DY 27: Fluid Physics 3 - organized by Stephan Weiss and Michael Wilczek (Göttingen)

Time: Tuesday 14:00–17:10 Location: DYa

Invited Talk DY 27.1 Tue 14:00 DYa
Human exhaled particles from nanometres to millimetres — •Gholamhossein Bagheri — Max Planck Institute for Dynamics and Self-Organization, Goettingen, Germany

COVID-19 and other airborne diseases are transmitted to healthy individuals by inhalation of pathogen-containing particles exhaled by infectious persons. Here I provide an overview of the mechanisms involved in formation of these particles and the flow physics of the exhaled air. I will present results of our comprehensive experimental study to characterise the size distribution of exhaled particles from more than 125 subjects aged 5-88 years using aerosol size spectrometers and in-line holography. I will also discuss the physics of the exhalation flows during different respiratory manoeuvres by presenting results from our size-resolved three-dimensional particle tracking imaged at 10-15 kHz, which are furthermore complemented by two-dimensional optical flow measurements. In total, we have collected and analysed 200 h of exhalation samples with the spectrometers, 9000 holograms, and more than three million images from the high-speed cameras. With this database, we are now able to predict risk of infection from human exhaled particles in indoor environments using conventional infection models as shown in our multilingual web application (https://aerosol.ds.mpg.de). Finally, we have further improved risk assessment models to account for particles containing multiple pathogens. This research is funded by the Max Planck Society, Universitätsmedizin Göttingen and Bundesweites Forschungsnetz Angewandte Surveillance und Testung project.

DY 27.2 Tue 14:30 DYa
Emergent transport in growing bacterial colonies — •Anupam Sengupta — Physics of Living Matter, Dept. of Physics and Materials Science, University of Luxembourg

Bacteria are known to mediate vital processes in ecology, medicine and industry. Morphology, a key bacterial trait, has been long studied for its biophysical functions. Yet, only recently we have started to uncover the role of morphology in tuning the emergent properties in active cellular micro-environments[1]. Here, I will present recent results that elucidate how non-motile bacteria harness morphology to regulate transport properties over colony scales. We examine the geometric and mechanical properties of growing colonies, with a particular focus on the emergence of topological defects that act as active hydrodynamic sites. Our experimental results indicate that the number of topological defects depends on the cell geometry and colony dimensions, which in turn regulate the emergent transport properties within the bacterial colonies. Our results are supported by MD simulations and continuous modelling [2, 3], suggesting that defect mediated mechanics can potentially lead to biological functions, owing to the active hydrodynamics at scales that are orders of magnitude larger than individual cells. [1] A. Sengupta, Microbial Active Matter: A Topological Perspective, Front. Phys. 8, 184, 2020; [2] You, Pearce, Sengupta, Giomi, Phys. Rev. X. 8 (2018); [3] You, Pearce, Sengupta, Giomi, Phys. Rev. Lett. 123 (2019).

DY 27.3 Tue 14:50 DYa
Hydrodynamically coupled cilia: synchronization and noise — •Anton Solovev and Benjamin M. Friedrich — TU Dresden, Germany

Motile cilia on ciliated epithelia in mammalian airways, brain ventricles and oviduct can display coordinated beating in the form of metachronal (=traveling) waves [1]. Past research proposed hydrodynamic coupling as a mechanism of synchronization, yet if such synchronization is stable in the presence of noise (corresponding to active fluctuations of cilia beating) has been addressed only for $n = 2$ cilia [2], while the question of multi-stable synchronization in cilia carpets ($n >> 1$) remains open.

Using multi-scale simulations [3] that map hydrodynamic interactions between cilia on a generalized Kuramoto model of phase oscillators with local coupling, we predict many multi-stable metachronal wave states, yet only one or two of them have considerable basins of attraction.

In the presence of noise, we observe stochastic transitions between different waves [4]. Active noise excites long-wavelength perturbations (which take relatively long time to decay). Strong noise impedes global synchronization and causes a break-up into smaller synchronized patches (similar to a chimera state).

[1] W. Gilpin, M.S. Bull, and M. Prakash, Nat Rev Phys 2, 74 (2020)
[2] R. Ma et al., Phys. Rev. Lett. 113, 048101 (2014)
[3] A. Solovev, B.M. Friedrich, preprint arXiv:2010.08111 (2020)
[4] A. Solovev, B.M. Friedrich, preprint arXiv:2012.11741 (2020)

DY 27.4 Tue 15:10 DYa
Boundary conditions for polar active fluids exhibiting mesoscale turbulence — •Sebastian Heidenreich[1], Henning Reinken[2], Daiki Nishiguchi[3], Andrey Sololov[4], Igor S. Aranson[5], and Sabine H. L. Klapp[2] — [1]Physikalisch Technische Bundesanstalt Braunschweig und Berlin, Germany — [2]Technische Universität Berlin, Germany — [3]University of Tokyo, Japan — [4]Argonne National Laboratory, USA — [5]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).

DY 27.5 Tue 15:30 DYa
Non-equilibrium phase transitions in bacterial vortex lattices — •Henning Reinken[1], Sebastian Heidenreich[2], Markus Bär[2], and Sabine H. L. Klapp[1] — [1]Technische Universität Berlin, Germany — [2]Physikalisch-Technische Bundesanstalt, Berlin, Germany

Recent theoretical and experimental studies have shown that the turbulent vortex structures emerging in bacterial active fluids can be organized into regular vortex lattices by weak geometrical constraints such as small pillars [1,2].

