.

[55] Müller, F., Escobar, L., Xu, F., Wegrzyn, E., Nainytė, M., Amatov, T., Chan, C., Pichler, A., Carell, T. (2022).

6.7 Quantum Biology

[1] McFadden, J., Al-Khalili, J. (1999). A quantum mechanical model of adaptive mutation. *Physica A: Statistical Mechanics and its Applications*, *274*(1), 265–284.

[2] Slocombe, L., Sacchi, M., Al-Khalili, J. (2022). An open quantum systems approach to proton tunnelling in DNA. *Communications Physics, 5*, 109. `https://doi.org/10.1038/s42005-022-00881-8`

[3] ZerahHarush, E., Dubi, Y. (n.d.). Do photosynthetic complexes use quantum coherence to increase their efficiency? Probably not. *Science Advances.*

[4] Zerah-Harush, E., Dubi, Y. (2020). Effects of disorder and interactions in environment-assisted quantum transport. *Journal Name.* `https://doi.org/10.XXXX/XXXXXX`

[5] Vattay, G., Csabai, I. (2015). Environment assisted quantum transport in organic molecules. *Journal Name.* `https://doi.org/10.XXXX/XXXXXX`

[6] Rebentrost, P., Mohseni, M., Kassal, I., Lloyd, S., Aspuru-Guzik, A. (2009). Environment-assisted quantum transport. *Journal Name.* `https://doi.org/10.XXXX/XXXXXX`

[7] Fornés, J. A. (Year). *Springer Series in Biophysics* (Vol. 26). Springer. Series Editor: Martinac, B.

[8] Brixner, T., Stenger, J., Vaswani, H. M., Cho, M., Blankenship, R. E., Fleming, G. R. (Year). Two-dimensional spectroscopy of electronic couplings in photosynthesis. *Journal Name*, *Volume*(Issue), Page range.

6.8 Computational Life

[2] Thatcher, J. W. (1964). *Universality in the von Neumann Cellular Model: Technical Report.*

[3] Wikipedia contributors. (2023, May 20). *Von Neumann cellular automaton.* Wikipedia. `https://en.wikipedia.org/wiki/Von_Neumann_cellular_automaton`

[4] Wikipedia contributors. (2023b, December 25). *Von Neumann universal constructor.* Wikipedia. https://en.wikipedia.org/wiki/Von_Neumann_universal_constructor

[5] Rendell, P. (January 2014). *Turing Machine Universality of the Game of Life.*

[6] Carlson, M. (2020, November 22). A computer in the game of life. *Hackaday.* https://hackaday.com/2020/11/21/a-computer-in-the-game-of-life/

[7] ConwayLife.com. *Replicator.* https://conwaylife.com/wiki/Replicator

[8] Sievers, D., von Kiedrowski, G. (1994). Self-replication of complementary nucleotide-based oligomers. *Nature, 369*(6478), 221–224.

[9] Ottelé, J., Hussain, A. S., Mayer, C., Otto, S. (2020). Chance emergence of catalytic activity and promiscuity in a self-replicator. *Nature Catalysis, 3*(7), 547–553.

[10] Kim, D., Joyce, G. F. (2004). Cross-catalytic replication of an RNA ligase ribozyme. *Chemistry & Biology, 11*(11), 1505–1512.

[11] Miras, H. N., Mathis, C., Xuan, W., Long, D., Pow, R., Cronin, L. (2020). Spontaneous formation of autocatalytic sets with self-replicating inorganic metal oxide clusters. *Proceedings of the National Academy of Sciences of the United States of America, 117*(20), 10699–10705.

[12] Yang, S., Schaeffer, G., Mattia, E., Markovitch, O., Li, K., Hussain, A. S., Ottelé, J., Sood, A., Otto, S. (2021). Chemical fueling enables molecular complexification of self-replicators. *Angewandte Chemie International Edition, 60*(20), 11344–11349.

[13] Yang, S. (2021, April 22). For the first time, large self-replicating molecules win evolution. *Sciworthy.* https://sciworthy.com/for-the-first-time-self-replicating-molecules-win-evolution/

[14] Automatic Mechanical Self Replication. *YouTube.*

[15] Arrighi, P. (September 9, 2019). An overview of Quantum Cellular Automata. https://www.cnet.com/science/the-milky-way-is-flush-with-habitable-planets-study-says/

[17] Menor-Salván, C. (2018). From the dawn of organic chemistry to astrobiology: urea as a foundational component in the origin of nucleobases and nucleotides. In *Nucleic acids and molecular biology* (pp. 85–142).

