

ILASOL 2021 – Book of Abstracts:

- Dana Azouri, Itay Mayrose, TAU:

The tree reconstruction game: phylogenetic reconstruction using reinforcement learning

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The following two fields have never interacted before: reinforcement learning and molecular evolution. Here we propose to develop reinforcement-learning algorithms to solve a fundamental step in evolutionary studies; the reconstruction of phylogenetic trees, which are used to describe the evolutionary relationships among a set of organisms, genes or genomes. The current algorithms for phylogenetic tree reconstruction use various heuristics approaches to make tree inference feasible for problems involving more than a handful of sequences, thus all suffer from the known trade-off between accuracy and run-time. The novel methodology we propose here can greatly reduce the computing time without jeopardizing the likelihood of the obtained tree; considering the task of searching for the most-likely phylogenetic tree as a dynamic process which can be viewed as a game, we aim to use reinforcement-learning techniques to learn an optimal strategy rather than only optimize the progress made in each single move. As a preliminary analysis we utilized a standard machine-learning algorithm (i.e., Random Forest) to learn which phylogenetic tree moves are optimal for the next step. Our results clearly show that artificial-intelligence-based-learning can substantially improve our ability to accurately and efficiently reconstruct phylogenetic trees.

- Tanaya Bose, Ada Yonath, WIS:

Origin of life: peptide bonds formed by protoribosome constructs links the RNA world to RNA/protein lives

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High resolution ribosomal structures of ribosomes from various organisms, determined by us and elsewhere, highlight the peptidyl transferase center (PTC) as a semi-symmetrical RNA-made pocket, located in the core of the otherwise asymmetric ribosome. The three-

dimensional structure and the nucleotide sequence of this region are highly conserved among all domains of life, hinting at its prebiotic origin and implying that it is a remnant of a prebiotic entity. These characteristics, in addition to the findings that RNA can create itself and may possess catalytic activities, led to our “proto-ribosome” concept, which was recently proven experimentally via the successful peptide bond formation (monitored by MALDI) by our lab constructs. Hence, it is conceivable that this entity represents the origin of the ribosome, and perhaps also the origin of life, which existed in the RNA dominated world. Furthermore, it is suggested to be the missing link from the RNA dominating world to the contemporary protein/nucleic acids life.

- Amir Sapir, HaifaU:

Nematodes as a platform for understanding fundamental aspects of animal life in extreme environments on earth and in space

Amir Sapir, Department of Biology and the Environment, University of Haifa-Oranim.

Nematodes are among the most common animals in many extreme environments including the deep sea and toxic lakes on land. Thus, we use nematodes as a gateway for the understanding of biological processes in extreme environments. In deep-sea methane seeps and hydrothermal vents, we identified complex interactions of nematodes with parasitic fungi and with the particular chemical composition of these environments. Extending our studies inland, we found nematodes in Mono Lake, CA, an alkali (pH~10) hypersaline and arsenic-rich environment previously thought to host only alkali flies and brine shrimp animals. In Mono Lake nematodes, we identified a molecular mechanism of arsenic-resistance. Finally, to understand how space missions may affect the onset and development of neurodegenerative diseases we study disease-model nematodes that we sent to the International Space Station*.

* In collaboration with SHAKIM high school STEM program, Nahariya; Supported by The Ramon Foundation and NASA.

- Itay Fayerverker, Tal Mor, Technion:

Emergence of translation via autocatalytic sets – a minimal model

Understanding the characteristics of prebiotic tRNA molecules is fundamental to the presentation of a feasible scenario for the emergence of life, and especially for the emergence of translation, i.e., the emergence of “coded life”. In a recent work by Agmon, Fayerverker and Mor (AFM) published in FEBS Letters (2021), statistical analysis of bacterial tRNA sequences reveals that for six specific amino acids, a substring (of length 10 nucleotides) preceding the NCCA-tail carries cognate coding triplets to a very high extent.

Significantly, for five out of these six amino-acids, that is for Ala, Gly, Asp, Pro and Ser, there is a consensus that they are among the most ancient ones (Trifonov, 2004).