Using a deterministic continuum-theoretical approach for the effective microswimmer velocity [3], we show that the emergence and disappearance of these non-equilibrium structures shares many similarities with second-order equilibrium phase transitions including critical behavior, e.g., long-range correlations and divergent susceptibility at the critical point. The exponents are very close to those of the 2D Ising model with nearest-neighbor interactions. A mapping to the Onsager solution allows us to identify an effective temperature linear in the strength of nonlinear advection.

[1] D. Nishiguchi, I. S. Aranson, A. Snezhko, and A. Sokolov,
    Nat. Commun. **9**, 4486 (2018)
[2] H. Reinken, D. Nishiguchi, S. Heidenreich, A. Sokolov, M. Bär,
    S. H. L. Klapp, and I. S. Aranson, Commun. Phys. **3**, 76 (2020)
[3] H. Reinken, S. H. L. Klapp, M. Bär, and S. Heidenreich,
    Phys. Rev. E **97**, 022613 (2018)

DY 27.6 Tue 15:50 DYa
Impact of the gut motility on nutrient absorption and bacterial growth — •Agnese Codutti[1,2] and Karen Alim[1,2] — [1]MPIDS, Goettingen, Germany — [2]TUM Physics, Munich, Germany

The small intestine malfunctioning and its microbiome have been linked to serious diseases (from obesity, diabetes, Crohn disease to depression and anxiety). Therefore, the study of the physics underlaying such malfunctioning and the healthy gut behavior is of vital importance. In our work, we aim to theoretically model the tight link between gut motility, fluid flows, nutrients absorption and bacterial growth. We extend the Taylor dispersion approach to the case of an absorbing tube with moving walls, and we use a system of coupled equations to model nutrients and bacteria. We show that the gut motility deeply impacts the nutrient absorption: motility patterns

with slow flows such as segmentation increase the nutrient absorption due to the long permanence times, while motility patterns with strong flows such as peristalsis reduce the absorption. On the contrary, segmentation favours the bacterial growth, while peristalsis reduces it. Therefore, we prove that the gut alternates such patterns to maximize nutrient absorption and minimise bacterial growth.

DY 27.7 Tue 16:10 DYa

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 zonated 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 25, 1885.

DY 27.8 Tue 16:30 DYa

Resistive force theory and wave dynamics in swimming flagellar apparatus isolated from C. reinhardtii — Samira Goli Pozveh[1], Albert Bae[2], and •Azam Gholami[1] — [1]MPI for Dynamics and Self-organization, Göttingen, Germany — [2]Department of Biomedical Engineering, University of Rochester, USA

The-biflagellated micro-swimmer Chlamydomonas reinhardtii is a model organism to study dynamics of flagellar synchronization. Hydrodynamic interactions, intracellular mechanical coupling or cell body rocking are believed to play crucial role in synchronization of flag- ellar beating in green algae. Here, we use freely swimming intact flagellar apparatus isolated from wall-less strain of Chlamydomonas to investigate wave dynamics. Our analysis in phase coordinates show that, when the frequency difference between the flagella is high (10-41% of the mean), neither mechanical coupling via basal body nor hydrodynamics interactions are strong enough to synchronize two flagella, indicating that beating frequency is perhaps controlled internally by the cell. We also examined the validity of resistive force theory for a flagellar apparatus swimming freely in the vicinity of a substrate and found a quantitative agreement between experimental data and simulations with drag anisotropy of ratio 2. Finally, using a simplified wave form, we investigated the influence of phase and frequency differences, intrinsic curvature and wave amplitude on the swimming trajectory of flagellar apparatus. Our analysis shows that by controlling phase or frequency differences between two flagella, steering can occur.

DY 27.9 Tue 16:50 DYa

Rectified Diffusion of E. coli in Microfluidic Labyrinths — •Ariane Weber[1,2,3], Marco Bahrs[4], Zahra Alirezaeizanjani[4], Xingyu Zhang[1,2], Carsten Beta[4], and Vasily Zaburdaev[1,2] — [1]Department Biologie, Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen — [3]Max-Planck-Institut für Menschheitsgeschichte, Jena — [4]Institut für Physik und Astronomie, Universität Potsdam

In many natural environments such as tissue or soil, bacteria have to orient through and interact with complex surroundings. To describe the bacterial dispersal in such environments, the movement of bacteria in the presence of spatial restrictions has to be understood qualitatively and quantitatively. In the present work, we take a first step in this direction by studying the spreading of E. coli in labyrinths of square and hexagonal geometry, both experimentally and theoretically. Using a microscopic tracking system, we first generate experimental data quantifying the dispersal of the bacteria in quasi-two-dimensional microfluidic labyrinths. Second, we formulate a two-dimensional random walk model of the bacterial movement within the labyrinths to (i) find theoretical expressions quantifying the diffusive motion and (ii) produce numerical results by implementing it in computer simulations. We then verify the analytical results by comparing them with the simulation statistics and the experimental data. Taken together, we are able to quantify the bacterial dispersal on short time scales and model it on large time scales, predicting faster dispersal and a prolonged time of non-Gaussian diffusion within the labyrinths.