[18] Linday, B. (2020, May 18). Skin's outermost defense mechanisms: the microbiome, acid mantle, and lipid layer. https://www.dermascope.com/skin-care/11449-skin-s-outermost-defense-mechanisms-the-mi

[19] Saha, A., Yi, R., Fahrenbach, A. C., Wang, A., Jia, T. Z. (2022). A physicochemical consideration of prebiotic microenvironments for self-assembly and prebiotic chemistry. *Life, 12*(10), 1595.

[20] Mohseni, M., Rebentrost, P., Lloyd, S., Aspuru-Guzik, A. (2008). Environment-assisted quantum walks in photosynthetic energy transfer. *The Journal of Chemical Physics, 129*(17).

[21] Isogai, Y., Itoh, T. (1984). Fractal analysis of tertiary structure of protein molecules. *Journal of the Physical Society of Japan, 53*(6), 2162–2171.

[22] Tejera, E., Nieto-Villar, J., Rebelo, I. (2014). Protein sequence complexity revisited: Relationship with fractal 3D structure, topological and kinetic parameters. *Physica A: Statistical Mechanics and Its Applications, 410*, 287–301.

[23] Menor-Salván, C. (2018). From the dawn of organic chemistry to astrobiology: urea as a foundational component in the origin of nucleobases and nucleotides. In *Nucleic acids and molecular biology* (pp. 85–142).

[24] Linday, B. (2020, May 18). Skin's outermost defense mechanisms: the microbiome, acid mantle, and lipid layer. https://www.dermascope.com/skin-care/11449-skin-s-outermost-defense-mechanisms-the-mi

[25] Saha, A., Yi, R., Fahrenbach, A. C., Wang, A., Jia, T. Z. (2022). A physicochemical consideration of prebiotic microenvironments for self-assembly and prebiotic chemistry. *Life, 12*(10), 1595.

[26] Mackiewicz, D., Kowalczuk, M., Mackiewicz, D., Nowicka, A., Dudkiewicz, M., Łaszkiewicz, A., Dudek, M. R., Cebrat, S. (2002). How many protein-coding genes are there in the *Saccharomyces cerevisiae* genome? *Yeast, 19*(7), 619–629.

[27] Blattner, F. R., Plunkett, G., Bloch, C. A., Perna, N. T., Burland, V., Riley, M. W., Collado-Vides, J., Glasner, J. D., Rode, C. K., Mayhew, G. F., Gregor, J. W., Davis, N. W., Kirkpatrick, H., Goeden, M. A., Rose, D. J., Mau, B., Shao, Y. (1997). The Complete Genome Sequence of *Escherichia coli* K-12. *Science, 277*(5331), 1453–1462.

[28] Agüera y Arcas, B., Alakuijala, J., Evans, J., Laurie, B., Mordvintsev, A., Niklasson, E., Randazzo, E., Versari, L. (2024). Computational life: How well-formed, self-replicating programs emerge from simple interaction. *Google, Paradigms of Intelligence Team and The University of Chicago.*

[29] Walker, S. I., Davies, P. C. W. (2016). The "hard problem" of life. *Beyond Center for Fundamental Concepts in Science, Arizona State University, Tempe, AZ, USA; School of Earth and Space Exploration, Arizona State University, Tempe, AZ, USA; Blue Marble Space Institute of Science, Seattle, WA, USA.*

[30] davbrdavbr. (2022, July 24). Langton's Loops: The cellular automaton that copies itself [Video]. *YouTube.* `https://www.youtube.com/watch?v=xsLX390SJM4`

[31] LegenDUST. (2019, July 14). Nobili-Pesavento self-replicator original [Video]. *YouTube.* `https://www.youtube.com/watch?v=FPM8esG1Los`

[32] Phillip Bradbury. (2012, May 13). Life in life [Video]. *YouTube.* `https://www.youtube.com/watch?v=xP5-iIeKXE8`

6.9 Computational theory

[1] Deutsch, D. (1985). Quantum theory, the Church–Turing principle and the universal quantum computer. *Proceedings of the Royal Society of London A Mathematical and Physical Sciences, 400*(1818), 97–117. `https://doi.org/10.1098/rspa.1985.0070`

[2] Gyongyosi, L., Imre, S. (2011). Quantum cellular automata controlled self-organizing networks. In *InTech eBooks.* `https://doi.org/10.5772/15750`

[3] Arrighi, P. (2019, September 9). An overview of quantum cellular automata.

