BP 36: Statistical Physics of Biological Systems IV (joint session BP/DY)

Time: Friday 9:30–12:45 Location: BAR/SCHÖ

Invited Talk BP 36.1 Fri 9:30 BAR/SCHÖ

Swimming in complex environments — •Christina Kurzthaler — Max Planck Institute for the Physics of Complex Systems

Microorganisms are omnipresent in the ocean, the human body, and our soils and therefore play an important role for various geological, biological, and medical processes. To optimize their survival and perform biological functions many microorganisms convert chemical energy into directed motion. In this talk, I will illustrate the underlying physical concepts and show concrete examples of our research, focusing on the interactions of microorganisms with their complex habitats. I will first discuss the motion of sperm in complex fluids and address their emergent dynamics in the presence of a hyperactivation agonist, modifying the sperm beating pattern. Second, I will focus on the first-passage-time statistics of active agents moving towards a target boundary. Our results highlight how swim gait impacts spreading and search efficiency in active systems with potential consequences for sperm motion in the reproductive tract and the accumulation of microbial communities.

BP 36.2 Fri 10:00 BAR/SCHÖ

Motor shot noise explains active fluctuations in a single cilium — •Maximilian Kotz[1], Veikko F. Geyer[2], and Benjamin M. Friedrich[1] — [1]Cluster of Excellence Physics of Life, TU Dresden, Dresden, Germany — [2]B CUBE, TU Dresden, Dresden, Germany

Molecular motors drive seemingly regular motion, making living matter move - yet also cause non-equilibrium fluctuations that can serve as a probe of internal motor dynamics. Here, we use motile cilia as a model system to investigate how small-number fluctuations shape collective dynamics. Motile cilia exhibit regular bending waves; this motion is driven by the self-coordinated activity of thousands of molecular motors inside the cilia's cytoskeletal core. By developing, to the best of our knowledge, the first stochastic model of cilia beating, we show that the finite number of motors leads to active fluctuations on the mesoscale, sufficient to explain frequency jitter in beating cilia observed in experimental data. We rigorously compare observables of this model, including the quality factor of the oscillation, to experimental data in which motors have been partially extracted from cilia. This is a strong test of this stochastic model. The model also reproduces other phenomena of experimental data, like correlation lengths of intra-cilium synchronization and noise-induced phase slips. We propose that active fluctuations are important new observables, which can guide theoretical models of motor dynamics in beating cilia and other motor systems.

BP 36.3 Fri 10:15 BAR/SCHÖ

Theory of Forces Between Crosslinked Filaments — •Cedrik Barutel and Sebastian Fürthauer — Institute of Applied Physics TU Wien Austria

The cytoskeleton drives essential cellular processes like cell division and chromosome segregation. It consists of filaments that are crosslinked by proteins, many of which are molecular scale motors that consume ATP to do work. The forces that crosslinking proteins generate between cytoskeletal filaments are the key drivers of active cellular mechanics. We derive a generic theory to describe such crosslinking forces.

We construct a theory to describe and predict the forces generated collectively by crosslinking proteins between biofilaments using symmetries, conservation laws, and out-of equilibrium thermodynamic principles. Our approach identifies the full set of phenomenological coefficients governing entropic, active, and frictional crosslinking forces, which allows a quantitative comparison between the effects of different crosslinker mixtures between two filaments. We demonstrate the power and validity of this framework by quantitatively explaining a set of different experimental setups, which combine the effects of passive and active crosslinks

BP 36.4 Fri 10:30 BAR/SCHÖ

Modeling Cooperative Remodeling and Energy Landscapes in the Bacterial Flagellar Motor — •Nils-Ole Walliser — Laboratoire Charles Coulomb, University of Montpellier, Montpellier, France

Bacteria use the flagellar motor to adapt their motility to changing mechanical conditions. This rotary motor tunes its torque by recruiting and releasing torque-generating stator units. I will present statistical-physics-based models that use single-motor measurements to infer interaction potentials and energy landscapes in the bacterial flagellar motor. First, using single-motor bead assays that resolve stepwise changes in rotation speed and thus stator occupancy, we model stator recruitment as a finite-size lattice gas and infer stator-stator cooperativity from occupancy fluctuations. This reveals moderate attractive interactions and shows that the motor operates in a regime that balances responsiveness to load changes with noise in stator number. Second, I will discuss experiments where the motor load is actively perturbed, uncovering a strong asymmetry in the relaxation to the steady state when starting from higher versus lower stator occupancy. A two-state catch-bond model quantitatively explains this stoichiometry-dependent asymmetry and captures the mechanosensitive nature of stator anchoring to the cell wall. Finally, I will show how high-temporal-resolution rotation traces can be used to reconstruct, in a model-independent way, the tilted periodic energy landscape of the rotor/LP ring within a Smoluchowski framework, yielding barrier heights, torque and internal friction.

