BP 31: Active Matter IV (joint session BP/CPP/DY)

Time: Friday 9:30–13:00 Location: H44

Invited Talk BP 31.1 Fri 9:30 H44

Wave propagation in systems of active filaments — •Kirsty Y. Wan — Living Systems Institute, University of Exeter, UK

Active hair-like protrusions called cilia are found in many eukaryotes where they produce physiological flows for a variety of functions. Cilia assume a myriad of configurations both external to an organism for the purposes of feeding or swimming motility, but also internally where they mediate mucociliary clearance in vertebrate tissues. Single cilia can propagate large-amplitude non-decaying bending waves, even in the absence of a cell body. These waves assume a variety of stereotyped forms and frequencies, depending on the species. Multiple cilia also interact to produce different types of local and global coordination patterns, including robust metachronal waves. Do these dynamic states of coordination arise spontaneously, or do they require some form of internal control by the cell or animal? We propose new and emerging organisms to address these questions.

BP 31.2 Fri 10:00 H44

Metabolic activity controls the emergence of coherent flows in microbial suspensions — •Florian Böhme[1], Alexandros Fragkopoulos[1,2], Nicole Drewes[2], and Oliver Bäumchen[1,2] — [1]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [2]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany

Photosynthetic microbes have evolved and successfully adapted to the spatio-temporal variations of environmental parameters within their habitat. In the abscence of light, they can still sustain their biological functionality and metabolic activity through aerobic respiration. However, for the soil-dwelling microalga *Chlamydomonas reinhardtii*, their environment may be deprived of both oxygen and light, resulting in a significant reduction of their swimming velocity [1]. Here, we study the effect of motility and cell density of *C. reinhardtii* in a confined system, on the emergence of bioconvection [2]. This collective phenomenon can be reversibly switched by light and arises due to the natural tendency of the bottom-heavy cells to move against gravity. We show that the rate at which the system evolves, as well as the dominant wavelength of the instability can both be directly controlled by the number density of cells. Further, we provide insights on the internal flow fields and density profiles of single bioconvection plumes for different parameters.

[1] A.A. Fragkopoulos et al., *J. R. Soc. Interface* **18**, 20210553 (2021).
[2] A.A. Fragkopoulos et al., *arXiv*:2407.09884 (2024)

BP 31.3 Fri 10:15 H44

Tumbling *E.coli* in bulk and close to surfaces — •Pierre Martin[1], Tapan Chandra Adhyapak[2], and Holger Stark[1] — [1]Institute of Theoretical Physics, Hardenbergstr. 36, 10623 Berlin, Germany — [2]Indian institute of science education and research (IISER), Tirupati, India

Escherichia coli (*E. coli*) swims by rotating multiple flagella which are connected to the cell body forming a thick bundle. To change direction, *E. coli* performs tumble events by reversing the rotation of one or more flagella. The involved filaments undergo a series of polymorphic transformations, altering both their helicity and handedness. This complex phenomenon involves the interplay of semiflexible filaments and hydrodynamic flow fields.

Here, we have developed a detailed numerical framework to simulate *E. coli*, capturing the full dynamics of flexible flagella, including their polymorphism and their hydrodynamic interactions. The filaments and the cell body are embedded in a viscous fluid, which we model using multi-particle collision dynamics. We analyzed a large number of tumble events, with fixed tumble time or taken from a gamma distribution, exploring the roles of hook and flagellar flexibility as well as flagellar polymorphism. We find that they strongly influence the distribution of tumble angles. Finally, we also show that close to a flat surface the mean tumble angle is strongly shifted to smaller values. This indicates that tumble events may not be recognized, which could give the impression of suppressed tumbling near surfaces.

BP 31.4 Fri 10:30 H44

***Trypanosoma brucei* (un)chained - effects of confinement on a parasitic microswimmer** — •Hannes Wunderlich[1], Marinus Thein[2], Lucas Brehm[2], Klaus Ersfeld[2], and Matthias Weiss[1] — [1]Experimental Physics I, University of Bayreuth — [2]Laboratory of Molecular Parasitology, University of Bayreuth

Trypanosoma brucei is a parasitic unicellular microswimmer that causes the African sleeping sickness. An active spiral movement of the parasite, mediated by a microtubule-driven flagellum that wraps around the cell body, is mandatory to evade the host's immune system while exploring tissues and blood vessels. In addition, the nematic subpellicular micotubule array plays a pivotal role in the elasticity, propulsion, and navigation of the parasite. To study the features and mechanisms behind the cell's motion in such complex environments, we have mimicked spatial confinement in microfluidic devices with different geometries. Our data show that spatial constraints in narrow channels and channel networks can improve cell locomotion of wild-type trypanosomes, supposedly due to the interaction of the elastic cell body and nearby walls. The addition of microtubule-disrupting drugs or the use of mutant strains with altered post-translational modifications of microtubules resulted in significantly altered swimming velocities and marked changes in the intermittent switching between run and tumble phases. Shape analyses of individual cells suggest that microtubules in the sub-pellicular array, the corset that keeps trypanosomes in their native spindle-like shape, are most affected in these cases.

