# BP 8: Systems and Networks Biophysics

Time: Monday 16:45–18:30 Location: BAR/0106

BP 8.1 Mon 16:45 BAR/0106

**Origins of the Fittest: Clonal interference in the World Aviation Network** — •Adrian Zachariae, Pascal Klamser, and Dirk Brockmann — Technische Universität Dresden, Dresden, Deutschland

Clonal interference, the competition between strains carrying different beneficial mutations, plays a crucial role in shaping evolutionary outcomes in asexual populations. Since the spread of new mutations is critical for CI, it is strongly influenced by the structure of the population. For example, long-range connections can rapidly distribute new mutations, reducing CI. We investigate how this phenomenon unfolds in the the World Aviation Network, which shapes the population structure of microorganisms that use humans as hosts, including pathogens. We developed a novel analytical framework that models the succession of adaptive mutations as a Markov Renewal Process. The process is built by leveraging epidemic modeling methods to model mutation spread in the network. Or approach reveals how the interplay between mutation rate and network topology gives rise to distinct evolutionary regimes: At low mutation rates, strains originating from globally central nodes have higher fixation probabilities, while at higher mutation rates, meso-scale and local properties become more important. Applied to the WAN, affluent, western regions are most likely origins of high-fitness lineages in the low-rate regime, shifting to more populous nations in Asia at high rates. The framework provides valuable insights how spatial structure shapes evolutionary outcome, with particular relevance for pandemic preparedness.

BP 8.2 Mon 17:00 BAR/0106

**Polymerization of prebiotic building blocks in a wet-dry cycling system** — •Almuth Schmid — LMU, Geschwister-Scholl-Platz 1, München

When it comes to the question on how life could have emerged on an early Earth, not only the setting plays an important role but also the chemistry that helped forming the first building blocks of life. Prebiotic chemistry is limited in multiple ways since many of the common catalysts life uses nowadays are too complex to have been present in such an early stage. In addition, the existing compounds were diluted and only available in low concentration. To overcome these problems, systems like wet-dry cycles can help accumulating molecules while at the same time lowering the reaction activation barrier.[1] In addition, amino acids promote RNA copolymerization more than 100-fold via acid-base catalysis, starting from prebiotically plausible ribonucleoside-2',3'-cyclic phosphates.[2] MD simulations and X-ray crystallography confirmed that water is still present in the dry state, limiting the condensation reaction and hydrolyzing the material. Preliminary experiments showed that by using ammonium salts instead of sodium salts, including nucleotides and hydroxide to adjust the pH, overall longer polymers and yields 5-fold higher than before were obtained. Expanding this adapted wet/dry cycling system with an NH3/CO2 enriched atmosphere [3] would re-create a day and night rhythm on the early Earth, providing a prebiotic way to synthesize RNA.

**Invited Talk** BP 8.3 Mon 17:15 BAR/0106

**Constructing synthetic life-like vesicle systems by integration of artificial metabolic reaction networks** — •Laura Heinen — DWI - Leibniz Institut für interaktive Materialien, Aachen, Germany

Life emerges as a systemic property of the interplay of complex chemical reaction networks out of equilibrium. Living cells, for example, need energy to grow, divide, process information and synthesize their own constituent building blocks. In my group we develop minimal metabolic reaction networks to fuel out of equilibrium behavior in synthetic lipid vesicles, to finally, build active cell-like compartments bottom-up, called synthetic cells. In my talk I will demonstrate the construction of autonomous, active behavior in vesicles by the example of cross-feeding in between synthetic vesicles. Key to such sustained out-of-equilibrium behavior is the selective transport of energy molecules across the lipid membrane. One population of vesicles produces and exports adenosine triphosphate (ATP) while a second population of vesicles takes up the ATP and uses this chemical energy to fuel ATP-consuming reactions. The hydrolyzed ATP feeds back into the first vesicle population where it will be recycled, and the interdependent metabolic cycle can be sustained. The vesicles are a platform to enable active behavior in synthetic systems in a continuous, autonomous and adaptive fashion. Fundamentally, they allow us to study non-equilibrium processes in an energy-controlled environment and will promote our understanding of constructing life-like materials and systems.