BP 36.5 Fri 10:45 BAR/SCHÖ

Anisotropic (sub)diffusion of organelles in living cells — •Aranyak Sarkar, Pooja Yadav, and Matthias Weiss — Experimental Physics I, University of Bayreuth, Universitätsstraße 30, 95447 Bayreuth

Eukaryotic cells are neatly organized into distinct, membrane-enclosed compartments ('organelles') with specific duties. A prominent example are peroxisomes, which feature vesicle-like shapes with radii $0.1-1\ \mu$m that are dispersed across the cytoplasm. Using time-lapse fluorescence microscopy, we have tracked the motion of individual peroxisomes over extended periods. Analysis of the experimental data revealed two distinct modes of motion: a prevailing (sub)diffusive motion and a quite rare super-diffusive characteristics that is associated with motor-driven transport along microtubules. Focussing on the seemingly unremarkable subset of (sub)diffusive trajectories, we have found a significant anisotropy in the motion that persisted even when microtubules were disrupted. In particular, diffusive steps along the cells' long axis were seen to be favored over steps in the perpendicular direction, indicating an anisotropic materials characteristic of the cytoplasm. Using a simple model, we were able to capture and explain the observed features of the anisotropic diffusion of organelles.

15 min. break

BP 36.6 Fri 11:15 BAR/SCHÖ

Understanding Influenza A Virus particles detaching from reconstructed cell surfaces — •Thomas Kolbe[1,2], Pierre Gaspard[1], and Bortolo Matteo Mognetti[1,2] — [1]CENOLI, Université Libre de Bruxelles (ULB) — [2]IB2 - Interuniversity Institute of Bioinformatics in Brussels

Influenza infection is a multistage process that involves the trafficking of viral particles across the cell membrane. Before endocytosis, virions target the membrane by binding hemagglutinin ligands to sialic acid residues on cell receptors. After budding, neuraminidase cleaves these residues, enabling virions to detach from the infected cell surface.

We examine detachment dynamics through simulations and theoretical analysis. We explain experimental findings showing that the time required for virions to detach can decrease as the single-trajectory average number of bonds increases - a counterintuitive result specific to neuraminidase activity. Furthermore, we demonstrate that the detachment time is not governed by a Poisson distribution but depends on multiple factors, including ligand-receptor reaction rates, virion size, and receptor diffusion constant. These results clarify how biochemical parameters regulate the residence time of virions at the cell surface.

BP 36.7 Fri 11:30 BAR/SCHÖ

Band pattern formation of erythrocytes in density gradients is due to competing aggregation and net buoyancy — •Felix Maurer[1], Camila Romero[1], Nikolas Lerch[1], Thomas John[1], Lars Kaestner[1,2], Christian Wagner[1,3], and Alexis Darras[1,4] — [1]Experimental Physics, Saarland University, Saarbruecken, Germany — [2]Department of Theoretical Medicine and Biosciences, Saar-

land University, Homburg, Germany — [3]Physics and Materials Science Research Unit, University of Luxembourg, Luxembourg — [4]School of Physics, University of Bristol, Bristol, United Kingdom

Centrifugation of biological matter in density gradient solutions is a standard method for separating cell types or components. It is also used to separate RBCs by age, as they lose water and become denser over their lifespan. When the density gradient is prepared with Percoll, discrete bands of RBCs are systematically observed, despite the continuous density distribution of RBCs. We developed a continuity equation incorporating cell aggregation to describe the macroscopic evolution of RBC volume fraction in a density gradient, considering a continuous RBC density distribution. Numerical solutions demonstrate that the competition between net buoyancy and aggregation is sufficient to create band patterns. Our model reproduces the temporal evolution observed in experiments, but also predicts several types of bifurcation-like behaviors for the steady-state patterns in constant gradients, depending on RBC volume fraction and aggregation energy.

BP 36.8 Fri 11:45 BAR/SCHÖ

Adaptive self-organization in excitable biological collectives — •Bianca Ariani[1,3], Yunus Sevinchan[2,3], and Pawel Romanczuk[2,3] — [1]Bernstein Center for Computational Neuroscience, Berlin — [2]Science of Intelligence, TU Berlin — [3]Institute for Theoretical Biology, HU Berlin

Biological collectives often display complex, context-dependent behavior, such as coordinated responses to predators, despite individuals following simple local rules. This class of phenomena is broadly understood as self-organization.

