BP 10: Evolution and Origin of Life

Time: Tuesday 9:30–12:15 Location: BAR 0106

Invited Talk BP 10.1 Tue 9:30 BAR 0106

Protein evolution in sequence landscapes: from data to models and back — •Martin Weigt — Sorbonne University, Paris, France

In the course of evolution, proteins diversify their sequences via mutations, while keeping their 3D structure and biological functions remarkably conserved. Modern sequence databases provide us with increasingly large samples for this sequence diversity. In my talk, I will describe how these samples can be used to infer data-driven protein sequence landscapes, using approaches borrowed from statistical physics or machine learning. In turn, we can model the interplay between mutation and selection in protein evolution as a stochastic process in these landscapes. I will illustrate these ideas in three examples: (i) the prediction of the effect of individual mutations in proteins, (ii) the modeling of experimental protein evoltuion, and (iii) the statistical design of artificial but functional proteins.

BP 10.2 Tue 10:00 BAR 0106

Non-equilibrium approaches to the origin of life — Thomas Matreux[1], Paula Aikkila[1], Corinna Kufner[2], Dominik Bucher[3], Almuth Schmid[1], Wolfgang Zinth[1], Dieter Braun[1], and •Christof Mast[1] — [1]LMU, Munich, Germany — [2]Harvard, Cambridge, USA — [3]TUM, Munich, Germany

Life is an out-of-equilibrium process, so its emergence must also have been decisively shaped and driven by the non-equilibrium systems present 4 billion years ago. We investigated how simple heat fluxes through geological networks of interconnected chambers created chemical niches from complex mixtures of prebiotically relevant substances, each with different prevailing concentration ratios. These "micro-labs" could thus enable a wide variety of prebiotic reactions and massively increase their yield and selectivity compared to bulk systems. We further measured the sequence selectivity of UV radiation on pseudogenomes built from subsets of codon sequences. Comparison with existing chronologies for codon and amino acid evolution suggests the importance of UV light as a selection pressure during the evolution of early life.

BP 10.3 Tue 10:15 BAR 0106

Unpredictable repeatability in evolutionary dynamics — •Suman Das and Joachim Krug — Institute for Biophysics, University of Cologne, Germany

Biological evolution proceeds through occurrence and fixation of mutations. But how repeatable are evolutionary trajectories? Is the evolution of specific well-adapted genotypes largely a matter of chance, or should we expect the same genotypes to evolve repeatedly? The answer depends in part on the probability distribution of mutational effect sizes. Repeatability is itself a random variable, and for light-tailed distributions it converges to its mean value in the limit of a large number of available mutations. However, for heavy-tailed distributions, we show that the repeatability is much higher but the distribution remains broad, and consequently the repeatability cannot be predicted based on the distribution. This non-self averaging effect is similar to those observed in certain disordered systems, and arises from the fact that the fixation process is dominated by a few mutations even in the limit of infinite mutation number. We discuss the behavior in various heavy-tailed regimes, and illustrate it with applications to empirical data on drug resistance evolution.

REF: S G Das and J Krug (2022). Unpredictable repeatability in molecular evolution. Proceedings of the National Academy of Sciences, 119(39):e2209373119.

BP 10.4 Tue 10:30 BAR 0106

Kinetics of Information Content in a Virtual Circular Genome — •Ludwig Burger, Tobias Thun, and Ulrich Gerland — Technical University of Munich

We study the kinetics of information content in an ensemble of oligonucleotides that undergo hybridization, dehybridization, non-enzymatic templated ligation and single-strand cleavage. The stability of hybridized complexes depends on the sequence because the dehybridization rate depends on the free hybridization energy. Mismatches are possible, but they lead to a thermodynamic and kinetic penalty. The information that is supposed to be "stored" in the ensemble is a circular genome as well as its complementary strand. Therefore, the oligonucleotides in the initial ensemble are chosen such that every element in the ensemble is part of the true genomic sequence. In most investigated scenarios, the initial ensemble loses its information content and no information amplification can be observed. Depending on the choice of ligation and cleavage rate, the loss of information can be driven by cleavage or ligation. Information loss by ligation is caused by templated ligation processes that produce long strands that do not resemble the true genomic sequence. This is the case if the hybridization site is too short or contains too many mismatches to guarantee correct alignment of template and ligated strands. Even though information amplification appears to be difficult to achieve, the timescale of information loss can be extended by tuning the hybridization energy or the concentration of short oligomers.

15 min. break

BP 10.5 Tue 11:00 BAR 0106

Evolutionary rescue of resistant mutants is governed by a balance between radial expansion and selection in compact populations — Serhii Aif[1,2], Nico Appold[1,2], Lucas Kampmann[3], Oskar Hallatschek[3,4], and •Jona Kayser[1,2] — [1]MPI für die Physik des Lichts, Erlangen, Germany — [2]MPZ für Physik und Medizin, Erlangen, Germany — [3]University of California, Berkeley, USA — [4]Leipzig University, Leipzig, Germany

Mutation-mediated treatment resistance is one of the primary challenges for modern antibiotic and anti-cancer therapy. Yet, how slower-growing resistant lineages may escape purifying selection via continued evolution is still unclear. Here, we introduce a system of fluorescence-coupled synthetic mutations to track the entire evolutionary trajectory of thousands of resistant lineages in expanding yeast colonies. We uncover that an underlying quasi-stable equilibrium between the opposing forces of radial expansion and natural selection, a phenomenon we term inflation-selection balance, enhances the evolutionary rescue of resistant lineages. Tailored computational models and agent-based simulations corroborate the fundamental nature of the observed effects and demonstrate the potential impact on drug resistance evolution in cancer. The described phenomena should be considered when predicting multi-step evolutionary dynamics in any mechanically compact cellular population, including pathogenic microbial biofilms and solid tumors. The insights gained will be especially valuable for the quantitative understanding of response to treatment, including emerging evolution-based therapy strategies.