[4] Syropoulos, A. Hypercomputation: Computing beyond the Church–Turing barrier. ISBN 978-0-387-30886-9. e-ISBN 978-0-387-49970-3. DOI `10.1007/978-0-387-49970-3`.

[5] Evans, D. J. (1971). Analog and hybrid computing. *D. E. Hyndman.* Pergamon Press, Oxford, 1970. 218 pp. Illustrated. £2.25. (Flexi-cover £1.50). *The Aeronautical Journal, 75*(732), 861. `https://doi.org/10.1017/s000192400004700x`

[6] Shore, R. A., Slaman, T. A. Defining the Turing jump.

[7] Savage, J. E. (1998). Models of computation: Exploring the power of computing. `http://ci.nii.ac.jp/ncid/BA35517629`

[8] Timler, J., Lent, C. S. (2003). Maxwell's demon and quantum-dot cellular automata. *Department of Electrical Engineering, University of Notre Dame, Notre Dame, Indiana 46556.*

[9] Coutinho, S. C. (2010). Quantum computing for computer scientists. In N. S. Yanofsky M. A. Mannucci (Eds.), *Cambridge University Press, 2008.* ACM SIGACT News, 40(4), 14–17. https://doi.org/10.1145/1711475.1711479

[10] Draeger, J. (n.d.). Quantum Turing machines. In *Contribution to the Encyclopedia of Mathematics.*

[11] Sipser, M. (2012). *Introduction to the theory of computation* (3rd ed.). Cengage Learning. ISBN 978-1133187790.

[12] Childs, A. M. (2009). Universal computation by quantum walk. *Physical Review Letters, 102*(18). https://doi.org/10.1103/physrevlett.102.180501

[13] Potgieter, P. H. (2005). Zeno machines and hypercomputation. *Journal of Universal Computer Science*, 11(6), 948–961. Received 6 December 2004; received in revised form 14 November 2005; accepted 29 November 2005. Communicated by M. Hirvensalo.

[14] Barendregt, H. (1984). Introduction to lambda calculus. *Nieuw Archief Voor Wiskunde, 4*, 337–372. `https://www.ii.uni.wroc.pl/~kosciels/rl/lambda.pdf`

[15] Chaitin, G. J. (1977). Algorithmic information theory. *IBM Journal of Research and Development, 21*(4), 350–359. `https://doi.org/10.1147/rd.214.0350`

[16] Shen, A. Algorithmic information theory and Kolmogorov complexity.

[17] Wetterich, C. (2022). Fermionic quantum field theories as probabilistic cellular automata. *Physical Review D, 105*(7). https://doi.org/10.1103/physrevd.105.074502

[18] Schwartz, J. T., Von Neumann, J., Burks, A. W. (1967). Theory of Self-Reproducing Automata. *Mathematics of Computation, 21*(100), 745. `https://doi.org/10.2307/2005041`

6.10 Thermodynamics of Computing

[1] Tadaki, K. (2019). A statistical mechanical interpretation of algorithmic information theory. In *SpringerBriefs in Mathematical Physics.* `https://doi.org/10.1007/978-981-15-0739-7`

[2] Zhu, J. (2023). A thermodynamically universal Turing machine.

[3] Duwell, A. (2021). Physics and computation. ISSN 2632-413X (online).

[4] Bennett, C. H. (1982). The thermodynamics of computation—a review. *International Journal of Theoretical Physics, 21*(12).

[5] Wolpert, D. H., Kolchinsky, A. (2020). Thermodynamics of computing with circuits. *New Journal of Physics, 22*(6), 063047. https://doi.org/10.1088/1367-2630/ab82b8

[6] Kolchinsky, A., Wolpert, D. H. (2020). Thermodynamic costs of Turing machines. *Physical Review Research, 2*(3). https://doi.org/10.1103/physrevresearch.2.033312

[7] Strasberg, P., Cerrillo, J., Schaller, G., Brandes, T. (2015). Thermodynamics of stochastic Turing machines. *Physical Review E, 92*(4). https://doi.org/10.1103/physreve.92.042104

6.11 Cosmology

[1] Kaluza Klein Theory: Unifying Forces Through Extra Dimensions. (2024). *YouTube.* `https://www.youtube.com/watch?v=your_video_id`

[2] Susskind, L. (n.d.). String Theory, Fine-Tuning, and the Physics of the Multiverse. YouTube. `https://www.youtube.com/watch?v=5JtzDueKX_Q`

[3] Susskind, L. (2006). *The Cosmic Landscape: String Theory and the Illusion of Intelligent Design* (Illustrated ed.). New York: Little, Brown and Company.