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**abstracts**

**Beyond physics: The emergence and evolution of life**

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The emergence and evolution of life is based on physics but is beyond and not reducible to physics. First, evolution is an historical process arising from the non-ergodicity of the universe above the level of atoms. Most complex things will never get to exist. But human hearts exist. How comes this to be? Prebiotic chemistry on the early earth probably saw the evolution of many organic molecules in complex reaction networks, and the formation of low energy structures such as micelles and bilipid membranes. The latter could have served as constraints, or boundary conditions, on the release of energy by the same chemical non-equilibrium reaction processes. Atkins notes that “work” is the constrained release of energy into a few degrees of freedom, as in the cylinder, piston and working gas expanding to do thermodynamic work on the piston, pushing it down the cylinder. The cylinder and piston are the constraints or boundary conditions on this non-equilibrium release of energy. Newton does not tell where the boundary conditions come from. Physicists “cheat” and merely put in fixed and moving boundary conditions to solve for the work done on the piston. But it takes WORK to construct the cylinder and piston and assemble them. Thus something new: It typically takes work to construct constraints on the release of energy into a few degrees of freedom, which then constitutes work. No work, no constraints. No constraints, no work. The work done in such a process can itself be used to construct further constraints, or boundary conditions, on some further non-equilibrium process achieving still further work that can construct yet further constraints. A living cell achieves what Mael Montevil calls a “constraint closure”. Here a set of coupled and constrained non-equilibrium processes harnesses both these constrained non-equilibrium processes to do work that thereby constructs constraints, into a feedback system where the total system literally does work to construct its own boundary conditions on the non-equilibrium processes that construct those very constraints. A collectively autocatalytic set of peptides, such as the nine peptide set of G. Ashkenasy, achieves this closure. Constraint closure is something new: Biological organization. It is not matter alone, energy alone, entropy alone, or non-equilibrium process, such as dissipative structures, alone. None of these involves a system that does work to construct its own constraints, or boundary conditions. Such systems are fundamentally living, and can propagate their organization with heritable variations, hence can be subject to Darwin’s natural selection. In this evolution, these proto-organisms emerge unprestatably, and afford novel niches enabling, not causing, yet further types of proto-organisms to emerge. With this, new functions arise unprestatably. The ever-changing phase space of evolution includes these functionalities, such as hearts pumping blood. We cannot prestate these ever new functionalities, so can write no laws of motion for this evolution, which is therefor entailed by no laws at all, and thus not reducible to physics. Beyond entailing law, the evolving biosphere literally constructs itself and is the most complex system we know in the universe.

## **From Cosmology to life**

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## **Major extinctions and Gamma ray bursts**

**Tsvi Piran**

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## **Conditions for liquid water on M-dwarf planets**

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The recent detection of small planets within the Habitable Zone of Proxima Centauri, Trappist-1 and many other M-type stars raises the question whether such planets actually have liquid water. We investigate the surface temperature distribution of tidally locked planets, with a simple model including an atmosphere and heat transport. We explore the parameter space defined by the atmospheric properties and the heat redistribution mechanism. We identify the domain in the parameter space for which such planets have surface temperatures that can support liquid water. Our results suggest that planets orbiting in the Habitable Zone of M-type stars, in particular Proxima b, may support liquid water for a wide range of properties, including their atmospheric pressure, greenhouse effect (IR optical depth), albedo, insolation and heat transport. We suggest an observational procedure that could test the abundance of planets with water or oxygen in the Habitable Zone of nearby M dwarfs, using advanced telescopes such as JWST and ELT. We estimate that TESS may detect 10-40 transiting candidates within 30 pc and discuss the implications for oxygenic photosynthesis.

## **Potential for Life on Trappist-1 and other Red Dwarf Star Planets**

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To date seven planets have been detected orbiting the “nearby” Red Dwarf star Trappist-1, but the number may be significantly greater. The star is relatively small (0.12 R<sub>sun</sub>) and cool (2,550K) compared to our Sun (5,780K). Consequently its radiation flux is low (0.05% that of the Sun), mainly in the infrared, with a spectral peak at ~1mm, well above the Photosynthetically Active Radiation (PAR) waveband of 400 – 700nm, used by Earth vegetation. At least three of the planets are in the Habitable Zone (defined as regions where surface temperatures may support liquid water), but all six inner planets could have such temperatures, depending on their atmospheres. The six inner, closely orbiting planets (at 0.1-0.35AU), receive a radiation flux 0.3-4 that of Earth, but only ~10% of this is PAR, compared with ~40% on Earth. However, the star-facing hemisphere of tidally locked Trappist-1 planets would receive a continuous PAR flux, comparable with that received on Earth at high northerly or southerly latitudes, during only 3-4 months per Earth year – which

produces lush vegetation. XUV radiation from Trappist -1 is  $\sim 10^3$ - $10^4$  that of the Sun. This radiation could (possibly, but not necessarily) erode the primary atmosphere and oceans, and directly endanger life, unless life evolves in water or under a dense atmosphere. Given an atmosphere thick enough to protect life from flares of XUV radiation, dry land plants on Trappist-1 and other RDS planets could possibly evolve to utilize the infrared radiation between 700-1,000nm, which is energetically sufficient to drive water splitting oxygenic photosynthesis, an important precursor of complex life. These considerations and the abundance RD stars, enhance the chance of finding life clement abodes in the Milky Way.

