CPP 18: Active Matter III (joint session BP/CPP/DY)

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

CPP 18.1 Tue 9:30 BAR/SCHÖ

inertia-driven re-entrant coil-Globule transition of active ring polymers — •Sunil P Singh[1], Roland G Winkler[2], Rakesh Palariya[1], and Arindam Panda[1] — [1]Indian Institute of Science Education and Research Bhopal, India — [2]Theoretical Physics of Living Matter, Institute for Advanced Simulation, Forschungszentrum Jülich, 52425 Germany

The role of inertia in the collective dynamics of active systems has been a subject of increasing interest in recent studies. The present study investigates the inertial effects on active agents. We present the conformational and dynamical characteristics of an active Brownian ring polymer using Langevin dynamics simulations. We show that a long active ring polymer shrinks into globular-like structures even in the absence of attractive interactions. This transition becomes sharper and the structures more compressed as the reduced moment of inertia of the monomers increases, particularly in the intermediate range of activity. We demonstrate that the ring polymer undergoes a coil-globule-coil transition, which is modulated by both activity and rotational inertia. The coil-to-globule transition is mapped in the inertial parameter space (J-M) using the radius of gyration. Additional physical quantities, including bond-bond correlations, scaling behavior in the compressed state, monomer contact probability, geometric distances, coordination number, and effective temperature, further elucidate the physical mechanism driving the collapse. Finally, we show that the effective diffusivity of the ring polymer increases with the reduced moment of inertia as $D_p \sim \sqrt{J}$.

CPP 18.2 Tue 9:45 BAR/SCHÖ

Shape selectivity by complex buckling dynamics in poroelastic active gels — •Kinjal Dasbiswas[1], Subhaya Bose[1], Arnab Roy[1], Michael Vennettilli[1], and Anne Bernheim[2] — [1]University of California, Merced, USA — [2]Ben Gurion University, Israel

Shape change in animal cells is prototypically driven by active forces, generated by myosin molecular motors bound to the actin cytoskeleton. Inspired by experiments on disc-shaped extracts of crosslinked actomyosin gels, we aim to show how a family of 3D shapes can arise from buckling caused by non-uniform active stresses. Although synthesized with identical composition of actin, myosin and the crossliker fascin, these gels contract and buckle into different shapes depending on the initial aspect ratio of the disc: thinner gels tend to wrinkle, while thicker gels tend to form domes. By incorporating active stresses, actin alignment, and stress-dependent myosin binding kinetics into a 2D poroelastic gel model, we qualitatively capture trends in gel contraction dynamics observed from quantitative particle image velocimetry (PIV). Next, we carry out numeric simulations of a geometric elastic model for thin sheets to obtain 3D buckled shapes from the strain rates predicted by the poroelastic model. Our results show that the coupling of elasticity to solvent flow, motor binding and fiber alignment play an important role in shape changes in living matter. Our studies have implications for shape changes during tissue morphogenesis and cell migration.

CPP 18.3 Tue 10:00 BAR/SCHÖ

The energy cost to build a spindle — •Dongliang Zhang[1], Xingbo Yang[4], Jan Brugués[2,1,3,4], and Frank Jülicher[1,3,4] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]Center for Systems Biology Dresden, Dresden, Germany — [4]Physics of Life, Cluster of Excellence, TU Dresden, Dresden, Germany

Spindle is a structure actively build from microtubules (MTs), and plays an important role for chromosome segregation during cell cycle. It's observed in experiments that the spindle size and shape depends on the cell level metabolic rate. In this work, we developed a minimal model that captures the active, energy-consuming processes such as MT turnover and active stress generation, which shows the energy cost for spindle mass maintenance and spindle-shape formation. We show that a spindle can be self-organized through these active processes. We aim to predict how the size and shape of the spindle depends on the energy input, and explain relative experimental phenomena, e.g. spindle shrinkage when the metabolism level is reduced.

CPP 18.4 Tue 10:15 BAR/SCHÖ

Cytoskeletal oscillations drive large-scale flows and nuclear organization in early embryonic systems. — •Lara Koehler, Elissavet Sandaltzopoulou, and Jan Brugués — Physics Of Life, TU Dresden

Synchronization drives early embryonic development, enabling simultaneous cell divisions and the spatial organization of nuclei within the embryo. In organisms such as Xenopus, Drosophila, and zebrafish, mitotic waves coordinate cell cycles across distances that exceed diffusion limits, guided by a chemical oscillator. At the same time, global cytoplasmic flows in these syncytial tissues contribute to the large-scale self-organization of nuclei, yet the coupling between biochemical signaling and cytoskeletal mechanics that underlies these directed flows remains poorly understood. Here, we relax the geometric constraints of the embryo and investigate nuclear dynamics in Xenopus egg extracts and complementary simulations. We show that the periodic polymerization and depolymerization of microtubule asters are sufficient to generate robust large-scale directed flows, even though the asters are intrinsically isotropic. Furthermore, we demonstrate that cell division stabilizes short-range order in a global synchronized system. Together, these findings reveal a minimal physical mechanism by which cytoskeletal dynamics and biochemical oscillations jointly organize flows and patterns, with implications for understanding the emergent principles that shape early development across species.

