BP 31: Statistical Physics of Biological Systems I (Joint Session with DY)

Joint session with DY organized by BP.

Time: Tuesday 12:00–13:00 Location: H43

BP 31.1 Tue 12:00 H43

Interplay of directed transport and diffusive motion inside cellular protrusions — •Isabella Krämer and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians-Universität, München, Deutschland

Linear cellular protrusions are characterized by their finger-like structure that is connected to the cell body at one end, the base, and extends into the surroundings at the other end, the tip. A membrane enclosing the protrusion separates the inside from the extracellular and prevents in- and outflux other than at the base. Inside the protrusion bundles of parallel actin filaments are embedded into cytoplasm so that different types of motion interact: directed transport of cargo towards the tip on the actin filaments and diffusive motion inside the cytoplasm.

Motivated by this biological process we study the steady-state behaviour of a totally asymmetric simple exclusion process (TASEP) that is weakly coupled to different diffusive environments and focus on systems that are closed at the tip of the TASEP. We derive an exact equation that relates the average total occupation on the TASEP to the average total occupation on the diffusive lattice coupled to it. This mass balance equation represents a global detailed balance for the exchange between the two lattices, where detailed balance does not hold locally for any pair of sites but for the two lattices in total. We show that the steady-state profile on the TASEP is given by a localized domain wall whose position can be determined using the mass balance equation. By further exploiting this equation we find an analytic expression for the nearest-neighbour correlations on the TASEP.

BP 31.2 Tue 12:15 H43

Physical driving of chemical reactions — •Vladimir Palyulin and Ulrich Gerland — Theory of Complex Biosystems, Physik-Department, Technische Universität München, James-Franck-Str. 1, 85748 Garching, Germany

Out-of-equilibrium physical processes can generate a chemical disequilibrium, if a suitable coupling mechanism exists. Such a physical driving of chemical reactions is relevant in contexts ranging from prebiotic evolution to atmospheric chemistry. Inspired by recent microfluidic experiments, we introduce a minimal model that couples biased diffusion as a generic form of physical non-equilibrium to reversible dimerization as the simplest nonlinear reaction. The model demonstrates explicitly that the effective coupling strength, i.e. the amplitude of the chemical response to a given amount of physical driving, depends on the boundary conditions as well as the relative speeds of the physical and chemical kinetics.

BP 31.3 Tue 12:30 H43

Growth and Division of Active Droplets: A Model for Protocells — David Zwicker[1,2], •Rabea Seyboldt[1], Christoph A. Weber[1], Anthony A. Hyman[3], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]School of Engineering and Applied Sciences, Harvard University, Cambridge, MA 02138, USA — [3]Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany

It has been proposed that during the early steps in the origin of life, small droplets could have formed by phase separation from a surrounding complex mixture. These droplets could have provided chemical reaction centers to generate and evolve organic molecules. However, whether these droplets could divide and propagate is unclear. Here we study the dynamics of such droplets by combining the physics of phase separation with chemical reactions that are maintained away from thermodynamic equilibrium by an external supply of energy. Outside the droplets, these reactions turn precursors into droplet material, which then gets incorporated into droplets, where it is eventually converted into a waste product that leaves the droplet. Surprisingly, our theoretical study shows that the resulting chemically driven fluxes can lead to shape instabilities that trigger division of droplets into two smaller daughters, which can then grow again. Therefore, chemically active droplets can exhibit cycles of growth and division that resemble the proliferation of living cells. Dividing active droplets could serve as a model for prebiotic protocells, where chemical reactions in the droplet play the role of a prebiotic metabolism.

BP 31.4 Tue 12:45 H43

Robustness of nucleosome patterns in the presence of DNA sequence-specific free energy landscapes and active remodeling — •Johannes Nuebler[1], Benedikt Obermayer[2], Wolfram Moebius[3], Michael Wolff[1], and Ulrich Gerland[1] — [1]Physik-Department, TU München, James-Franck-Str. 1, 85748 Garching — [2]Max-Delbrück-Center for Molecular Medicine, Robert-Rössle-Str. 10, 13125 Berlin — [3]Department of Physics, Harvard University, Cambridge, MA 02138, USA

Proper positioning of nucleosomes in eukaryotic cells is important for transcription regulation. When averaged over many genes, nucleosome positions in coding regions follow a simple oscillatory pattern, which is described to a surprising degree of accuracy by a simple one-dimensional gas model for particles interacting via a soft-core repulsion. The quantitative agreement is surprising given that nucleosome positions are known to be determined by a complex interplay of mechanisms including DNA sequence-specific nucleosome affinity and active repositioning by remodeling enzymes. We rationalize the observed robustness of the simple oscillatory pattern by showing that the main effect of several known nucleosome positioning mechanisms is a renormalization of the particle interaction. For example, "disorder" from sequence-specific affinities leads to an apparent softening, while active remodeling can result in apparent softening for directional sliding or apparent stiffening for clamping mechanisms. We suggest that such parameter renormalization can explain the apparent difference of nucleosome properties in two yeast species, S. cerevisiae and S. pombe.