DY 5: Active Biological Matter I (joint session BP/DY/CPP)

Time: Monday 9:00–11:00 Location: BPb

Invited Talk DY 5.1 Mon 9:00 BPb

The tortoise and hare: how moving slower allows groups of bacteria to spread across surfaces — Oliver Meacock[1,2], Amin Doostmohammadi[3], Kevin Foster[1], Julia Yeomans[1], and •William Durham[1,2] — [1]University of Oxford, United Kingdom — [2]University of Sheffield, United Kingdom — [3]University of Copenhagen, Denmark

Bacteria use tiny grappling hook like appendages called pili to pull themselves across solid surfaces. While pili-based motility has been widely studied in solitary Pseudomonas aeruginosa cells, this species also uses pili to collectively migrate across surfaces when they are densely packed together in a colony. Interestingly, we find genotypes that individually move slower can collectively migrate faster as a group. Using theory developed to study liquid crystals, we demonstrate that this effect is mediated by the physics of topological defects, points where cells with different orientations meet one another. Our analyses reveal that when defects with a topological charge of $+1/2$ collide with one another, the fast-moving mutant cells rotate vertically and become trapped. By moving more slowly, wild-type cells avoid this trapping mechanism, allowing them to collectively migrate faster. Our work suggests that the physics of liquid crystals has played a pivotal role in the evolution of collective bacterial motility by exerting a strong selection for cells that exercise restraint in their movement.

Full paper in Nature Physics available free of charge at: https://rdcu.be/cbcgc

DY 5.2 Mon 9:30 BPb

Light-regulated cell aggregation in confinement — •Alexandros Fragkopoulos[1], Jeremy Vachier[1], Johannes Frey[1], Flora-Maud Le Menn[1], Marco Mazza[1,2], Michael Wilczek[1], David Zwicker[1], and Oliver Bäumchen[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), D-37077 Göttingen, Germany — [2]Department of Mathematical Sciences, Loughborough University, Loughborough, Leicestershire LE11 3TU, United Kingdom — [3]Experimental Physics V, University of Bayreuth, D-95447 Bayreuth, Germany

Photoactive microbes live in complex environments with spatially and temporally fluctuating light conditions. They survive in such habitats by switching their metabolic activity from photosynthesis to aerobic respiration in unfavorable light conditions. We demonstrate that this adaptation in a suspension of soil-dwelling *Chlamydomonas reinhardtii* cells under confinement leads to a spontaneous separation into regions of high and low cell densities. We show that the inhibition of the photosynthetic machinery is necessary but insufficient to generate the observed aggregation. Microfluidic experiments, simulations, and mean-field theory approaches demonstrate that the emergence of microbial aggregations is governed by the oxygen concentration field inside the microhabitat. In fact, in regions where the energy production is completely arrested by both, the photosynthetic and respiratory systems, the cell speed decreases resulting in an aggregation, which thus takes the form of the underline oxygen field.

DY 5.3 Mon 9:50 BPb

Emergent activity of motile phytoplankton in nutrient landscapes — •Jayabrata Dhar, Francesco Danza, Arkajyoti Ghoshal, and Anupam Sengupta — Physics of Living Matter Group, Department of Physics and Materials Science, University of Luxembourg, 162 A, Avenue de la Faencerie, L-1511, Luxembourg City, Luxembourg

Despite their minuscule size, microbes mediate a range of processes in ecology, medicine, and industrial settings that span orders of nutrient concentrations. Yet, to date, we lack a biophysical framework that could link nutrient availability to phytoplankton behavior and predict the impact of dynamic nutrient conditions on motility. Using a combination of micro-scale imaging, microbiology and fluid dynamic models, we quantify how nutrient availability regulates motility, at both individual and population scales [1]. We extract the time-scales over which phytoplankton actively regulate swimming and morphological characteristics, thus shedding light on the finely tuned biophysical mechanisms that equip cells to tackle spatial and temporal heterogeneity of nutrient landscapes. Our results propose local nutrient levels as a handle to control the activity of motile phytoplankton species, promising an exciting model of tunable motile active matter.

[1] Danza, Dhar, Ghoshal and Sengupta (in prep.)

DY 5.4 Mon 10:10 BPb

Chemotaxis strategies of bacteria with multiple run-modes — Zahra Alirezaeizanjani[1,2], •Robert Grossmann[1], Veronika Pfeifer[1], Marius Hintsche[1], and Carsten Beta[1] — [1]Institute of Physics and Astronomy, University of Potsdam, 14476 Potsdam, Germany — [2]Max Planck Institute of Colloids and Interfaces, 14476 Potsdam, Germany

Bacterial chemotaxis – a fundamental example of directional navigation in the living world – is key to many biological processes, including the spreading of bacterial infections. Many bacterial species were recently reported to exhibit several distinct swimming modes – the flagella may, for example, push the cell body or wrap around it. How do the different run modes shape the chemotaxis strategy of a multimode swimmer? Here, we investigate chemotactic motion of the soil bacterium *Pseudomonas putida* as a model organism. By simultaneously tracking the position of the cell body and the configuration of its flagella, we demonstrate that individual run modes show different chemotactic responses in nutrition gradients and thus constitute distinct behavioral states. Based on an active particle model, we demonstrate that switching between multiple run states that differ in their speed and responsiveness provide the basis for robust and efficient chemotaxis in complex natural habitats.

30 min. Meet the Speaker