Here we search for prebiotic para-codons (De Duve, 1988) that potentially played a role in a secondary code. Such para-codons could potentially also be hidden in that same (length 10) tRNA arm. We present statistical evidence to suggest a novel quintuplets-based secondary code: By performing a statistical analysis on the same data used for AFM's analysis, but this time searching for longer strings containing cognate coding triplets rather than searching for the coding triplets themselves, we find a potentially interesting result. The same 10-mer substring also carries quintuplets to a high extent, but only for the tRNA of Ala, Gly and Asp, three amino-acids that are considered to be among the four most ancient ones (Trifonov, 2004). Could it be that these three amino-acids were sufficient for the emergence of the genetic code?

Combining this observation, Agmon and Mor's (2015) notion of code-prompting autocatalytic sets, and several papers presenting non-enzymatic template replication by Szostak and his team (2016-2018), we suggest a minimal model for the emergence of translation.

- Philippe Schmitt-Kopplin, Helmholtz Zentrum München, Germany:

Describing the early Abiome: a molecular inventory in meteorites

Understanding complex (bio/geo)systems is a huge challenge in modern sciences and implies constant development of modern analytical technology with innovative solutions for their resolved analysis. In this introduction presentation to the ILASOL 2021 in biogeochemistry we aim to present concepts of complexity, complex chemistry in biotic and abiotic systems and to introduce the analytical possibilities to disentangle chemical complexity into its elementary "bio" and "geo" parts (i.e. compositional and structural resolution). The concept will be applied to samples of highest abiotic complexity – soluble organic matter from meteorites and we will show that the description of organic compositional profiles in the CHNOSMg space enables us to reconstruct thermal, pressure and water alteration history on the parent body.

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- Nuphar Gedulter, HUJI:

Insights into formation and preservation of biosignatures from the study of Dead-Sea stromatolites

Stromatolites represent some of the most ancient forms of life on Earth, bearing information regarding the primitive environment in which early life has appeared and evolved. The quest to shed light on such processes on livable planets has motivated thorough investigations of stromatolites. Currently, the main practical attraction regarding these stromatolite textures is analogies with potential life and fossils on Mars.

Stromatolites are laminated bio-sedimentary structures formed by sediment trapping and binding of microbially-assisted mineral precipitation. They are generally created by photosynthetic activity of anaerobic microbial communities in shallow water environments. At the Dead Sea these communities comprise halophiles surviving under extremely arid environmental conditions.

In order to understand the formation of ancient Dead Sea stromatolites, we sampled modern microbial communities living in ponds, supplied with fresh-water seepages, on the retreating Ein-Gedi shore. Our research focuses on aragonite forming-microbial mats, more likely to build-up on fossil stromatolites, thereby preparing the ground for studies of the primary chemical and isotopic compositions. Microsensing techniques assist in determining how the bioactivity of these organisms may lead to the formation and the preservation of biosignatures and textures in fossil stromatolite reefs.

The Dead Sea shoreline is suited for our research as stromatolite reefs there offer a testing ground for developing integrated methods for identifying sites of geobiological interest. Detecting and mapping formations of ancient life forms can contribute to better deciphering the paleo-environmental conditions that had governed the Dead Sea area. In particular, we seek diagnostics to securely identify microbial mats that lived near lake shoreline environments.

We use remote sensing and in-situ hyperspectral technologies for characterization of biosignatures inherent to stromatolites and living microbial mats. We commenced developing spectral detection for automated mapping from drone and satellite imaging.

