

## BP 27: Fluid Physics of Life (joint session DY/BP)

Time: Wednesday 15:00–17:45

Location: ZEU 160

**Invited Talk**

BP 27.1 Wed 15:00 ZEU 160

**Light-regulated microbial dynamics and self-organization in complex geometries** — ●OLIVER BÄUMCHEN — Max Planck Institute for Dynamics and Self-Organization (MPIDS), Am Fassberg 17, D-37077 Göttingen, Germany

Life on Earth has evolved under the periodic exposure to sunlight and many microorganisms are equipped with a photosynthesis machinery enabling them to convert light into chemical energy. Their habitats include liquid-infused soil, porous rocks and microdroplets, featuring complex geometric architectures that induce strong spatial and temporal light fluctuations. Thus, biological functionalities to sense and rapidly respond to light fluctuations are pivotal for microbial life.

In this presentation I will discuss how concepts from non-equilibrium statistical physics, in conjunction with novel experimental approaches from soft matter and biophysics [1], enable us to decipher fundamental physical principles of microbial responses to light cues. We discovered that light regulates the transition of motile microbes from the free-swimming to the surface-adhered state [2]. I will further elaborate on how interfacial interactions govern the motility and navigation of individual cells in complex geometries [3] and demonstrate that the light-regulated motility controls the emergence of self-organization and phase separation of microbial populations in confinement.

[1] M. Backholm & O. Bäümchen, *Nature Protocols* 14, 594 (2019).

[2] C. Kreis et al., *Nature Physics* 14, 45 (2018).

[3] T. Ostapenko et al., *Phys. Rev. Lett.* 120, 068002 (2018).

BP 27.2 Wed 15:30 ZEU 160

**Wet-tip versus dry-tip regimes of osmotically driven bile flow in the liver** — OLEKSANDR OSTRENKO, MICHAEL KÜCKEN, and ●LUTZ BRUSCH — Center for Information Services and High Performance Computing (ZIH), Technische Universität Dresden, Germany

The secretion of osmolites into a lumen and thereby caused osmotic water inflow drive fluid flows like saliva, sweat and bile in organs without a mechanical pump, as opposed to the heart in blood circulation. The effects of elevated fluid pressure and the associated mechanical limitations of organ function remain largely unknown. We consider the pressure profile of the coupled osmolite-flow problem with combined velocity and pressure boundary conditions. Notably, the entire lateral boundary acts as a fluid source, the strength of which is determined by feedback from the emergent pressure solution itself. Hence, the pressure difference between the boundaries is not imposed but self-organises. Our theoretical results reveal fundamental parameter dependencies and a phase boundary separating the commonly considered “wet-tip” regime with steady flow out of the very tip of a channel from a “dry-tip” regime suffering stalled flow and a self-organised block of osmotic water inflow [1]. We validate model predictions against intra-vital video microscopy data from mouse liver [2] and propose a relation between the predicted phase boundary and the onset of zoned cholestasis, a pathological liver condition [3].

[1] Ostrenko et al. (2019) *Scientific Reports* 9, 4528. [2] Meyer et al. (2017) *Cell Systems* 4, 277. [3] Segovia-Miranda et al. (2019) *Nature Medicine and bioRxiv* 572073.

BP 27.3 Wed 15:45 ZEU 160

**Memory capacity of a flow network** — ●KOMAL BHATTACHARYYA<sup>1</sup>, DAVID ZWICKER<sup>1</sup>, and KAREN ALIM<sup>1,2</sup> — <sup>1</sup>Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany — <sup>2</sup>Physik-Department, Technische Universität München, Garching, Germany

The slime mould *Physarum polycephalum* is a very simple unicellular but seemingly intelligent organism with a network-like body. Its complex behaviour requires the ability to propagate, store and process information. Recently, it has been shown that *Physarum* propagates information about stimuli with the fluid flows throughout its network. Most inspiringly, *Physarum* was observed to adapt its networks tube radii globally in response to stimuli, reaching a steady-state as a long term response that keeps a memory of the stimuli in its network morphology. Inspired by this observation we here investigate the capacity to store information about previous stimuli in the morphology of an adaptive flow network. We model the organism as a flow network whose radii can change when optimising the network to have the least energy dissipation. We observe how the system reacts to localised changes

and the timescale of its responses to applied stimuli by numerical simulation. Through theoretical understanding, we aim to pinpoint the information storing and processing capabilities of adaptive flow networks in general and *Physarum* networks specifically.

