DY 46: Microswimmers (joint session BP/CPP/DY)

Time: Wednesday 15:00–17:30   Location: H 1028

Invited Talk   DY 46.1   Wed 15:00   H 1028
Emergent Dynamics of Active Particles — •Roland G. Winkler — Institute for Advanced Simulation, Forschungszemtrum Jülich, 52425 Jülich, Germany

The stationary-state structural and dynamical properties of microswimmers are governed by their shape and hydrodynamic interactions, but also the effective dimensionality of the system matters, i.e., three-dimensional bulk versus thin film. As a generic approach for microswimmers, we have developed a model for a spheroidal squirmer, with hydrodynamics implemented by the multiparticle collision dynamics approach [1,2]. We study the swimming behavior, cooperative motion, and motility-induced phase separation (MIPS) of such squirmers in a narrow slit. For two squirmers, surface hydrodynamic interactions strongly influences their cooperative motion [2]. Considering the phase behavior of many squirmers, hydrodynamic interactions suppress MIPS for spherical squirmers. In contrast, hydrodynamic interactions enhance MIPS for elongated squirmers. Moreover, the shape affects the rheological properties of squirmers in shear and Poiseuille flow.

[1] J. Elgeti, R. G. Winkler, G. Gompper, Rep. Prog. Phys. 78, 056601 (2015)
[2] M. Theers, E. Westphal, G. Gompper, R. G. Winkler, Soft Matter 12, 7372 (2016)

DY 46.2   Wed 15:30   H 1028
Magnetic behavior and chemotaxis of magnetic bacteria — •Agnese Codutti[1], Damien Faivre[1], and Stefan Klumpp[2] — [1]Max Planck Institute of Colloids and Interfaces, Am Mühlenberg 1, 14476 Potsdam, Germany — [2]Georg-August-Universität Göttingen Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

Chemotaxis is the bacterial ability to bias their motility toward a preferred concentration of attractants or repellents. This chemotactic ability can be used by magnetic bacteria, coupling it to a passive alignment to external magnetic fields. Magnetic bacteria include the naturally-occurring magnetotactic bacteria, and lab-produced biohybrids, in which for example E. coli can be coupled to external magnetic beads. Therefore, a model to understand the coupling between magnetic fields, active swimming, and chemotaxis is needed to predict the behavior of these systems. We perform simulations based on an Active Brownian Particle model, modified to include active swimming, active changes of directions, chemotaxis, and passive alignment with external magnetic fields. The model allows us to reproduce the capillary experiments, and to throw some light on the possible aerotaxis models shown by magnetotactic bacteria. As main results, we show how run and tumble motion hinders the chemotactic/aerotactic abilities of the bacteria when coupled with magnetic fields, while run and reverse motility benefits from the magnetic field, leading to faster chemotaxis. We explore different magnetic behaviors of magnetotactic bacteria, where cells are either simply aligned by the external field or alternatively using it as proxy of oxygen gradient.

DY 46.3   Wed 15:45   H 1028
The bacterial soliton in a nutrient field – re-examined — •Andrzej Palugniok[2], Maximilian Seyrich[1], and Holger Stark[1] — [1]Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstrasse 36, 10623 Berlin, Germany — [2]Worcester College, University of Oxford, Walton Street, OX1 2HB Oxford, United Kingdom

The gut bacterium E. coli with its run-and-tumble walk is a well-studied model swimmer in the active-matter field. One of the various interesting collective phenomena is a bacterial soliton or a traveling concentration pulse of bacteria [1]. It develops when bacteria start to consume a nutrient in an initially uniform field, in which they also perform chemotaxis.

To describe such a situation, we start from a Smoluchowski equation of a run-and-tumble particle in a chemotactic field. A Markovian tumble rate is derived from the usual linear response theory. We perform a multipole expansion to derive equations for the bacterial density and the local polar order decribed by the bacterial polarization. On times longer than the typical relaxation time for the polarization, one recovers the Keller-Segel equation. Solving it together with the diffusion equation for the nutrient, we are able to reproduce the bacterial soliton. Thereby, we demonstrate that one does not need a second, signalling

chemical field as introduced in Ref. [1] nor a singular chemotactic drift term as demanded in Ref. [2].