### **In Favor of our Uniqueness**

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Several models have been proposed under the general term *Multiverse*, where “our” universe is only one out of infinitely many co-existing universes. In a series of papers [1-5] we have claimed that this multitude is dispensable and moreover, subjected to various conceptual difficulties. I will first outline the *Two-Time interpretation* of quantum mechanics, which entails a solution to the measurement problem and allows macroscopic time-reversibility at the level of a single branch of the wavefunction. These and other related results weaken the motivation for employing the many-worlds interpretation. I will then briefly present some thermodynamic considerations suggesting that other notions of a multiverse are not self-consistent.

### **ncRNA: cellular activity controller?**

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Except for DNA viruses, RNAs are widespread in biological systems and are involved in multilaterally adapted systems that control numerous cellular processes, the dimensions of which are still being explored. Principally, there are two broad categories of RNAs, namely coding and non-coding (ncRNA) and this abstract refers to the latter. The ncRNA molecules can form primary structures of approximately 22 nucleotides, as in “guided single stranded microRNAs” (ss(mi)RNA); double stranded miRNA interference segments can exist as a secondary shape; tertiary architectures are common in self-splicing group I and II introns; and, in association with proteins, quaternary structures can be formed eg RNA-induced silencing complex (RISC) and ribosomes. Such structures are multifunctional and are broadly regulatory, being involved in gene regulation as well as interfering with and the processing of both small and large RNAs. Such processing actions are well orchestrated, even to the point of efficient shredding of any unwanted RNAs - for example “used” mRNA within the cell is degraded rapidly (via RISC centres), so as to prevent them from being translated further. Recent discoveries have also demonstrated that ncRNAs can act as riboswitches (eg glmS ribozymes), whereby they regulate their own activity; and perform genetic control by a metabolite binding mRNA. Furthermore, ncRNAs can act as triggers against invading mobile genetic elements, thereby affording protection against incoming attacks by “parasitic” nucleotide sequences, viruses, transposons, etc. ncRNAs, in addition to ribozymatic activities and carrying genetic

codes such as influenza (RNA virus) are significant in that the hallmark of their modular architectural structure implies that structural and possible functional similarities exist among ncRNAs. A unique aspect of ncRNAs is that they are highly conserved and it is thought that they are molecular relics which delineated a 'hypothetical' entity called the "last universal common ancestor" (LUCA), which pre-dated the three domains of life, namely Archaea, Bacteria and Eukarya. The conserved nature of ncRNAs allows us to posit that it is highly probable that these molecules still have overall control of cellular activity. This is particularly relevant as there are large number of newly discovered ncRNAs whose functions are still to be explained and validated. During this oral presentation, I will put a case for ncRNAs being involved in the overall control of cellular activity and speculate that this 'cellular activity control' is passed on from one generation to the next.

## **Metabolic GARD: replicating mutually catalytic network of lipid-anchored metabolites and cofactors**

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The graded autocatalysis replication domain (GARD) model is a chemistry-based formalism that simulates network dynamics within amphiphile-containing compositional assemblies. In the GARD model, amphiphilic molecules join and leave assemblies, in a probabilistic fashion which is biased by a network of mutual catalysis (rate enhancement) parameters dictated by current assembly composition. Upon assembly growth, occasional assembly fission results in the generation of "progeny". GARD provides a detailed microscopic description of the walk in compositional space between fission events, and portrays the emergence of quasi-stationary states in compositional space termed composomes. These preserve their composition, by homeostatic growth, across many growth-fission cycles. In other words, composomes show similarity of "mother" to "daughter" assembly, a phenomenon that resembles cell replication. Composomes have been shown to serve as targets for selection [4], and to exhibit ecology-like constant population dynamics. As GARD assemblies store information in the form of non-random molecular compositions, and transfer this information to fission-generated progeny, they represent possible pre-RNA information carriers. GARD thus embodies two of the three widely accepted cornerstones of life's origin: compartmentalization- being rooted in lipid micelles and vesicles, and information storage/copying - via the propagation of assembly composition. A crucial open question is how GARD assemblies, with their immutable amphiphiles, might undergo Darwinian evolution, leading to increasingly complex molecular ensembles, and potentially to the appearance of biopolymers like RNA and proteins. We posit that this could be addressed by the addition of the third prebiotic cornerstone to GARD - a network of metabolism-like covalent molecular transformations. We are therefore exploring a novel computer-simulated model, metabolic GARD or M-GARD. Importantly, some of M-GARD's invoked metabolic conversions are set to involve amphiphiles, so as not to lose the forte of basic GARD. And just as in present-day living cells, we propose that M-GARD chemical reactions take place on both the outer and inner leaflets of the vesicle membrane, and in addition, involve compounds within the inner aqueous vesicular volume (lumen). Importantly, just as basic GARD's compositional replication and inheritance make it possible to temporarily forgo polynucleotides, it is possible for M-GARD to make do without protein enzymes. For this we invoke Kauffman's concept of the prebiotic importance of mutually catalytic sets of small molecules. In a generalization of Kauffman's formalism, early metabolism is enacted by having some low molecular weight compounds serve as non-protein catalysts for the