BP 31.5 Fri 10:45 H44

Micro-swimmer motility in presence of signaling factors — Agniva Datta, Robert Grossmann, and •Carsten Beta — Institute of Physics and Astronomy, University of Potsdam, Germany

The navigation of bacteria through aqueous environments, driven by the rotation of helical flagella, has been a significant region of interest in the biophysics community for the last few decades. In this study, we focus on the motility of our model organism, Pseudomonas putida, which exhibits persistent mobile episodes (Active Brownian motion) interrupted by stochastic reorientation events (turns), driven by flagellar self-propulsion, thereby leading to a run-and-turn motility.

Key motility parameters including tumbling rates, run lengths, trajectory persistence (rotational diffusion coefficient), and the characteristics of the self-propulsion force*are hypothesized to depend on the density of quorum-sensing autoinducer molecules, produced by the bacteria themselves as signaling factors. To test this hypothesis, we expose swimming bacteria to aqueous environments with controlled autoinducer concentrations and analyze the resulting changes in motility patterns. Through a combination of experimental data and theoretical modeling, we aim to elucidate the principles of micro-swimmer motility in presence of signaling molecules.

BP 31.6 Fri 11:00 H44

Collective dynamics of active dumbbells near a circular obstacle — •Chandranshu Tiwari[1] and Sunil Singh[2] — [1]Department of Physics, Indian Institute of Science Education and Research, Bhopal 462066, India. — [2]Department of Physics, Indian Institute of Science Education and Research, Bhopal 462066, India.

We present the collective dynamics of active dumbbells in the presence of a static circular obstacle using Brownian dynamics simulation. The active dumbbells aggregate on the surface of a circular obstacle beyond a critical radius, and the aggregate size increases with the activity and the curvature radius. The dense aggregate of active dumbbells displays persistent rotational motion with a certain angular speed, which linearly increases with activity. Furthermore, we show a strong polar ordering of the active dumbbells within the aggregate. The polar ordering exhibits long-range correlation, with the correlation length corresponding to the aggregate size. Additionally, we show that the residence time of an active dumbbell on the obstacle surface increases rapidly with area fraction due to many-body interactions that lead to a slowdown of the rotational diffusion. This article further considers the dynamical behavior of a tracer particle in the solution of active dumbbells. Interestingly, the speed of the passive tracer particle displays a crossover from monotonically decreasing to increasing with the size of the tracer particle upon increasing the dumbbells' speed. Furthermore, the effective diffusion of the tracer particle displays non-monotonic behavior with the area fraction; the initial increase in diffusivity is followed by a decrease for a larger area fraction.

BP 31.7 Fri 11:15 H44

Free growth under tension

•Chenyun Yao and Jens Elgeti — Forschungszentrum Jülich GmbH, Jülich, Germany

Ever since the ground breaking work of Trepat et al. in 2009, we know that cell colonies growing on a substrate can be under tensile mechanical stress. The origin of tension has so far been attributed to cellular motility forces being oriented outward of the colony. Works in the field mainly revolve around how this orientation of the forces can be explained, ranging from velocity alignment, self-sorting due to self-propulsion, to kenotaxis.

In this work, we demonstrate that tension in growing colonies can also be explained without cellular motility forces! Using a combination of well established tissue growth simulation technique and analytical modelling, we show how tension can arise as a consequence of simple mechanics of growing tissues. Combining these models with a minimalistic motility model shows how colonies can expand while under even larger tension. Furthermore, our results and analytical models provide novel analysis procedures to identify the underlying mechanics.

15 min. break

BP 31.8 Fri 11:45 H44

A route to active turbulence in circular activity spots

•Arghavan Partovifard and Holger Stark — Institute of Theoretical Physics, Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstr. 36, 10623Berlin, Germany.

Active nematics exhibit distinctive behavior such as active turbulence and regular flow patterns under spatially varying activity [1]. Utilizing the Doi-Edwards theory supplemented by an active stress tensor [1], we investigate active nematics confined to a circular spot by switching off activity outside the spot. The open boundary allows topological defects to enter and leave the spot.

We calculate the total topological defect charge inside the spot using three approaches: counting all defects, measuring the rotation of the director field along the rim of the spot, and integrating the diffusive charge density. All methods agree that for spot radii just larger than the nematic coherence length, the system has a total topological charge of $+1$, where two $+1/2$ defects perform a regular swirling motion. As the radius increases, more defects enter and their motion becomes more and more chaotic. Ultimately, the charge per unit area saturates at the value characteristic of bulk active turbulence. For the range of radii where the total charge in the spot is $+1$, the nematic director exhibits shear-induced anchoring at an angle of 45° with respect to the tangent at the spot rim. With increasing radius, when more defects enter, the anchoring angle deviates from 45° but its distribution still peaks around this value.