[1] J. Saragosti et al., PNAS **108**, 39 (2011).
[2] E.F. Keller and L.A. Segel, J. Theor. Biol., **30**, 2 (1971).

DY 46.4   Wed 16:00   H 1028
Dynamic Propulsion Force Measurements of Chlamydomonas Microalgae using Micropipette Force Sensors — •Thomas Josef Böddeker, Christian Titus Kreis, Quentin Magdelaine, and Oliver Bäumchen — Max Planck Institute for Dynamics and Self-Organization (MPIDS), Am Faßberg 17, D-37077 Göttingen, Germany

Although the swimming dynamics of microbes, such as bacteria and microalgae, have received a lot of attention in recent years, methods for direct propulsion force measurements are still limited. We present a new approach utilizing micropipettes as force sensors to study the propulsion forces and wall interactions of the unicellular, biflagellated microswimmer *Chlamydomonas*. Fourier signal analysis of the micropipette deflection reveals a clear signature of the energy output of the microswimmer and provides a handle to measure the frequency and energy associated to the flagella beating. Continuous measurements in a liquid cell allow us to characterize the propulsion of individual cells and to probe the extent of steric and hydrodynamic interactions between beating flagella and solid interfaces. For controlled environmental conditions, we quantify the difference in propulsion energy and beating frequency between swimming in bulk and in close proximity to solid interfaces.

DY 46.5   Wed 16:15   H 1028
Applying an Extended Kalman Filter to extract bacteria statistics — •Oliver Köhn — Universität des Saarlandes

Bacteria tend to swim in liquids in absence of food facilitated by creation of flagella. The trajectories are determined by slightly curved lines (running states) and randomly interrupted by short intervals with strong direction changes (tumbling state)[1]. This behavior seems to be efficient in finding food in unknown environments. We assume an intrinsic randomness in the running states as well in the appearance of the tumbling intervals.[1] Furthermore in real experiments the extracted positions are influenced by a detection noise. Estimating the stochastic trajectory properties requires the distinction between bacteria intrinsic randomness and the measurement noise. From the engineers it is known that the Kalmann filter algorithm provide this in an optimal way [2]. We adapted and implemented this filter for simulated as well as measured bacteria trajectories.

[1] Enhancing bacterial motility and search efficiency by genetic manipulation of flagellar number; Javad Najafi, M. Reza Shaebani, Thomas John, Florian Altegoer, Gert Bange & Christian Wagner; submitted to PNAS [2] Forecasting, structural time series models and the Kalman filter; Andrew C. Harvey; 1989; Cambridge University Press

DY 46.6   Wed 16:30   H 1028
Phase diagram of a low Reynolds number swimmer near a wall — •Abdallah Daddi-Moussa-Ider[1], Maciej Lisicki[2,3], Christian Hoell[1], and Hartmut Löwen[1] — [1]Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, Universitätsstraße 1, Düsseldorf 40225, Germany — [2]Department of Applied Mathematics and Theoretical Physics, Wilberforce Rd, Cambridge CB3 0WA, United Kingdom — [3]Institute of Theoretical Physics, Faculty of Physics, University of Warsaw, Pasteura 5, 02-093 Warsaw, Poland

The hydrodynamic flow field generated by self-propelled active particles and swimming microorganisms is strongly altered by the presence of nearby boundaries in a viscous flow. Using a simple model swimmer composed of three-linked spheres, we show that the swimming trajectories near a non-slip wall reveal various interesting scenarios of motion depending on the initial orientation and the distance separating the swimmer from the wall. Accordingly, the swimmer can either be trapped by the wall, totally escape from the wall, or undergo an oscillatory gliding motion at a constant mean height above the wall. Using a far-field approximation, we find that the wall-induced correction at leading order has a quadrupolar flow structure where the translational and angular velocities of the swimmer decay as inverse third and fourth

power with distance, respectively. The resulting equations of motion for the trajectories and the relevant order parameters fully characterize the transition between the phases and allow for an accurate description of the swimming behavior near a wall.

