BP 26: Synthetic life-like systems and Origins of Life

Time: Thursday 9:30–12:15 Location: H46

BP 26.1 Thu 9:30 H46

Heat flows through rock cracks purify life's building blocks and protect RNA from hydrolysis — •Paula Aikkila[1], Thomas Matreux[2], Dieter Braun[1], and Christof Mast[1] — [1]Ludwig-Maximilians-Universität München — [2]ESPCI Paris

The emergence of biopolymer building blocks is a crucial step during the origins of life. However, their synthesis pathways usually require feedstocks of pure reactants and defined purification and mixing steps to suppress unwanted side reactions, which is required for high product yields. We show that heat flows through thin crack-like compartments purify complex mixtures of prebiotically relevant building blocks and drive prebiotically relevant reactions such as the dimerization of glycine. In these same compartments, we furthermore study how heat-flows can locally switch on and off pH gradients, thereby enabling or disabling RNA hydrolysis depending on their hybridization state. We seek to explore how this enables spontaneous symmetry breaking in the sequence and folding space, possibly facilitating the emergence of functional ribozyme.

BP 26.2 Thu 9:45 H46

Membraneless protocell confined by a heat flow — •Alexander Floroni[1], Noël Yeh Martín[2], Thomas Matreux[1], Laura Weise[3], Sheref Mansy[4], Hannes Mutschler[5], Christof Mast[1], and Dieter Braun[1] — [1]Systems Biophysics, LMU Munich; München, Germany — [2]Institute of Biotechnology HiLIFE, University of Helsinki, Helsinki, Finland — [3]MPI of Biochemistry; Martinsried, Germany — [4]Department of Chemistry, University of Alberta; Edmonton, Canada — [5]Department of Chemistry and Chemical Biology, TU Dortmund; Dortmund, Germany

In living cells, a complex mixture of biomolecules is assembled within and across membranes. This state is maintained by a sophisticated protein machinery. It imports nutrients, removes waste, and orchestrates cell division. Here we show how the molecular contents of a cell can be coupled in a coordinated way to the non-equilibrium of a heat flow. A temperature difference across a water-filled pore accumulated the core components of a modern cell to make a functional reaction. The mechanism arose from the interplay of convection and thermophoresis. Protein synthesis was triggered as a direct result of the up-concentration. The same non-equilibrium setting continued to attract nutrients from an adjacent fluid stream, while keeping the cellular molecules confined. Our results show how a simple and archaic non-equilibrium physical process can assemble the many different molecules of a cell and trigger its basic functions. The framework provides a membrane-free environment to bridge the long evolutionary times from an RNA world to a protein-based cell-like proto-metabolism.

BP 26.3 Thu 10:00 H46

A game of life with dormancy — •Daniel Henrik Nevermann[1], Claudius Gros[1], and Jay Lennon[2] — [1]Institute for Theoretical Physics, Goethe-University Frankfurt, Germany — [2]Department of Biology, Indiana University, Bloomington, IN 47405, USA

The factors contributing to the persistence of life are fundamental for understanding complex living systems. Many species contend with harsh environments by entering a reversible state of reduced metabolic activity, a phenomenon known as dormancy. Here, we develop Spore Life, a model to investigate the effects of dormancy on population dynamics. It is based on Conway's Game of Life, a deterministic cellular automaton where simple rules govern the metabolic state of an individual based on its neighborhood. For individuals that would otherwise die, Spore Life provides a refuge in the form of an inactive state. These dormant individuals (spores) can resuscitate when local conditions improve. The model includes a parameter $\alpha \in [0, 1]$ that controls the survival probability of spores, which yields stochastic dynamics between the limits $\alpha = 0$ (Game of Life) and $\alpha = 1$ (Spore Life). In addition to identifying the emergence of unique periodic configurations, we find that spore survival increases the average number of active individuals and buffers populations from extinction. Contrary to expectations, the population stabilization does not require large and long-lived seed bank. Instead, the demographic patterns in Spore Life only require a small number of resuscitation events. Spore Life can be interactively explored at `https://itp.uni-frankfurt.de/spore-life/`.

BP 26.4 Thu 10:15 H46

Continuous Evolving Game of Life with Diversity — •Alexandre Guillet and Frank Jülicher — MPI-PKS, Dresden, Germany

The complex phenomenology of J. Conway's "Game of Life" cellular automaton, in particular its gliders, has been translated into continuous fields in space and time in a 2011 preprint by S. Rafler. The striking organic feel associated with these artificial life simulations in isotropic space has attracted the attention of a growing online community at the intersection of citizen science and computer art, which has recently culminated in the exploration and classification of the diverse morphologies of the "Lenia" gliders by BWC. Chan and others.

Our research focuses on a minimal variant of these continuous nonlinear dynamical systems that is capable of generating gliding, self-replicating and vanishing patterns, with striking resemblance to cell division, motility and death. Elaborating upon the governing partial integro-differential equation, we allow each cell to carry individual variations of the parameters, thus introducing a spatial diversity of rules. A conservation law is enforced on the resources of the cells as a selection pressure, together with a mutation process as a random source of diversity. The spontaneous evolution of the system from a single cell leads to a rich phenomenology, ranging from mycelial growth to epithelia and amoeboid motion.

This continuous and evolving model with diversity raises the Game of Life into a toy model for the morphogenesis and evolution of primordial lifeforms.