- Avshalom Elizur, Chapman University, USA / Iyar, and Tzachi Pilpel, WIS:

When Structure Outlasts its Substance: Platonist Idealism and Physical Invariants Highlighting the Physical Uniqueness of Life

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Tzachi Pilpel, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot 76100, ISRAEL

Evolution adapts the organism to the subtlest aspects of the environment, namely to the physical laws which remain invariant above probabilistic randomness. Examples are constants like G on which plants rely for growing upwards, or the space and time invariances that dictate the bilateral symmetry of motile animals. This correspondence offers a novel understanding of the physical uniqueness of life. Matter constantly changes its form over time. But sometimes it is the form which persists while its material content changes. Examples are a sound signal maintaining its modality while propagating from air to water, or a tornado exchanging air and debris with the environment while its whirling pattern persists. The living organism displays an even greater feat of this kind. Its extraordinarily complex structure outlasts all its material contents, whether by individual metabolism or by genetic reproduction. But then, this structure itself changes over time, whether through ontogenetic development or phylogenetic evolution. What it is, then, which outlasts the living structure which had outlasted its matter? Intriguingly, these are the structure's most abstract components, such as spatial and temporal ratios, and topological and even mathematical invariants. We speculate that genes responsible for these properties associate, dissociate and reassociate into numerous complex structures. Adaptation, then, increases the correspondence between the invariants of the living structure and those of its environment. This echoes Plato's argument about form's priority over matter, now augmented by physical and biological principles. A new characteristic of life thereby emerges. Life is a process by which a structure outlasts its substance, and in turn is outlasted by factors that encode invariants of the environment. This definition offers some experimental predictions.

- Yael Yair, Reut Sorek-Abramovich, TAU:

Temporal and spatial analysis of forward and backward microbial contamination in a Mars analog mission

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As human exploration missions to Mars are on the horizon, there is intense emphasis on both ethical and practical aspects of planetary protection. Microbial cross-contamination remains a key issue to address before executing human missions to any planetary body. These issues can be approached today using the advances in molecular metagenomics methods. These methods include rapid and sensitive sequencing platforms for characterizing microbial population. Combined with space analog missions, they provide powerful tools for assessing the challenges associated with space exploration. Here, we designed a protocol to monitor forward and backward contamination events and progression in an analog mission setup of 11-days Mars analog mission in the Ramon crater in Israel. Forward contamination soil samples were collected daily from three sites – two sites in close proximity to the habitat and one reference site. Backward contamination was determined in samples from nitrile gloves of

six analog astronauts (AA), before and after extra vehicular activities (EVAs). Temperature, relative humidity and soil composition data were also collected. Environmental DNA samples were extracted in the main habitat and 16S (bacterial) and 18S (eukaryotic, fungal) rRNA gene amplicons were sequenced and analyzed to study the composition of microbial population. Shannon Diversity index analysis and Principal Coordinates analysis (PCoA) of rRNA genes indicated that differences in the diversity and population composition were significant in sites closer to the habitat when compared to a reference site. These samples also demonstrated the introduction of human-associated taxa to the environment. Backward contamination consisted of bacterial taxa found on gloves upon the AAs' return from EVA and also detected in soil, altogether 44 genera, indicating backward contamination events. To the best of our knowledge, this is the first protocol to utilize advanced molecular technologies to investigate forward and backward contamination in a Mars analog mission.

- Jonathan Gropp, Itay Halevy, WIS:

A metabolic-isotopic model of biological methane production

Jonathan Gropp, Qusheng Jin, Itay Halevy

Methane-producing organisms (methanogens) were among the first organisms to evolve on Earth. Methanogens are capable of using electrons from H₂ or small organic molecules such as propionate to fix inorganic carbon via the Wood–Ljungdahl pathway, and they emit methane (CH₄) as a byproduct of energy conservation which then plays a major role as a greenhouse gas in the atmosphere. Remarkably, the main metabolic pathway of methanogenesis was highly conserved during methanogens' evolution over the past 4 billion years, and thus modern methanogens are suitable model organisms for methanogenic activity also in early Earth. It is still not clear how much of the methane in early Earth was biogenic. The isotopic composition of methane is a useful tool to distinguish between different biotic and abiotic sources and is widely used for samples of methane from natural environments, but in many cases, it is limited by overlapping signals from different sources. There is currently only limited understanding of the biological processes that produce the large observed range of isotopic compositions of methane.