formation of others. This notion obtains further support from the experiment-based proposals that present-day low molecular weight cofactors may have been early non-protein catalysts, as exemplified by a recently proposed scenario of thioester-based early metabolism. M-GARD assumes the environmental existence of a large number of compounds, with different degrees of lipophilic characteristics, related to bilayer-forming capacity, bilayer solubility and leaflet preference. Some of these compounds will generate amphiphile vesicles, allowing the classical GARD dynamics to emerge. The membrane components would have a large diversity of hydrophilic headgroups that could take part in mutually-catalytic metabolism on the lipid bilayer surface. Some of M-GARD's simulated covalent transitions are headgroup clipping, and when these occur on the inner leaflet, they contribute to intra-vesicular content. The reverse of such reactions would modify lipophilic chains dissolved in the bilayer to form new amphiphile types. Additional reactions to be simulated are the spontaneous or catalyzed transport of molecules across the vesicular membrane, to become part of M-GARD's intra-vesicle metabolism. Finally, photochemically driven and high energy compound-dependent reactions would constitute part of the simulated chemical dynamics of M-GARD. Crucially, as in basic GARD, both the bilayer and luminal content are reproduced upon vesicle's homeostatic growth and fission. All the M-GARD simulations are carried out by chemistry-rigorous kinetic equations, using evidence-based numerical parameters, as done for the "artificial chemistry" of basic GARD. Important dynamic behaviors expected to emerge from M-GARD simulations include: a) gradual transition from pure heterotrophy (all compound are extraneously supplied) to higher and higher levels of heterotrophy, as specific instances of M-GARD assemblies become capable of endogenous metabolic generation of some compounds; b) Cross-generation gradual increase of homeostatic growth capacity of M-GARD assembly instances, including membrane components and inner content. This in turn will get translated into more effective replication, hence evolutionally advantage in multi-vesicle reactor GARD simulations; c) Portrayal of open-ended evolution, by allowing "open chemistry" – i.e. the generation of novel compounds absent or scarcely present in the environment.

### **The Ski-Lift: A unique thermodynamic Pathway with biological ubiquity**

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Thermodynamics has intensively studied "vertical" entropy transformations, *e.g.*, from low to high and vice versa. Little consideration has been given to "horizontal" transformations between states of similar entropy but different levels of complexity, or to "half way" transitions between high entropy and complexity. The latter ones, however, are of great importance for life sciences, complexity being one of life's hallmarks. We show that such transitions take a unique thermodynamic pathway: First a low entropy state is attained, of much higher order than that of the desired complex one. This ordered state is then "degraded" back towards the desired complex state. We give the mathematical proof for the efficiency of this pathway in comparison to the expected direct pathway, and point out several examples for it across life phenomena.

### **Evaluation of homochirality as an indicator for extraterrestrial life**

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## **Chemical evolution of functional peptides and proteins**

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## **Bistability, bifurcation and multistability in prototype models for understanding living systems and the origin of life**

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Bistability, bifurcation and multistability, present in a wide range of biochemical networks, are essential functions of living systems and arguably prerequisites of life. By looking at relatively simple catalytic reaction networks as representative prototypes for modeling chemical logic and complexification, we have investigated the theoretical and computational requirements for observing bistability, namely, higher order catalysis and feedback effects that lead to a mismatch between forward and reverse processes. Furthermore, by extending our networks to allow for multiple templates, we can observe the onset of multistability. Our findings may have far-reaching implications for potentially understanding early evolutionary processes of complexification, emergence and the origin of life.

## **Computing by nowhere increasing complexity**

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Order is the imprint of life. Negentropy is commonly used to refer to the process in which a biological system exchanges energy with its surrounding thereby "concentrating a stream of order on itself and thus escaping the decay into atomic chaos". Order may also be the imprint of a computational process. An orderly pattern embedded within disordered data conceivably matches the rules of a computer program that is likely to discover it. The program thus acts on the disordered data only to exert its own order on it. Here computation brings about order. But can the converse also be true, can the enforcement of order bring about computation? Here we show that computation can indeed be realized by enforcing order. In particular, we present a cellular automaton whose only governing rule is that the Kolmogorov complexity of a cell's neighborhood may never increase. Using an approximation of Kolmogorov complexity this automaton is shown to be functionally complete { it is capable of simulating any Boolean circuit. It is also shown to capture trianry logic described by a quandle, a non-associative algebraic structure underlying certain knots and links. This in turn suggests that some quantum computations may also be simulated by such an automaton. In digital physics, the universe itself is speculated to be a gigantic cellular automaton. Our study suggests that such a universe may come to thrive by employing a single rule, that of locally imposing order.