We examine a system showing rich spatio-temporal dynamics: Sulphur Mollies, Mexican freshwater fish whose group behavior resembles a stochastic excitable medium. To probe the mechanisms behind their collective activity, we study a bio-inspired agent-based model in which individuals estimate the shoal's mesoscale activity from the cues they perceive as they move. Each agent adjusts its sensitivity to cues through a simple homeostatic plasticity rule, allowing the group to regulate its collective state. This formulation links individual adaptation to population-level patterns.

Our results show that local adaptive regulation reproduces key qualitative features of the biological system. More generally, they illustrate how distributed plasticity mechanisms can support robust self-organization in complex biological collectives.

BP 36.9 Fri 12:00 BAR/SCHÖ

Visual-based Collective Shepherding in Swarm Robotic System — •Yating Zheng[1,2] and Pawel Romanczuk[1,2] — [1]Department of Biology, Humboldt Universität zu Berlin, Berlin, Germany — [2]Research Cluster of Excellence 'Science of Intelligence', Berlin, Germany

Collective shepherding presents a rich example of two interacting multi-agent systems coupled through non-reciprocal interactions. While most existing models assume that shepherd agents have global knowledge of the flock-an unrealistic premise for physical or biological systems-we introduce a vision-based, locally interacting model that captures the essential physics of shepherd-flock coordination. The model produces robust, self-organized behavior among shepherds without explicit communication, and we analyze how key control parameters, such as flock size and the number of shepherds, shape the resulting dynamics.

The framework also performs effectively in more challenging regimes, including the manipulation of non-cohesive agents and passive (non-self-propelled) agents, demonstrating its broad dynamical applicability. We further validate the model on a mixed-reality swarm-robotic platform, where physical robots successfully shepherd a virtual flock.

Overall, these results provide a minimal yet powerful physics-based description of multi-agent herding using only local visual information, offering insight into non-reciprocal collective behavior and enabling scalable real-world implementations in swarm robotics.

BP 36.10 Fri 12:15 BAR/SCHÖ

Polymer theory shows DNA motors extrude loops in the monomeric mode — Kirill Polovnikov[1,2] and •Dmitry Starkov[2] — [1]Institute for Physics and Astronomy, University of Potsdam, Potsdam-Golm, Germany — [2]Moscow, Russia

Cohesin-dependent loop extrusion is a key active mechanism of DNA organization, yet it remains unclear whether chromatin loops in living cells are generated primarily by individual cohesin motors or by higher-order structures. To fill this major gap, we build an analytical polymer-physics model that extracts a missing parameter - *the linear density of loops* - directly from Hi-C data. We focus on short genomic distances, where contact statistics simplify, resulting in a perturbative expression for the contact probability of a looped chain under a finite contact-detection radius. Our theory recapitulates a characteristic dip in the *logarithmic derivative* of the contact-probability that is *broadly observed in experiments*. By fitting this minimal model to a diverse range of mammalian Hi-C datasets, we infer approximately six loops per megabase. Independent imaging and mass spectrometry measurements of cohesin density are consistent with our inferred loop density, supporting the monomeric mode of DNA motors extrusion.

BP 36.11 Fri 12:30 BAR/SCHÖ

Universal loop statistics from active extrusion — •Anastasia Chervinskaya[1] and Kirill Polovnikov[1,2] — [1]Moscow, Russia — [2]Institute for Physics and Astronomy, University of Potsdam, Potsdam-Golm, Germany

Cohesin-dependent loop extrusion is a key active mechanism of genome organization, yet quantitative links between extrusion kinetics and measurable loop statistics remain incomplete. We develop an analytical model that predicts the mean loop scale, full loop-length distributions, state composition, and arm-arm correlations for one-sided versus two-sided extrusion. The theory maps the master equations onto diffusion on a state graph yielding state-resolved loop-length PDFs.

We show that one-sided extrusion yields a universal exponential loop-length distribution, whereas two-sided extrusion generates a sum of exponentials that approaches a gamma-like form at high barrier density. The model also predicts a strictly positive lower bound of $1/4$ on arm-arm correlations.

Parameterized with independent measurements for HeLa G1 (cohesin residence and spacing; barrier densities and lifetimes), our model quantitatively accounts for the observed loop size. Also, it reproduces the experimentally measured distribution of CTCF-CTCF loop lengths under the assumption of two-sided extrusion, providing additional evidence that cohesin extrusion in living cells is predominantly bidirectional. Our results provide a compact route to infer biophysical parameters of active extrusion from experimental data.