To bridge this gap, we have developed a bio-isotopic model that can predict the expected isotopic compositions of methane depending on the availability of H₂ and CO₂ in the environment, and other physiological parameters. We calibrated the model to results from lab cultures and modern natural environments, spanning 10 orders of magnitude of cell-specific methanogenic activity. We found that the isotopic compositions are controlled by the rate of methanogenesis, and that a combination of signals from carbon, hydrogen and clumped isotopologues may aid in pinpointing the source of methane. In the modern oxygenated Earth, methanogens are limited only to strictly abiotic environments, which are often energy (substrate) limited. We found that in these conditions, methanogenesis usually proceeds close to the thermodynamic limit, producing unique isotopic signals that reflect chemical and

isotopic equilibrium between the reactants and products. However, methanogens that have more available energy in lab cultures generate a wide range of isotopic effects that depend on the concentration of H₂, and the enzyme-specific kinetic isotope effects.

During Earth history methanogens experienced extreme changes of the redox state of the planet, which we found was the main driver of generating the observed isotopic effects. We suggest that our model can be used to interpret the link between the metabolic state of methanogens and the isotopic fingerprints that they leave behind, throughout Earth history and also in the search of methanogenic life in exoplanets.

- Tony Z. Jia, BMSIS / ELSI, Japan:

DNA Liquid Crystal Coacervates and Other Phase-Separated Systems as Primitive Compartments

Phase separation of nucleic acids and proteins is a ubiquitous phenomenon regulating subcellular compartment structure and function. While complex coacervation of flexible single-stranded nucleic acids is broadly investigated, coacervation of double-stranded DNA (dsDNA) is less studied because of its propensity to generate solid precipitates. Here, we reverse this perspective by showing that short dsDNA and poly-l-lysine coacervates can escape precipitation while displaying a surprisingly complex phase diagram, including the full set of liquid crystal (LC) mesophases observed to date in bulk dsDNA. Short dsDNA supramolecular aggregation and packing in the dense coacervate phase are the main parameters regulating the global LC-coacervate phase behavior. LC-coacervate structure was characterized upon variations in temperature and monovalent salt, DNA, and peptide concentrations, which allow continuous reversible transitions between all accessible phases. A deeper understanding of LC-coacervates can gain insights to decipher structures and phase transition mechanisms within biomolecular condensates, to design stimuli-responsive multiphase synthetic compartments with different degrees of order and to exploit self-assembly driven cooperative prebiotic evolution of nucleic acids and peptides.

- Andres de la Escosura, Universidad Autónoma de Madrid, Spain:

Programming of self-assembly and replication networks with minimal nucleobase sequences

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(2) Institute for Advanced Research in Chemistry (IAdChem), Campus de Cantoblanco, 28049 Madrid, Spain.

The study of complex molecular networks and supramolecular assemblies is a clear objective in the field of systems chemistry [1], which is expected to have a great impact in the area of origins-of-life research and as biohybrid functional systems in materials science [2,3]. With regards to the origins of life, a pertinent question is whether protocells could be constructed from non-natural components. To answer this question, we have research lines towards synthetic nucleic acid hybrids, replicating nucleopeptide networks [4] and nucleolipid compartments [5]. Merging these components is an interesting approach because it allows exploring some properties of life without the restrictions of the historical pathway that Darwinian evolution took. In this respect, in the talk I will present results on how self-assembly processes and replication networks can be programmed with minimal nucleobase sequences in hybrid synthetic molecules built from simple biological building blocks.

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2. A. de la Escosura, "The Informational Substrate of Chemical Evolution: Implications for Abiogenesis". *Life* 2019, 9, 66.
3. K. Ruiz-Mirazo, C. Briones, A. de la Escosura, "Chemical Roots of Biological Evolution: The Origins of Life as a Process of Development of Autonomous Functional Systems". *Open Biol.* 2017, 7, 170050.
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- Sergey Semenov, WIS:

Thiolate-Based Autocatalytic Reaction Networks.