BP 27.4 Wed 16:00 ZEU 160

**Fluid transport by metachronal waves in cilia chains** — ●ALBERT VON KENNE, THOMAS NIEDERMAYER, and MARKUS BÄR — Physikalisch-Technische Bundesanstalt (PTB), Berlin 10587

Motile cilia are hair-like cell extensions that undergo a cyclic motion with the purpose to transport the extracellular fluid at a low Reynolds number, providing crucial functionality of living matter such as cell locomotion or molecular transport in tissue. A striking feature of populations of cilia is a state of collective motion known as metachronal wave. In proximity to a cell surface a symmetry breaking of the flow field is due that affects the properties of metachronal waves and facilitates transport generation. We generalize a simple phase oscillator model for the elasto-hydrodynamic coupling in ciliated systems [1] to include this asymmetry. We obtain analytical results for the linear stability of metachronal waves in presence of long-range hydrodynamic interactions, illustrate their properties by numerical simulations and relate the change in transport ability to the specific properties of metachronal waves.

[1] Niedermayer et. al., *Chaos*: 18(3) 2008.

BP 27.5 Wed 16:15 ZEU 160

**Boundary conditions for polar active fluids exhibiting mesoscale turbulence** — ●SEBASTIAN HEIDENREICH<sup>1</sup>, HENNING REINKEN<sup>2</sup>, DAIKI NISHIGUCHI<sup>3</sup>, ANDREY SOKOLOV<sup>4</sup>, IGOR S. ARANSON<sup>5</sup>, SABINE H. L. KLAPP<sup>2</sup>, and MARKUS BÄR<sup>1</sup> — <sup>1</sup>Physikalisch Technische Bundesanstalt Braunschweig und Berlin — <sup>2</sup>Technische Universität Berlin — <sup>3</sup>University of Tokyo, Japan — <sup>4</sup>Argonne National Laboratory, USA — <sup>5</sup>Pennsylvania State University, USA

Bacterial suspensions are intriguing examples for active polar fluids which exhibit large-scale collective behaviour from mesoscale turbulence to vortex lattices. The bulk collective motion is well described by a continuum equation with derivatives up to the fourth order [1]. That simple model reproduces experimental findings of mesoscale turbulence and was recently derived from a minimal micro-swimmer model. However, the treatment of boundaries to describe the collective motion in a confinement or near walls remains so far unknown. In the talk, we propose boundary conditions for active polar fluids suitable to describe recent experiments of *Bacillus subtilis* bacteria moving in an array of lithographic designed pillars [2]. Furthermore, we describe the collective motion of bacteria around single pillars of different sizes in experiments and show that the model with the mentioned boundary conditions reproduces this behavior faithfully.

[1] J. Dunkel, S. Heidenreich, M. Bär and R. E. Goldstein, *New J. Phys.* 15, 040516 (2013). [2] D. Nishiguchi, I. S. Aranson, A. Snezhko and A. Sokolov *Nat. Comm.* 9, 4486 (2018).

**15 min. break.**

BP 27.6 Wed 16:45 ZEU 160

**Artificial topological defects organize bacterial motion** — ●HENNING REINKEN<sup>1</sup>, SEBASTIAN HEIDENREICH<sup>2</sup>, DAIKI NISHIGUCHI<sup>3</sup>, ANDREY SOKOLOV<sup>4</sup>, IGOR ARANSON<sup>5</sup>, MARKUS BÄR<sup>2</sup>, and SABINE KLAPP<sup>1</sup> — <sup>1</sup>Technische Universität Berlin — <sup>2</sup>Physikalisch-Technische Bundesanstalt Berlin — <sup>3</sup>University of Tokyo, Japan — <sup>4</sup>Argonne National Laboratory, USA — <sup>5</sup>Pennsylvania State University, USA

Active systems spontaneously self-organize into complex spatio-temporal structures such as flocks, bands, vortices, and turbulence. These collective states are susceptible to weak geometrical confinement, as has been demonstrated in experiments on suspensions of *Bacillus subtilis*, where turbulent motion is organized into a highly ordered bacterial vortex lattice by arrays of tiny obstacles [1]. Using a continuum-theoretical approach [2], we show how self-induced topological defects imposed by artificial obstacles guide the flow profile of the active fluid and enable the stabilization of vortex patterns with tunable properties. Beyond the stabilization of square and hexagonal

lattices, we also provide a striking example of a chiral, antiferromagnetic lattice induced by arranging the obstacles in a Kagome-like array. In this setup, the interplay of lattice topology, activity and length-scale selection generates a net rotational flow. Further, we investigate how the properties of the stabilized patterns impact the transport of tracer particles in the active fluid.