CPP 18.5 Tue 10:30 BAR/SCHÖ

Geometric control of cell migration in disordered porous media — •Laeschkir Würthner[1] and Frederik Graw[2] — [1]European Molecular Biology Laboratory, Heidelberg, Germany — [2]Friedrich-Alexander-Universität Erlangen-Nürnberg and Universitätsklinikum Erlangen, Erlangen, Germany

Cell migration is a dynamic process that plays a central role in development, wound healing, and immune responses. Active cell movement is controlled by several biochemical and mechanical cues, including chemokine gradients and the mechanical properties of the extracellular matrix (ECM). Although the biochemical pathways underlying directed cell motion are increasingly well understood, the influence of the porous structure of the ECM on active cell motion remains largely unexplored. Using a combination of computational modeling and theory, we investigate how active cells move through 3D disordered porous environments. We show that cell migration in disordered porous media can be understood as a generalized random walk among "traps", with the effective diffusivity determined by the geometry of the microenvironment. A key implication of our work is that spatial heterogeneities in porosity effectively direct cell motion, revealing a guidance mechanism that we refer to as porotaxis. Overall, our work connects geometry with cell motility and underscores the microenvironment as a key regulator of cell migration.

CPP 18.6 Tue 10:45 BAR/SCHÖ

Motility-induced mixing transition in exponentially growing multicellular spheroids — •Torben Sunkel[1,2], Lukas Hupe[1,2], and Philip Bittihn[1,2] — [1]MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, University of Göttingen, Germany

Growth drives cellular dynamics in various dense aggregates, but its effects on other relevant activities have only received limited attention. Here, we investigate the interplay of unconstrained growth, steric repulsion and motility in a minimal agent-based model of exponentially growing, three-dimensional spheroids. Our results reveal a diverging mixing time scale at a critical motility threshold, below which mixing of cells is completely suppressed. Above the threshold, large-scale mixing is enabled. Using an effective phenomenological model parameterized from full simulations, we identify two fundamental mechanisms governing this transition: On the cell scale, weak motility-induced active motion is locally suppressed by growth-induced steric repulsion, consistent with an Active Brownian Particle type description of single-cell dynamics. Beyond this, the expanding nature of the system inhibits global mixing purely geometrically by limiting the exploration range of diffusive cell motion. Both mechanisms naturally scale with the growth rate, highlighting the nature of the transition as an interplay between proliferation and motility. The results provide a baseline for

identifying additional biological mechanisms in experiments and could be relevant for competition, heterogeneous tumor evolution and other manifestations of motile proliferating active matter.

15 min. break

CPP 18.7 Tue 11:15 BAR/SCHÖ

Fluctuation-Response Theory of Non-Equilibrium Complex Fluids — •Ryota Takaki[1] and Frank Jülicher[1,2,3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Center for Systems Biology Dresden, Dresden, Germany — [3]Cluster of Excellence Physics of Life, TU Dresden, Dresden, Germany

Active soft materials such as cytoplasm and tissues are constantly driven by chemical reactions and often retain long-lived mechanical memory. In this work, we develop a generalized hydrodynamic framework applicable to non-equilibrium fluids with memory at finite wavevectors and frequencies. Our approach is based on exact correlation-function identities, leading to a fluctuation-response relation for steady states, including non-equilibrium. Applying the theory to chemically driven active fluids, we uncover Active Viscoelastic Memory, in which reaction cycles dynamically renormalize the viscous response and can generate negative storage moduli at finite frequency, absent in conventional viscoelastic materials. Our results provide a first-principles basis for modeling memory-dependent dynamics in a broad class of biological and synthetic active systems, and suggest concrete rheological signatures of chemical driving that can be tested experimentally.

CPP 18.8 Tue 11:30 BAR/SCHÖ

Chemically Active Liquid Bridges Generate Repulsive Forces — •Noah Ziethen — DAMTP, University of Cambridge, UK

Intracellular droplets help organize cells by compartmentalizing biomolecules and mediating mechanical interactions. When such droplets bridge two structures, they generate capillary forces that depend on the surface properties and the separation between the structures. While the forces exerted by passive liquid bridges are well understood, the impact of active chemical reactions, ubiquitous in biological condensates, remains unclear.

Here, we investigate a single liquid bridge with continuous chemical turnover, in which the production and degradation of droplet material maintain a non-equilibrium steady state. In this active bridge, the reactions dynamically set the bridge radius, thereby controlling the force-distance relation. In striking contrast to passive systems, we find that activity can generate purely repulsive forces over a broad range of separations. These results show that chemical activity can qualitatively alter capillary forces generated by liquid bridges, suggesting a potential route for cells to actively regulate mechanical coupling via droplets.