The emergence of life on Earth is one of the most fundamental and difficult questions in modern science. Research on the origin of life mostly focuses on two directions: (i) the development of prebiotic synthetic routes to the nucleotides and amino acids and (ii) the development of a self-replicating ribozyme (RNA) that can undergo Darwinian evolution. However, the nonenzymatic template replication with simple substrates suffers from product inhibition and the formation of an exceptionally complex ribozyme, which overcomes product inhibition, seems highly improbable. An alternative approach proposed by Eigen [1], Dyson [2], and Kaufmann [3] assumes the formation of autocatalytic metabolic reaction networks before the genetic apparatus. Nevertheless, this approach lacks experimental evidence. In this work, we examined reaction networks which are based on small organic building blocks that are abundant in space or that could have been easily formed on early Earth. We pursued an idea that nucleophilic catalysis by thiolates can be a driving force for autocatalytic reactions involving cyano-compounds and studied reactions of hydrogen cyanide, cyanamide, thiourea, thiols, disulfides, thioesters. We observed that thiouronium salts react with some disulfides autocatalytically forming guanidines in a similar way as thioesters

autocatalytically form amides [4]. Hydrogen cyanide and mercaptoethanol form an autocatalytic reaction network that drives a self-propagating reaction front. This reaction formed a variety of oligomeric products such as oligomers of hydrogen cyanide and oligothiirane. We are currently studying the mechanisms underlying these reactions.

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2. Dyson, F. J., A Model for the Origin of Life. *J. Mol. Evol.* 1982, 18 (5), 344-350.
3. Kauffman, S. A., Autocatalytic sets of proteins. *J Theor Biol* 1986, 119 (1), 1-24.
4. Semenov, S. N.; Kraft, L. J.; Ainla, A.; Zhao, M.; Baghbanzadeh, M.; Campbell, C. E.; Kang, K.; Fox, J. M.; Whitesides, G. M., Autocatalytic, bistable, oscillatory networks of biologically relevant organic reactions. *Nature* 2016, 537, 656 - 660.

- Siddhant Sharma, H. James Cleaves, BMSIS / ELSI, Japan:

A computational simulation of a reaction networks involved in life essential reactions.

We used an automated rule-based reaction generation to simulate the reaction network generated during the alkaline hydrolysis of glucose and applied graph transformation rules and restricted the outputs by applying various constraints. We used isomorphism tests to match the output molecular structures to experimentally reported structures. The reaction network was further assessed for the existence of potentially autocatalytic loops. This was done by loading the network topology into a graph database where pattern matching queries could be executed to search for patterns of interest. This work demonstrates some efficient methods for finding reaction pathways and autocatalysis in in-silico modeled reaction networks.

- Dharm Dev, Gonen Ashkenasy, BGU:

Replication Driven Peptide-based Systems Far from Equilibrium

Origin of life has probably evolved from simple precursors interacting through multiple prebiotic chemical reactions, which were later on wired together into feedback-controlled autocatalytic networks. This is particularly true for systems that operate out of chemical equilibrium and show complex dynamic behavior, such as multi-stability, oscillations, and chaos [1]. In this approach, first, we have studied bistability behavior of thiopeptide-based non-enzymatic networks propelled by reversible replication processes out of equilibrium. The bistable system has been demonstrated by following the reversible formation of a thiopeptide (named R) from its precursor peptides, a shorter thioester (E) and a thiol-terminated (N). This reaction network contains a positive feedback, generated by efficient self-replication of R as a coiled coil template. The resulted disparity in forward and backward reactions is a network response that leads to bistability, where two distinct steady

states (high steady state, Hss and low steady state, Lss) obtained depending on the reaction's starting compositions [2-3]. Second, we have analyzed the propensity of the bistable network that reaches either Hss or Lss to regulate nanoparticle formation reaction and growth (NRG) processes and consequently, yielding variable output in Au NP morphology, self-assembly, and shape [4]. Finally, we are currently trying to demonstrate the non-enzymatic oscillatory behavior of peptides under out of equilibrium conditions. Altogether, our model supports the idea that research in Systems Chemistry would expand the chance for success in the design of life-like systems.