BP 26.5 Thu 10:30 H46

Cooperative effects in compartmentalized irreversible self-assembly — •Richard Swiderski, Severin Angerpointner, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians-Universität München, Germany

From biomolecular compartments, protein patterns to porous rocks: Many biological and chemical systems like living cells or prebiotic chambers exhibit some form of spatial organization which separates biochemical processes. This is known to play a key role in the assembly of virus capsids or the enrichment of prebiotic chemicals. We systematically explore the effects of such spatial separation on the self-assembly of irreversibly binding identical particles. We show that already in a simplified model of two coupled biochemical compartments cooperative effects emerge through limiting compartment exchange. Further, these findings generalize to spatially extended systems like intracellular chemical gradients or membrane-assisted assembly.

15 min. break

Invited Talk BP 26.6 Thu 11:00 H46

Theory for sequence selection via phase separation and oligomerization — •Christoph Weber — University of Augsburg, Universitätsstr. 1, 86159 Augsburg

Non-equilibrium selection pressures were proposed for the formation of oligonucleotides with rich functionalities encoded in their sequences, such as catalysis. Since phase separation was shown to direct various chemical processes, we ask whether condensed phases can provide mechanisms for sequence selection. To answer this question, we use non-equilibrium thermodynamics and describe the reversible oligomerization of different monomers to sequences at non-dilute conditions prone to phase separation. We find that when sequences oligomerize, their interactions give rise to phase separation, boosting specific sequences' enrichment and depletion. Our key result is that phase separation gives rise to a selection pressure for the oligomerization of specific sequence patterns when fragmentation maintains the system away from equilibrium. Specifically, slow fragmentation favors alternating sequences that interact well with their environment (more cooperative), while fast fragmentation selects sequences with extended motifs capable of specific sequence interactions (less cooperative). Our results highlight that out-of-equilibrium condensed phases could provide versatile hubs for Darwinian-like evolution toward functional sequences, both relevant for the molecular origin of life and de novo life.

BP 26.7 Thu 11:30 H46

Prebiotic RNA Replication through Templated Ligation by

Humidity and pH Cycles — •Felix T. Dänekamp and Dieter Braun — Systems Biophysics LMU, Munich, Germany

To replicate long RNA strands, templated ligation from 2',3'-cyclic phosphate RNA is a promising pathway. Preliminary screenings suggest that through tuning of monovalent salt content and through adding Lysine or other amino acids to the solution, no additional catalysts are required to attain yields of 50% ligation product in one day. Cycling physical conditions such as pH and salt/RNA concentration likely solves the strand inhibition problem. This opens up the possibility of prebiotic ligation chain reactions and thus open-ended evolution from short RNA strands.

BP 26.8 Thu 11:45 H46

Gravitationally induced oscillations of active droplets — •Advait Thatte[1], Judit Sastre[2], Alexander Bergmann[2], Michele Stasi[2], Marta Tena-Solsona[2], Job Boekhoven[2], and Christoph Weber[1] — [1]Faculty of Mathematics, Natural Sciences, and Materials Engineering, and Institute of Physics, University of Augsburg, Universitätsstrasse 1, 86159 Augsburg, Germany — [2]Department of Bioscience, School of Natural Sciences, Technical University of Munich, Lichtenbergstrasse 4, 85748 Garching, Germany

Oscillations in the formation and dissolution of compartments inside living cells are pivotal in orchestrating various cellular functions and processes. Recent experiments on synthetic cells showed the spontaneous emergence of spatio-temporal oscillations in the number of droplets, their size, and position. Oscillations occur because droplets grow via gravitationally induced fusion above their stationary size. As a result droplets shrink, feeding the nucleation of new sedimenting droplets, restarting the cycle. The stationary droplet size is a consequence of deactivating droplet material inside and activating outside. Here we present a theoretical model for phase separation with non equilibrium chemical fuelling including a sharp interface model for many active droplets. The model quantitatively describes the stationary droplet size and the oscillation frequency observed experimentally.

BP 26.9 Thu 12:00 H46

Linking fitness landscape topography to the characteristics of the underlying genotype-phenotype map — Malvika Srivastava[1,2], Ard A. Louis[3], and •Nora S. Martin[4] — [1]Institute of Integrative Biology, ETH Zurich, Zurich, Switzerland — [2]Swiss Institute of Bioinformatics, Lausanne, Switzerland — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, UK — [4]CRG (Barcelona Collaboratorium for Modelling and Predictive Biology), Dr. Aiguader 88, Barcelona 08003, Spain

The topographies of fitness landscapes are central in models of evolutionary processes. Key topographical features include the prevalence of fitness peaks, as well as the existence of accessible (i.e. fitness-increasing) paths to the global fitness optimum. Recent numerical work found that such accessible paths commonly exist in fitness landscapes based on biophysical models of genotype-phenotype (GP) maps, even when fitness values are randomly assigned to phenotypes [1]. Here, we examine such landscapes with random phenotype-fitness assignment more thoroughly to investigate, how their topography depends on the characteristics of the underlying GP map. By simplifying the GP map to a "neutral component" (NC) graph, we can compute the expected prevalence of fitness peaks based only on two GP map characteristics: the evolvabilities and sizes of NCs. Evolvabilities are also important for peak heights and for the existence of accessible paths to global optima. [1] S. F. Greenbury, A. A. Louis, S. E. Ahnert, Nat Ecol Evol. 6, 1742-1752 (2022).