[1] A. Partovifard *et. al.*, Soft Matter **20**, 1800 (2024)

BP 31.9 Fri 12:00 H44

Cognitive flocks: order-disorder transitions and threat evasion

•Priyanka Iyer[1], Cecilia Soroco[2], and Gerhard Gompper[1] — [1]Forschungszentrum Jülich — [2]University of British Columbia, Canada

Directed self-propulsion is ubiquitous in living organisms. From E.Coli dispersing in biofilms to migrating bird flocks, living organisms are constantly out-of equilibrium. By sensing their environment and adjusting their movement, organisms can exhibit emergent patterns and collective behaviors, such as self-organization in human crowds [1], bird flocks, and fish schools. The Inertial Spin Model (ISM) was introduced to explain the fast and robust propagation of information in bird flocks [2], when only alignment interactions are considered. However, more generally, agents exhibit a variety of interactions like local avoidance, cohesion and threat evasion. We show how such behaviors can be incorporated within the framework of the ISM. It is found that local avoidance introduces emergent noise in the system, triggering an order-disorder transition. Exploring the flock dynamics near this transition reveals a complex interplay between cohesion, alignment, and local avoidance, resulting in diverse behaviors such as pronounced shape and density fluctuations, and diffusive motion of the flock. Lastly, by applying the model to a stationary threat scenario, we analyze flock properties that govern threat information propagation in the flock.

[1] Iyer, P. et al. , Comm. Phys. 7.1 (2024): 379.
[2] Attanasi, A. et al. , Nat. Phys. 10, 691-696, (2014)

BP 31.10 Fri 12:15 H44

Myosin-independent amoeboid cell motility

•Winfried Schmidt, Alexander Farutin, and Chaouqi Misbah — Univ. Grenoble Alpes, CNRS, LIPhy, F-38000 Grenoble, France

Mammalian cell motility is essential for many physiological and pathological processes, such as the immune system, embryonic development, wound healing, and cancer metastasis. Cells have developed the amoeboid migration mode which allows them to move rapidly in a variety of different environments, including two-dimensional confinement, three-dimensional matrix, and bulk fluids. We introduce a model for an amoeboid cell where the cortex is described as a thin shell along the cell surface. The cell shape evolves due to polymerization of actin filaments and the forces acting on the cortex. We find analytically and numerically that the state of a resting, non-polarized cell can become unstable for sufficiently large actin polymerization velocities, resulting in the spontaneous onset of cell polarity, migration, and dynamical shape changes. Notably, this transition only relies on actin polymerization and does not necessitate molecular motors, such as myosin. These findings yield a deeper understanding of the fundamental mechanisms of cell movement and simultaneously provide a simple mechanism for cell motility in diverse configurations.

BP 31.11 Fri 12:30 H44

Active membrane deformations of a synthetic cell-mimicking system

Alfredo Sciortino[1], •Dmitry Fedosov[2], Gerhard Gompper[2], and Andreas Bausch[1] — [1]Physik Department, Technische Universität München, Garching bei München, Germany — [2]Institute for Advanced Simulation, Forschungszentrum Jülich, Jülich, Germany

Biological cells are fascinating micromachines capable of adapting their shape due to the complex interaction between a deformable membrane and the dynamic activity of the cytoskeleton. We investigate the behavior of an active synthetic cell-mimicking system using simulations and experiments. In simulations, the model consists of a fluid vesicle with a few encapsulated growing filaments. In experiments, giant vesicles contain an active cytoskeletal network composed of microtubules, crosslinkers, and molecular motors. These active vesicles show strong shape fluctuations reminiscent of shape changes of biological cells. We analyze membrane fluctuations and show how the intricate coupling between soft confinement and internal active forces results in fluctuation spectra with distinct spatial and temporal scales, differing significantly from those of passive vesicles. Simulations demonstrate the universality of this behavior, quantifying the impact of correlated activity on the dynamics of membrane deformations. This model makes a step toward quantitative description of shape-morphing artificial and living systems.

BP 31.12 Fri 12:45 H44

Force Generation by Enhanced Diffusion in Enzyme-Loaded Vesicles

Eike Eberhard, •Ludwig Burger, Cesar Pastrana, Giovanni Giunta, and Ulrich Gerland — Physik komplexer Biosysteme, Technische Universität München, Deutschland

Recent experiments show that the diffusion coefficient of some metabolic enzymes increases with the concentration of their cognate substrate, a phenomenon known as enhanced diffusion. In the presence of substrate gradients, enhanced diffusion induces enzymatic drift, resulting in a non-homogeneous enzyme distribution. In this work, we study the behavior of enzyme-loaded vesicles exposed to external substrate gradients using a combination of computer simulations and analytical modeling. We observe that the spatially inhomogeneous enzyme profiles generated by enhanced diffusion result in a pressure gradient across the vesicle, which leads to macroscopically observable effects, such as deformation and self-propulsion of the vesicle. Our analytical model allows us to characterize dependence of the velocity of propulsion on experimentally tunable parameters. The effects predicted by our work provide an avenue for further validation of enhanced diffusion, and might be leveraged for the design of novel synthetic cargo transporters, such as targeted drug delivery systems.