BP 8.4 Mon 17:45 BAR/0106

**Living Network Dynamics: From pH-Stimulated Growth to Resistance Optimization** — •Mathieu Le Verge-Serandour, Alexandra Bienau, Karen Alim, and Friedrich Simmel — School of Natural Sciences, Technical University of Munich

In this work, we explore how vascular-like functionality can be integrated into bioelectronic interfaces using the unicellular slime mold Physarum polycephalum. This organism forms a dynamic, self-organized tubular network that exhibits emergent behaviors such as optimization, adaptation, and self-healing, making it an ideal model for studying decentralized, stimulus-responsive growth. By leveraging electrochemically induced pH gradients, we experimentally translate designed network layouts into biological structures and characterize the key dynamics underlying their responses to pH stimuli.

We further analyze Physarum morphological evolution, where the network reorganizes over several hours to evacuate a defined area by sequentially pruning competing parallel veins, ultimately forming a tree-like architecture. Drawing an analogy with power-grid networks, we investigate how sequential pruning depends on the ratio of tube to network resistance. Analytical and numerical results show that regular graphs undergo pruning until the average node degree falls below four, a finding that remains robust in simulations of random networks. Incorporating mass redistribution into this process leads to resistance homogenization, revealing fundamental physical constraints that shape adaptive transport networks.

BP 8.5 Mon 18:00 BAR/0106

**Simulation of autoimmune and autoinflammatory diseases: the novel mechanism of psoriasis progression.** — •Nadezhda Esenkova[1,2], Lukas Pöschl[1,2], Gerard C. L. Wong[3], and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Germany — [3]University of California, Los Angeles, USA

Autoimmune and autoinflammatory diseases (AIIDs) still remain an unsolved problem. One of the most studied diseases which carries features of both types is psoriasis. In this study, we are focusing on the novel mechanism of disease enhancement, driven by antimicrobial peptides (AMPs) and AMP-like fragments organizing innate immune ligands for enhanced binding to Toll-Like Receptors in immune cells. These fragments have a diverse origin: there is strong recent evidence that serine proteases can digest viral and host proteins into AMP-like fragments. In order to explore the effect of this emerging pathway, we developed a new unified interaction network model for psoriasis, based on the current extant measurements. The model was reduced to a system of nonlinear differential equations, which were studied by using dynamical system theory and numerical methods. Importantly, we find that the proposed model can reproduce the full spectrum of disease progression from healthy response to uncontrolled inflammation and allows comparison of different therapeutic interventions. Finally, by expanding the model to include diffusion, we can successfully predict the geometry of psoriatic plaques, the precise measurements of which may inform modulation of treatment.

BP 8.6 Mon 18:15 BAR/0106

**Network-induced control of sustained oscillations in SIRS epidemics** — •Samuel Ropert[1,2], Tomas Perez-Acle[2], and Dirk Brockmann[1] — [1]Technische Universität Dresden, Dresden, Germany — [2]Universidad San Sebastián, Santiago, Chile

Sustained oscillations in SIRS epidemic models are well understood in well-mixed populations when infectious and immune periods deviate from exponential waiting times. In contrast, the role of contact network structure in generating or suppressing such oscillations has received little attention. Existing work on small-world networks reports oscillations but does not relate them to effective transition-time distributions. This work investigates how network topology shapes os-

cillatory SIRS dynamics by simulating a stochastic SIRS process on self-similar modular hierarchical (SSMH) networks. These networks interpolate between random-like graphs and strongly modular, hierarchical structures while preserving system size and mean degree. A single structural parameter controls edge placement across hierarchical levels, reshaping effective distances between communities. Preliminary results show that random-like networks support robust, coherent oscillations in global prevalence, whereas increasing hierarchical modularity desynchronizes outbreaks across communities and gradually destroys the global limit cycle, leading to damped or irregular fluctuations. These findings support an interpretation of epidemic oscillations as a synchronization phenomenon of individual SIRS cycles, where network topology promotes or inhibits global coherence by reshaping the time-to-infection distribution through changes in effective distances.