CPP 18.9 Tue 11:45 BAR/SCHÖ

Shared Laws of Pattern Formation in Reaction-Diffusion and Phase Separation — •Daniel Zhou[1] and Erwin Frey[1,2] — [1]Arnold Sommerfeld Center for Theoretical Physics — [2]Max Planck School Matter to Life

Many nonlinear field theories generate a strikingly similar repertoire of patterns: arrested coarsening, traveling waves, and spatiotemporal chaos appear both in phase-separating systems and in classical reaction-diffusion models. These descriptions have different physical origins, yet recent studies on Turing mixtures and foams in protein systems [1] and on chemotaxis-driven phase separation in cell populations [2] have already highlighted unexpected connections between these ostensibly different mechanisms, linking foam-like, phase-separating, and reaction-diffusion-type patterns. The present work revisits the relation between kinetic and phase-separating descriptions from a more general viewpoint. A unifying perspective is developed that places different modeling frameworks on comparable footing, identifies the conditions under which they yield effectively equivalent patterns, and suggests how stability criteria and design principles can be translated between them. This points toward a more systematic classification of pattern-forming dynamics that cuts across traditional divides between reaction-diffusion, chemotactic, and phase-separating systems.

[1] H. Weyer et. al, Deciphering the Interface Laws of Turing Mixtures and Foams, arXiv:2409.20070 (2024).

[2] H. Weyer et. al, Chemotaxis-Induced Phase Separation, Physical Review Letters 135, 208402 (2025).

CPP 18.10 Tue 12:00 BAR/SCHÖ

Spatial self-organization of enzymes in complex reaction networks — •Vincent Ouazan-Reboul[1,2], Ramin Golestanian[2,3], and Jaime Agudo-Canalejo[2,4] — [1]LPTMS, CNRS, Université Paris-Sud, 91400, Orsay, France — [2]Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, D-37077, Göttingen, Germany — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, OX1 3PU, Oxford, UK — [4]Department of Physics and Astronomy, University College London, WC1E 6BT, London, UK

Living systems contain intricate biochemical networks whose structure is closely related to their function and allows them to exhibit robust behavior in the presence of external stimuli. Such networks typically involve catalytic enzymes, which can have non-trivial transport properties, in particular chemotaxis-like directed motion along gradients of substrates and products. Here, we find that taking into account enzyme chemotaxis in models of catalyzed reaction networks can lead to their spatial self-organization in a process similar to biomolecular condensate formation. We develop a general theory for arbitrary reaction networks, and systematically study all closed unimolecular reaction networks involving up to six chemicals. Importantly, we find that network-wide propagation of concentration perturbations can be key to enabling self-organization, in a manner which is highly sensitive on the global network structure.

CPP 18.11 Tue 12:15 BAR/SCHÖ

Spatial organisation of the cell's metabolic power plant via phase separation — •Kathrin S. Laxhuber[1,2] and Frank Jülicher[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck School Matter to Life

Cell metabolism is the power plant that fuels the active processes essential to life. Recent experimental results show that glycolytic enzymes, central to sugar metabolism, phase-separate to form foci under energetic stress and can localise to sites of demand. To understand this phenomenon, we build and study a minimal theoretical model. We show that droplet formation can act as a metabolic switch that enables the system to maintain energetic homeostasis at higher output power. Notably, the metabolic droplets that emerge from this switch can self-organise to colocalise with demand. We discuss the non-equilibrium features and spatial energetic profiles in this system.

CPP 18.12 Tue 12:30 BAR/SCHÖ

Emergent interactions lead to collective frustration in robotic matter — •Onurcan Bektas[1,3], Adolfo Alsina[2,3], and Steffen Rulands[1,3] — [1]Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoSciences, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München, Germany — [2]GISC, Universidad Rey Juan Carlos, Tulipán, 28933, Móstoles, Spain — [3]Max-Planck-Institute for the Physics of Complex Systems, Noethnitzer Str. 38, 01187 Dresden, Germany

Current artificial intelligence systems show near-human-level capabilities when deployed in isolation. Systems with intelligent agents are deployed to perform tasks collectively. This raises the question of whether robotic matter, where many learning and intelligent agents interact, shows emergence of collective behaviour. And if so, what kind of phenomena would such systems exhibit? Here, we study a paradigmatic model for robotic matter: a system composed of a large collection of stochastic interacting particles where each particle is endowed with a deep neural network that optimizes its transitions based on the particles' environments. For a 1D model, robotic matter exhibits complex phenomena arising from emergent interactions, including transitions between long-lived learning regimes, the emergence of particle species, and frustration. We also find an abrupt, density-dependent change in the behaviour of particles. Using active matter theory, we show that this phenomenon is a reflection of a phase transition with signatures of criticality. Our model captures key phenomena observed in more complex forms of robotic systems.