DY 26: Active matter I (joint session BP/CPP/DY)

Time: Wednesday 9:30–13:00 Location: H4

DY 26.1 Wed 9:30 H4

Self-assembled active systems - from individuals to a collective behaviour — •Aitor Martin-Gomez, Gerhard Gompper, and Roland G. Winkler — Forschungszentrum Juelich (ICS-2), Juelich, Germany

Active matter is comprised of agents which either convert internal energy or exploit energy from the environment to generate directed motion. Its associated out-of-equilibrium character is the origin of a number of fascinating phenomena. In particular, active systems with many internal degrees of freedom like filamentous, polymer-like structures are involved in various biological processes and exhibit novel conformational and dynamical properties. Moreover, the study of collective behavior emerging from the non-linear contributions of many individuals is an ongoing, open question. In conclusion, to shed light onto the effect of such active systems, or their passive counterparts embedded in an active environment, we perform analytical calculations combined to advanced computer simulations.

DY 26.2 Wed 9:45 H4

Light-dependent microbial motility induces pattern formation in confinement — •Alexandros Fragkopoulos[1], Johannes Frey[1], Flora-Maud Le Menn[1], Jeremy Vachier[1], Michael Wilczek[1], Marco Mazza[1,2], and Oliver Bäumchen[1] — [1]Max Planck Institute for Dynamics and Self-Organization, D-37077 Göttingen, Germany — [2]Loughborough University, Loughborough LE11 3TU, United Kingdom

A collection of active swimmers can undergo complex dynamics due to hydrodynamic and steric interactions. For sufficiently concentrated suspensions, it is possible to form large-scale concentration patterns, where the active suspension separates into regions of high and low particle concentrations. Here we present that a collection of *Chlamydomonas reinhardtii* cells, a unicellular soil-dwelling microalgae and a model organism of puller-type microswimmers, form patterns of high and low cell density regions in confinement and under specific light conditions. We find that the motility of the cells differs significantly for different light intensities and cell densities, which regulate the pattern formation in such active suspensions. In addition, we observe that the emerged pattern follows the shape of the confinement that encloses the motile cells, which indicates that the boundaries enclosing the motile cells play a crucial role for pattern formation. Finally, by performing active Brownian dynamics simulations of active particles with the observed motility characteristics, we show that we can reproduce the experimentally observed patterns.

DY 26.3 Wed 10:00 H4

Active Matter Invasion into Capillaries — •Felix Kempf[1], Romain Mueller[2], Erwin Frey[1], Juila Yeomans[2], and Amin Doostmohammadi[2] — [1]Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Department of Physics, Ludwig-Maximilians-Universität München - Theresienstr. 37, D-80333 München, Germany — [2]The Rudolf Peierls Centre for Theoretical Physics - Clarendon Laboratory, Parks Road, Oxford, OX1 3PU, UK

Biological active materials such as bacterial biofilms and eukaryotic cells thrive in confined microspaces. Here, we numerically show that combining growth dynamics with their intrinsic activity active material can use confinement as a mechanical guidance to achieve distinct modes of collective invasion. We assess the dynamics of the growing interface and classify these collective modes of invasion based on the activity of the active substance. While at small and moderate activities the active material grows as a coherent unit, we find blobs of active materials collectively detaching from the cohort above an activity threshold in a process reminiscent of the intravasation in cancer cells. We further characterise the mechanical mechanisms of transition between different modes of invasion.

DY 26.4 Wed 10:15 H4

Collective Responses of Magnetic Swimmers in a Poiseuille Flow — •Fanlong Meng[1,2], Daiki Matsunaga[2], and Ramin Golestanian[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Goettingen, Germany — [2]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford OX1 3PU, United Kingdom

Magnetotactic bacteria can be focused at the radial centre of a microfluidic channel under an external magnetic field, and found to form clusters if the external magnetic field is strong or the flow speed is large [1]. However, the underlying mechanism was missing. We show that the magnetic microswimmers (not only for magnetotactic bacteria, but also applicable to synthetic magnetic microswimmers) can form interesting large-scale clusters when the magnetic attractive interaction dominates thermal fluctuations. By applying analytic techniques and conducting Brownian dynamics simulation, we provide the critical conditions for clustering of magnetic microswimmers, which matches well with the experiment. Hydrodynamic interactions between the microswimmers are also incorporated as a generalisation. Understanding the physics of magnetic active matter will help advance the cause of studying matter out of equilibrium, and provides new insight for technological applications of synthetic magnetic microrobots (for drug delivery, solution stirring, etc.) with desired collective properties. References: [1] N. Waisbord, C. T. Lefèvre, L. Bocquet, C. Ybert, C. Cottin-Bizonne, Phys. Rev. Fluids, (2016) 1, 053203 [2] F. Meng, D. Matsunaga, R. Golestanian, Phys. Rev. Lett., (2018) 120, 188101