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- Amit Kahana, Doron Lancet, WIS:

Micellar self-reproduction through dynamic compositional attractors: life is probable!

Due to their spontaneous emergence in prebiotic settings and their promiscuous growth and split dynamics, micellar assemblies have been proposed to have taken an essential part in the emergence of life [1, 2]. There is also growing experimental evidence for micellar autocatalytic reproduction without relying on templating biopolymers [3, 4]. This is in accord with the prediction of our chemical kinetics GARD model, suggesting that reproduction of mixed micelles occurs through composition-dependent non-covalent catalysis, leading to micellar homeostatic growth [1].

Excitingly, our GARD simulations also show that the privileged compositions that allow reproduction are reached much faster than expected, stemming from proven attractor properties of the GARD chemical kinetic equations [5]. By following accretion dynamics of mixed micelles, we were able to clearly illustrate gradual progression from random compositions towards these attractor states, and prove that this progression is the result of the inherent mutually-catalytic network at the basis of the GARD model. Further experimentations show that a dynamic advancement towards reproduction-prone compositions is evident even in large repertoires and varied concentrations of environmental monomeric lipids. These findings suggest that the advent of life-like properties in nanoscopic lipid assemblies, from prebiotic settings, is much more probable than previously thought, increasing the plausibility of a micellar origin.

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- Sandeep Ameta, Tata Institute, India:

Compositional identity and robustness of compartmentalized self-reproducing catalytic RNAs

Robust and dynamic compartmentalized self-replicating chemistries are an important step in understanding the emergence of life. Here, we demonstrate the encapsulation of a self-reproducing RNA system in coacervate droplets (compartments) where catalytic RNAs are synthesized from the autocatalytic assembly of smaller RNA fragments. We observe rate enhancement of the self-assembly process in the condensed compartment phase. Further, we demonstrate that cross-catalytic autocatalytic networks of RNA self-reproducers can be constructed, establishing a unique chemical compositional identity of the compartment. Not only the compatibility with network formation, coacervate compartments provide compositional robustness against perturbation by other RNA catalysts. Recently, these autocatalytic reaction networks have been shown to possess critical properties required for Darwinian evolution to occur. Combining them with dynamic compartments that are transient in nature, phase-separated systems have the potential to provide temporal and spatial protection to self-reproducing RNAs from other competing catalytic RNAs.

- Saurja DasGupta, Jack Szostak, Harvard, USA:

Prebiotic RNA assembly: chemistry, catalysis, and compartmentalization

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The ability of RNA to function as a carrier of heritable information as well as enzymes (ribozymes) have made it central to the emergence of life on earth. Non-enzymatic polymerization/ligation of monomers/oligomers activated by reactive moieties like prebiotically-relevant 2-aminoimidazoles (2AI) can generate short RNAs, but these processes

are inefficient. The appearance of ribozymes that catalyze RNA assembly was therefore a major transition in the chemical evolution of life. We used in vitro selection to identify ligase ribozymes that utilize the building blocks of non-enzymatic ligation as substrates, thus bridging chemical and biocatalytic RNA assembly. These ligases catalyze processive ligations with substrates as short as 4 nt and function under the chemical conditions of prebiotic 2AI activation of RNA oligomers, allowing in situ RNA activation chemistry to drive ribozyme-catalyzed ligation in one pot as it would have been on early earth.

But how did the complex ligase ribozymes emerge from chemistry? We demonstrated the non-enzymatic assembly of a functional ligase ribozyme from 3' aminoacylated RNA oligomers. This amino acid-bridged chimeric polymer unites the building blocks of RNA and protein presenting a potential intermediate between the RNA and protein worlds. To further connect primitive and modern biology, we evolved a pool of ligase ribozymes that use 2AI-activated RNAs as substrates to a pool of ligases that use RNA substrates activated with triphosphate, the activating group used in modern RNA building blocks (NTPs).