DY 46.7   Wed 16:45   H 1028

Three-dimensional simulation of sperm in structured microfluidic channels — •Sebastian Rode, Jens Elgeti, and Gerhard Gompper — Theoretical Soft Matter and Biophysics, Institute of Complex Systems (ICS-2) , Forschungszentrum Jülich, 52425 Jülich, Germany

Sperm cells propel themselves by a periodic wave-like beating of their flagellum [1-3]. At low Reynolds numbers and in confinement, the directed motion of sperm and other microswimmers is strongly influenced by steric and hydrodynamic surface interactions [1]. We model sperm motility in our mesoscale hydrodynamics simulations by imposing a planar traveling bending wave along the flagellum [2]. For swimming in zigzag shaped microchannels, we find that the deflection angle of a sperm cell at sharp corners depends on the orientation of its beating plane. Our results are in good agreement with recent microfluidic experiments, and help to improve the understanding of sperm cell navigation under strong confinement. We show that the emergence of a nonplanar component of the flagellar beat with increasing wavelength drastically increases surface attraction.

[1] J. Elgeti et al., Rep. Prog. Phys. 78, 056601 (2015) [2] J. Elgeti et al., Biophys. J. 99, 1018 (2010) [3] G. Saggiorato et al., Nat. Commun. 8, 1415 (2017)

DY 46.8   Wed 17:00   H 1028

Altering diffusion by interaction of microalgae with micronsized objects — •Francine Kolley[1,2], Patricia Dähmlow[2], Hajnalka Nadasi[2], Florian von Rüling[2], and Alexey Eremin[2] — [1]Technical University Dresden — [2]Otto-von-Guericke-University Magdeburg

The enhancement of passive particles, single silica spheres and their doublets, was studied in suspensions containing microswimmers Chlamydomonas reinhardtii. These green algae move with a flagellar motor, reaching typical velocities up to 150 μm/s. Stimulated by phototaxis, their motion is similar to humans doing breaststroke. The induced flow of the puller affects the translational as well as the rotational diffusion of the passive particles. The corresponding diffusion coefficients were obtained from the measurement of the mean square displacements of the passive particles for various concentrations of the algae. The Brownian Motion of the silica beads was observed in a quasi-2D system in flat cappilaries.To avoid cell immobilization by adsorption to the glass substrate the capillary surface was silanized. Additionally, a polymer was introduced to the suspension to optimize the diffusive behavior. In the range of small algae concentrations, the diffusion coefficients exhibited a linear dependence on the cell density of Chlamydomonas reinhardtii.

DY 46.9   Wed 17:15   H 1028

Dynamics of chemotactic and chemokinetic bacterial populations — •Theresa Jakuszeit[1], James Lindsey-Jones[1], François J. Peaudecerf[2], and Ottavio A. Croze[1] — [1]Cavendish Laboratory, University of Cambridge, J. J. Thomson Avenue, Cambridge CB3 0HE, United Kingdom — [2]Institute of Environmental Engineering, ETH Zürich, Stefano-Franscini-Platz 5, 8093 Zürich, Switzerland

Several motile bacteria are able to sense chemical gradients much larger than their own size, and perform a random walk biased up attractant gradients ('chemotaxis') by varying their reorientation rate. In addition to this well-known chemotactic behaviour, several soil and marine bacterial species are known to modify their swimming speed according to the local concentration of chemoattractant ('chemokinesis'). Therefore, a chemical field of attractant induces a spatially varying swimming speed, which results in a drift towards lower attractant concentrations – contrary to the drift created by chemotaxis.

Here, to explore the biological benefits of chemokinesis and investigate its impact on the chemotactic response, we extend a Keller-Segel type model to include a dependence of the swimming speed on the attractant concentration. Even though chemokinesis on its own results in a dispersion of the population away from high attractant concentrations, it can not only enhance the chemotactic response but also modify it qualitatively. We apply the model to predict the dynamics of bacteria capable of chemokinesis and chemotaxis in experimentally inspired chemoattractant fields, such as those generated in capillary migration assays and around environmental nutrient sources.