[1] D. Nishiguchi et al., Nat. Commun. **9**, 4486 (2018).

[2] H. Reinken et al., Phys. Rev. E **97**, 022613 (2018).

BP 27.7 Wed 17:00 ZEU 160

**Topological defects in growing bacterial colonies** — ANH LP THAI, ARKAJYOTI GHOSHAL, and ANUPAM SENGUPTA — Physics of Living Matter Group, University of Luxembourg, Luxembourg

Bacterial populations are known to mediate vital processes in ecology, medicine and industry. Morphology, a key biophysical trait, has been long studied for its biological relevance in uptake, motility and selection. Yet, only recently we have started to uncover the role of morphology in biophysical interactions between cells or with their micro-environment [1]. Here, I will present recent results that elucidate how non-motile bacteria harness morphology to regulate transport processes over colony scales. We examine the geometric and mechanical properties of growing colonies, with a particular focus on the emergence of topological defects. Our results indicate that the number of topological defects depends on the cell physiology and colony dimensions, which in turn regulate the active dynamics of the colony. We compare our experimental results with MD simulations and continuous modelling [2, 3], and demonstrate that an expanding colony of non-motile cells self-organizes into domains of aligned cells. Topological defects mediate the interactions between domains, ultimately yielding an active nematodynamic system. Topology mediated mechanics can potentially lead to physiological functions due to the active hydrodynamics at scales that are orders of magnitude larger than single cells. [1] A. Sengupta, Microbial Active Matter: A Topological Perspective (under rev.); [2] You, Pearce, Sengupta, Giomi, Phys. Rev. X. **8** (2018); [3] You, Pearce, Sengupta, Giomi, Phys. Rev. Lett. **123** (2019).

BP 27.8 Wed 17:15 ZEU 160

**Dynamics of Lithium Chloride Solutions in Nanopores of Various Diameters - a NMR Study** — CHRISTOPH SÄCKEL, SARAH SCHNEIDER, and MICHAEL VOGEL — Institut für Physik kondensierter Materie, TU Darmstadt

We analyse ion transport in aqueous salt solutions confined to

nanopores as part of a project that aims to develop a new generation of nanosensors by combining the effectiveness of biological ion channels with the robustness of synthetic silica nanopores. To this end it is necessary to understand the influence of the confinement on the temperature-dependent ion transport. We systematically vary the pore parameters and study effects on the dynamics of aqueous LiCl solutions using  $^2\text{H}$  and  $^7\text{Li}$  nuclear magnetic resonance (NMR). We combine homogeneous and gradient field NMR to selectively investigate water and ion dynamics on broad time and length scales from room temperature to the supercooled regime. Both the local and long-range dynamics of ions and water show a slowdown in silica confinement. In addition, our data indicates more heterogeneous dynamics for the liquid in confinement than in bulk. Moreover, NMR studies of solutions in functionalized silica pores reveal a significant influence of the chemical nature of the inner pore surfaces. The observed effects can be explained by a slower layer of solution at the pore walls and bulk-like dynamics in the pore centre. Self-diffusion shows an Arrhenius-like behaviour of the solution in confinements, while bulk samples are best described by a VFT fit.

BP 27.9 Wed 17:30 ZEU 160

**Self-organization of active microtubule networks** — SMRITHIKA SUBRAMANI, VISWA MAITREYI, and ISABELLA GUIDO — Max Planck Institute for Dynamics and Self-Organization, Goettigen, Germany

Transport in nature is a crucial task and simple diffusion is insufficient, especially in the intracellular confinement. Relying on cytoskeletal components and their motor proteins is a strategy that have been evolved to tackle this limitation. It was observed that inside large eukaryotic cells microtubule-motor protein networks display an activity that generates a flow, called cytoplasmic streaming, that contributes to transport and distribution of components. Many efforts have been made to understand the features and function of this intracellular streaming. However, the exact mechanism behind its establishment is still unknown. Here we present a study on a synthetic system made of active microtubule networks. When confined, they self-organize and show an interesting emergent behaviour that presents transitions through different regimes. Such transitions have similarities with the process examined in the intracellular space of *Drosophila* oocytes during their development. Our results show that the self-assembling of the active network as well as the generated synthetic streaming is dependent on the confinement geometry. This simplified approach allows the characterization of such dependence and can provide a deeper understanding of the natural process.