Next, we sought to establish RNA-catalyzed RNA assembly within protocells made with fatty acids. However, these prebiotic compartments are unstable at $[Mg^{2+}]$ required to support ribozyme function. To solve this problem, we identified a ligase sequence that functions at sub-millimolar $[Mg^{2+}]$ which enabled us to constitute the first instance of ribozyme-catalyzed RNA assembly within fatty acid protocells. In addition, our recent discovery that the presence of prebiotic small molecules such as ethylene glycol and D-ribose stimulate catalytic ligation at low $[Mg^{2+}]$, provide a more general 'systems' approach toward realizing catalytic RNA assembly within these protocells.

Our efforts to integrate various aspects of catalytic RNA assembly have brought us closer to assembling a self-replicating chemical system, capable of inventing Darwinian evolution.

- Sara Seager, MIT:

The Search for Signs of Life Beyond Earth by Way of Atmospheric Biosignature Gases

Thousands of exoplanets are known to orbit nearby stars and small rocky planets are established to be common. Driving the field is the study of exoplanet atmospheres, with the goal of detecting a gas that might be indicative of life. A suitable "biosignature gas" is not just one that might be produced by life, but one that: can accumulate in an atmosphere against atmospheric radicals and other sinks; has strong atmospheric spectral features; and has limited abiological false positives. Which gases might be potential biosignature gases in an as yet unknown range of exoplanetary environments? New computer simulations and next-generation telescopes coming online means the ambitious goal of searching for "biosignature gases" in a rocky exoplanet atmosphere is within reach.

- Amri Wandel, HUJI:

An extended Habitable Zone around Red Dwarfs

Because of their high abundance and relative ease of detecting HZ- planets around them, M-dwarfs have been the target of several surveys in the past decade, including the Kepler and TESS missions and the CARMENES and the MUSCLES projects. We apply the semi-analytical climate model for locked and synchronous planets of M stars (Wandel 2018, Wandel and Gale 2020) to suggest that the Habitable Zone around M-stars is significantly wider than previously thought. This is extremely relevant to understanding the evolution and biological potential of exoplanets, as M-dwarfs dominate planetary systems by number and their small masses and radii make their transiting planets comparatively easy to detect and characterize, in particular to look for bio-signatures. Earlier works assessed the potential habitability of such planets (e.g. Tarter et al., 2007; Gale and Wandel, 2017), in spite of such obstacles as tidally locked weather (e.g. Kopparapu et al., 2016), atmospheric and water erosion (Leconte et al., 2015; Lingam and Loeb, 2017; Tilley et al., 2019). Other works have shown that this need not be so, as planets may conserve or regain water and atmosphere (e.g. Wandel and Gale, 2020, and references therein). The recent discovery of water vapor in the atmosphere of K2-18b (Tsiaras et al. (2019)), a potentially habitable planet of an M-dwarf, demonstrated that at least in some cases the atmosphere and even water can survive, eventually supporting the extended HZ-model.

- Uri Malamud, TAU/Technion:

Water retention in icy bodies throughout the life of the host star: implications for habitability around white dwarfs

We performed large scale thermo-physical parameter studies of water retention, with thousands of simulations of minor planets of various sizes, orbits, compositions and formation times, evolving for billions of years around their host stars. As stars evolve, their luminosity increases by several orders of magnitude, and as they shed their mass, primarily in the AGB phase, minor planets around them experience orbital expansion. We thus have, for the minor planet's boundary condition, a temporal dependence on both accounts (the details of which were obtained using the MESA stellar evolution code). We applied our model to investigate the exo-planetary water composition associated with white dwarf pollution, of which 25-50% are known to accrete planetary material, being the only window we have to understand exo-planetary bulk composition. However, the collective water mass fraction inferred from their atmospheres is only of the order of a few %. Using our model, we were able to quantify the amount of water actually retained inside minor planets either in ice or in hydrated rocks. We evaluate water retention for small minor planets up to dwarf-planet size, around sun-like stars, in addition to the full range of stellar masses of white dwarf progenitors. To conclude our series of papers, we provided a code which calculates water retention for any combination of parameters, and may be freely used as a service to the community.