DY 26.5 Wed 10:30 H4

Hydrodynamic simulations of flagellated bacteria in polymer solutions and polymer networks — •Andreas Zöttl and Julia M Yeomans — University of Oxford, UK

Many cells in the human body have to move through dense complex fluids such as various cells in the extracellular matrix or bacteria in mucus. While the motion of swimming bacteria in simple Newtonian fluids can be well quantified using continuum low Reynolds number hydrodynamics, the presence of supramolecular elements such as biopolymers leads to a much more complex behavior. Although the presence of polymers generally lowers particle mobility, surprisingly, several experiments have shown that bacterial speeds increase in polymeric fluids, but there is no clear understanding why.

We perform extensive coarse-grained MPCD simulations of a bacterium swimming in explicitly modeled solutions of supramolecular model polymers of different lengths, stiffness and densities. We observe an increase of up to 60% in swimming speed with polymer density and show that this is a consequence of a non-uniform distribution of polymers in the vicinity of the bacterium leading to an effective slip. However, this alone cannot explain the large speed-up, but coupling to the chirality of the bacterial flagellum is essential. Finally we present results for swimming in crosslinked polymer networks where hydrodynamics is screened and speed enhancement is also observed.

DY 26.6 Wed 10:45 H4

Memory-induced persistent motion — •Bernhard Georg Mitterwallner, Laura Lavacchi, and Roland Netz — Institut für theoretisch Physik, Frei Universität Berlin, Berlin, Germany

We investigate the mean-square displacement (MSD) for random motion governed by the generalized Langevin equation for different two-scale memory-kernel models: In the first model, the memory kernel consists of a delta peak and a single exponential and in the second model of the sum of two exponentials. In particular, we investigate the scenario where the long-time exponential kernel contribution is negative. The competition between positive and negative friction contributions produces an enhanced transient ballistic regime in the MSD, which is relevant for biological motility and active matter systems.

15 minutes break.

Invited Talk DY 26.7 Wed 11:15 H4

Non-equilibrium dynamics in biological matter — •Christoph F Schmidt — Georg-August-Universität, Fakultät für Physik, Drittes Physikalisches Institut - Biophysik, Friedrich-Hund-Platz 1, 37077 Göttingen — Duke University, Department of Physics, 2316 French Family Science Center, 124 Science Drive, Durham, NC 27708, USA

Thermodynamic non-equilibrium is a defining feature of living systems on all levels of organization. Cells and tissues are built of active matter, dynamic materials with built-in force generators. Such materials self-organize in biological systems into well-ordered dynamic steady states, sustained by the dissipation of metabolic energy. The materials show

striking collective phenomena on a mesoscopic scale. We used light microscopy to characterize the complex mechanical properties of and the motion and stress patterns in biological active matter, in particular the actin cortex, both in reconstituted model systems and in cells. I will introduce a method to detect and quantitate thermodynamic non-equilibrium in the dynamics of primary cilia of kidney epithelial cells using the principle of detailed balance.

DY 26.8 Wed 11:45 H4

Enhanced rotational diffusion of squirmers in viscoelastic fluids — •Kai Qi[1], Elmar Westphal[2], Gerhard Gompper[1], and Roland Winkler[1] — [1]Theoretical Soft Matter and Biophysics, Institute for Advanced Simulation and Institute of Complex Systems, Forschungszentrum Jülich, D-52425 Jülich, Germany — [2]Peter Grünberg Institute and Jülich Centre for Neutron Science, Forschungszentrum Jülich, D-52425 Jülich, Germany

Squirmers are generic models for biological microswimmers and synthetic self-propelled particles. Fluid-mediated interactions are essential for their swimming behavior, which can be strongly affected by the fluid viscoelasticity. Here, we perform mesoscale hydrodynamic simulations via the multiparticle collision dynamics (MPC) method for a spherical squirmer in a viscoelastic fluid, which is composed of MPC fluid particles and polymers. Polymers are either of phantom nature or self-avoiding. The concentration of monomers on the squirmer surface is enhanced by introducing a short-range attraction between the squirmer and polymers. This leads to a decrease of the rotational diffusion for a passive colloid in the presence of polymers. Self-propulsion reduces the monomer concentration on the surface and the squirmer's rotational diffusion is enhanced considerably, up to a factor 20 for phantom polymers. The actual change of the rotational diffusion D_r depends on the polymer length. An increasing polymer length reduces D_r^0 of the passive colloid, but D_r of the squirmer is enhanced. Both effects contribute to the obtained substantial increase of the ratio D_r/D_r^0.