BP 10.6 Tue 11:15 BAR 0106

Heat flows drive ionic and pH gradients — •Thomas Matreux[1], Almuth Schmid[1], Paula Aikkila[1], Kristian Le Vay[2], Johannes Raith[3], Bernhard Altaner[3], Bettina Scheu[4], Ulrich Gerland[3], Hannes Mutschler[2], Dieter Braun[1], and Christof B. Mast[1] — [1]Systems Biophysics, LMU Munich, Germany — [2]Biomimetic systems, TU Dortmund, Germany — [3]Physics of Complex Biosystems, TU Munich, Germany — [4]Earth and Environmental Sciences, LMU Munich, Germany

The first steps in the emergence of life on Earth occurred on rocks and their constituent phases with a feedstock of simple molecules. Our aim is to combine this background with physical non-equilibria such as thermal gradients, offering unique opportunities for molecular selection on all levels.

In this scenario, ions leached from mineral samples are selectively accumulated by heat flows through water-filled fractures. In contrast to up-concentration by dehydration or freezing, this actively alters the Magnesium:Sodium ratio to an extent that permits key ribozyme activities.

Simple mixtures of formic acid and sodium hydroxide, exposed to thermal gradients, drive pH gradients which can be understood and predicted by a separation of timescales. Such proton gradients can locally acid-dissolve Apatite, a presumably abundant phosphate mineral that is close to insoluble at physiological pH. By thermal fractionation, significant concentrations of phosphate are provided at neutral pH.

BP 10.7 Tue 11:30 BAR 0106

Evolution Mechanics: a Framework of Hierarchy Formation

in Evolving Systems — •Yunus Sevinchan — Science of Intelligence Cluster, Technische Universität Berlin, Berlin, Germany — Institute for Theoretical Biology, Humboldt-Universität zu Berlin, Berlin, Germany — Institute of Environmental Physics, Universität Heidelberg, Heidelberg, Germany

The structures we observe around us are of a wide diversity and complexity, ranging from simple cells to intricate ecosystems and human societies. The question how these hierarchically modularized structures can arise from simpler ones is of central importance when desiring to understand our world.

I present the Evolution Mechanics framework [1] which aims to find a concise description of the mechanisms by which evolutionary systems unfold into hierarchically organized modules. Key elements of this conceptual framework are a so-called Self-Replicator and a set of processes that need to occur in order for an Evolutionary Transition in Individuality to take place, thus leading to a new hierarchical level. While inspired by the evolution of biological life, Evolution Mechanics is abstracted from it and takes a more general perspective, providing a consistent language to address the fundamental processes giving rise to the complexity we observe.

[1]: Yunus Sevinchan. Dissertation, 2021. Evolution Mechanics and Perspectives on Food Web Ecology. Heidelberg University Library. DOI: 10.11588/heidok.00030750

BP 10.8 Tue 11:45 BAR 0106

Sequence distributions in coexisting phases — •Ivar Svalheim Haugerud[1], Giacomo Bartolucci[2], and Christoph A. Weber[1] — [1]University of Augsburg, Augsburg, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Phase separation, sequence, and length distributions of heteropolymers such as RNA and DNA are essential in regulating functions and spatial organization in living cells and at the molecular origin of life. Here, we theoretically investigate the interplay between phase separation, polymer sequence, and length at non-dilute conditions. To this end, we developed a thermodynamic description for the reversible polymerization of different monomeric units. In the model, polymers can grow, shrink and phase separate from each other and the solvent. We show that growth in length facilitates phase separation already at low concentrations. Our key finding is that the distribution of sequences is entirely different in each phase. These results suggest that condensed phases can act as hubs for functionalities that rely on the sequence-specificity of RNA or DNA.

BP 10.9 Tue 12:00 BAR 0106

Controlling Alkaline Vent Morphologies in Microfluidic Models by pH and Fluid Flow — •Maximilian Weingart[1], Siyu Chen[2], Clara Donat[2], Dieter Braun[1], and Karen Alim[2] — [1]Systems Biophysics, Ludwig-Maximilians Universität München, Amalienstraße 54, 80799 München, Germany — [2]CPA and Department of Biosciences, School of Natural Sciences, Technische Universität München, Ernst-Otto-Fischer-Straße 8, 85748 Garching b. München, Germany

Alkaline vents provide the unique chemical composition for the precipitation of alkaline fluids in acidic, metal-ion containing ocean water, thereby providing the necessary gradients to drive molecular reactions at the origin of life. Yet, the 3D chimney-like structure of vents pre- vents any visualization of potentially reaction fueling gradients. Here, we develop a microfluidic model of alkaline vents permitting spatio-temporal visualization of precipitate formation and morphology. Varying concentration and inflow rate of an alkaline solution into a flat microfluidic-chamber pre-filled with an acidic Fe(II)-solution we observe a diverse set of precipitate morphologies. Visualizing the precipitation pattern we identify for which physical parameter vent morphologies allow for gradients in pH and molecular composition to arise. We establish our microfluidic model as a framework to investigate the potential of gradients across a permeable boundary for early compartmentalisation and molecular reactions at the Origin of life. The 2D microfluidic alkaline vent model shows that disordered precipitate morphologies allow for the formation of strong pH gradients.