- Joseph Gale, HUJI:

On the border between Science Fiction and Science in Astrobiology

Science fiction authors and early philosophers have long been way ahead of Astrobiology in considering the possibility of extraterrestrial life. They have had the advantage of employing the full and wonderful range of human imagination and longing, unhampered by the rules and requirements of rigorous science. In so doing, they have predicted many things in science and technology with which reality is slowly catching up. To mention only one example relevant to astrobiology - the ancient Greeks discussed the possibility of life on planets of other stars 2500 years ago; long before the first exoplanets were detected.

However, fiction and science should be kept separate. A recent paper¹ in Int. J. Astrobiology, by Matthew Edwards seems to cross this subtle border. The paper reviews numerous solutions to future human space flight to colonize exoplanets, which are not supported by today's, or any reasonable projection of future, science and technology. In particular, we point out that a much less ambitious plan for humanity to escape a depleted Earth would be to resettle within our planetary system, avoiding the need of interstellar space transportation of population. IJA will be publishing our rebuttal².

¹Matthew R. Edwards. Android Noahs and embryo Arks: ectogenesis in global catastrophe survival and space colonization. Int. J. Astrobiology, 04 February, 2021.

²Joseph Gale, Amri Wandel. On the border between Science and Science Fiction. IJA, 2021 (in press).

- David Avnir, HUJI:

Chirality indicators for extraterrestrial life

The major revolution in modern astronomy recognizing the universe as teeming with exoplanets, the discovery of liquid water in solar moons, and the continuing focus on Mars exploration, all accelerate the re-evaluation of potential biomarkers for extraterrestrial life. Based on life on planet Earth which relies heavily on chiral molecules and especially on homochiral families, molecules with these structural properties appear in all road-maps as prime indicators of extraterrestrial life. The lecture will focus on two related topics: First, analysis of the strengths, bounds and potential weaknesses of relying on chirality and on homochirality as such biomarkers, along with recommendations of how to practically use them. And second, evaluation of the abundance of chiral minerals in outer space and of their potential role in the synthesis of enantiomerically-excessed chiral molecules as catalysts and adsorbents.

- Avraham Binnendfeld, Shay Zucker, TAU:

Overcoming stellar activity in detecting earth-analogs

Current state-of-the-art spectroscopic efforts to detect earth-analog planets are majorly hindered by stellar activity. This is because of the effect changes in the spectrum have on the estimated radial velocity curves. Solar activity, for example, was shown to induce an 8–10 m/s RV variation. This is significantly larger than the expected signal due to the reflex motion of the sun relatively to earth. Stellar activity cycles were also shown to mimic planetary signals in RV data in numerous cases, resulting in false detections. We have recently developed an approach to study spectral variability that considers the global information in the spectrum, sparing the need to encapsulate it in a single number, such as scalar activity indices. Using the statistical concept of partial correlation, we further developed the method to disentangle RV bulk shifts, potentially originating from orbital signals, from periodic changes in the stellar spectrum (e.g. activity). The approach can be applied to any other system involving orbital signals combined with spectral shape variations, such as pulsating stars in binary systems.

- Seth Shostak, Center for SETI Research, USA:

Looking for Intelligence in the Cosmos

For six decades, a small group of researchers has used large antennas and specialized light detectors in a hunt for signals from extraterrestrial intelligence. Thanks to private funding, this effort has recently grown to a point where a million stellar systems will have been scrutinized for signals by the end of the decade. Nonetheless, these searches depend on the existence of (1) high intensity transmissions from the extraterrestrials; (2) a fortuitous synchronism in transmitting and receiving programs, and (3) a lack of inhibition on the part of the extraterrestrials to mark their existence and location. An alternative to the signal search – a hunt for the artifacts that very advanced societies might construct – circumvents all of these difficulties, and has the benefit of allowing discovery as a consequence of conventional astronomical research. Given this, what should be our strategy for uncovering other intelligence in the universe?