DY 26.9 Wed 12:00 H4

Modelling coordinated motion in simplest multicellular animals — •Stephan Meschede[1] and Pawel Romanczuk[2] — [1]Department of Physics, Humboldt Universität zu Berlin — [2]Institute for Theoretical Biology, Department of Biology, Humboldt Universität zu Berlin

Placozoa, Trichoplax adhaerens, are structurally simplest known multicellular animals. Their bodies are flat and irregular, up to few milimeters in diameter and $10-15\mu m$ thick [1]. They consists of three layers, an upper and a lower epithelium enclosing a fiber cell layer. The Trichoplax body plan is completely decentralized without any hierarchical structure or a central nervous system. However, they are capable of amoeba-like, coordinated active motion on substrates through ciliary locomotion. We show that individual Trichoplax motion behavior can be modeled as a two-dimensional 'sheet' of active particles coupled through elastic forces, building upon previous models of cellular migration model proposed by Szabo et al [2]. We discuss the emergence of coordinated motion and the role of animal size and elastic coupling strength for the stochastic motility. Our aim is to understand how the self-organized active sheet dynamics shapes and constrains the motion behavior of these simple animals and their ability to navigate the environment.

[1]: Miller, D. J., & Ball, E. E. (2005). Animal Evolution: The Enigmatic Phylum Placozoa Revisited. Current Biology, 15(1), 26-28.

[2]: Szabó, B. et al.(2006). Phase transition in the collective migration of tissue cells: Experiment and model. Phys. Rev. E, 74(6), 1-5.

DY 26.10 Wed 12:15 H4

Phase space geometry of reaction–diffusion systems — •Fridtjof Brauns, Jacob Halatek, and Erwin Frey — Arnold Sommerfeld Center for Theoret- ical Physics, Ludwig-Maximilians-Universität München, Germany

Self-organized pattern formation — typically studied in terms of spatially extended dynamical systems — is as ubiquitous in nature as it is difficult to deal with conceptually and mathematically. We build on the phase space geometric methods of Nonlinear Dynamics, using geometric structures like nullclines and fixed points, to develop a comprehensive theory for two-component mass-conserving reaction–diffusion systems — a paradigmatic model class for pattern formation, e.g. intracellular polarization. A dissection of space into (notional) compartments enables us to characterize the spatio-temporal dynamics based on the ODE phase space of local reactions. Diffusive coupling leads to mass redistribution between the compartments which, in turn, changes the local phase space properties.

We show that all aspects of pattern formation, from linear instability and excitability to the bifurcations of stationary patterns, can be extracted from the geometric features of the line of chemical equilibria in phase space. Furthermore, our analysis points towards a deep connection between the far from equilibrium reaction–diffusion dynamics to phase separation of binary mixtures near equilibrium, and thus offers a new perspective on phase separation far from equilibrium.

DY 26.11 Wed 12:30 H4

Diffusive dynamics of complex particles in active colloidal suspensions of motile algae — •Florian von Rüling and Alexey Eremin — Institute of Physics, Otto von Guericke Universität Magdeburg, Germany

We report experimental studies on the dynamics of complex passive particles in the presence of motile algae Chlamydomonas reinhardtii in thin capillaries. Employing video microscopy and particle tracking algorithm, the enhancement of the diffusion of elongated particles due to interactions with the microswimmers was explored. Depending on the number of motile algae, the translational and rotational diffusion constants of doublets of silica beads close to a solid boundary can be increased by several orders of magnitude in comparison to purely Brownian motion. At a high concentration of Chlamydomonas reinhardtii, the algae formed dense dynamic clusters at the lower capillary wall. In this state of the system, swimming and clustering algae interact with passive particles. Clustering algae can restrict both translational and rotational dynamics of the silica doublets. We explore the effect of the motion of algae in such active clusters on the dynamic of the passive silica doublets.

DY 26.12 Wed 12:45 H4

Self-propelled Dipolar Nanocubes — •Martin Kaiser[1], Sofia Kantorovich[1,2], Yeimy Martinez[3], and Annette Schmidt[3] — [1]University of Vienna, Austria — [2]Ural federal University, Russia — [3]Universität zu Köln, Germany

Microscopic active particles, including self-propelled cells, microorganisms and artificial swimming colloids, have gained a lot of attention due to their relevance in such important fields as biology, biomedicine, nanoscience and nanotechnology. The term "active" describes the ability of certain particles or units, to convert energy from their environment into motion, hence, kinetic energy.

In this study, we use active matter to create a new type of nanomotor, which is oriented by an applied magnetic field and propelled by an active particle. One of those units consists of a dipolar cube that can be directed due to its interaction with a magnetic field. A non-dipolar active particle attached to the cube, with a propulsion force directed into the cubes centre of mass, creates a field controlled swimming unit.

This scenario is investigated using molecular-dynamic simulations, setting the above described unit in an obstacle free environment while applying a constant magnetic field.

In collaboration with Dr. Schmidt from the University of Cologne, those nanomotors are also investigated experimentally.