

## DY 11: Microswimmers (joint session DY/ BP)

Time: Tuesday 9:30–12:30

Location: ZEU 146

DY 11.1 Tue 9:30 ZEU 146

**African trypanosomes swim faster in small capillaries and heterogeneous environment** — ●DAVOD ALIZADEHRAD and HOLGER STARK — Institut für Theoretische Physik, Technische Universität Berlin, Germany

Human African trypanosome (HAT), the causative agent of the deadly sleeping sickness in sub-Saharan Africa, is a protozoan or single-celled microorganism that propels itself with the help of a beating flagellum. Despite good recent progress [1], refined models and further numerical simulations are necessary to uncover the heavily debated propulsion mechanism of the trypanosome, in particular, how the flagellum is attached to the cell body.

In this study, to simulate the swimming trypanosome, we construct a refined elastic network model of trypanosome based on experimental data and combine it with the mesoscale simulation technique called multi-particle collision dynamics (MPCD) to model the fluid environment. We reproduce several key features of trypanosome motility. First, we simulate the swimming and rotation speed of the trypanosome and find excellent agreement with experiments [2]. Second, we show that confinement has profound effects on trypanosome locomotion. In narrow circular channels the swimming speed increases up to 6 times its bulk value. Finally, we demonstrate that randomly distributed obstacles in a fluid help the trypanosome to swim more efficient.

[1] S.B. Babu and H. Stark, *New J. Phys.* 14, 085012 (2012).

[2] N. Heddergott, et al., *PLoS Pathog.* 8, e1003023 (2012).

DY 11.2 Tue 9:45 ZEU 146

**Energetic efficiency of ciliary propulsion** — ●ANDREJ VILFAN and NATAN OSTERMAN — J. Stefan Institute, Ljubljana, Slovenia

Energetic efficiency of swimming has long been considered a non-issue in microorganisms, but newer studies show that ciliates can use more than half of their energy for propulsion. To estimate how close the ciliates are to the theoretically optimal way of swimming we address the following problems: i) we determine the optimal stroke of a cilium, ii) we determine the optimal beating pattern of a ciliated surface and iii) we calculate the optimal shape of a ciliated swimmer.

For a single cilium we define the efficiency in a scale-invariant way and show that the optimal stroke consists of a working stroke with a stretched cilium and a recovery stroke where the cilium bends and moves closer to the surface. When optimizing an array of cilia we additionally show that metachronal waves improve the efficiency and that the optimal efficiency is achieved for anti-plectic waves. The resulting beating patterns, as well as the optimal ciliary density, show remarkable similarity with those observed in ciliated microorganisms. In order to optimize the shape of the whole swimmer we use a simplified description where we replace the ciliated layer with a surface slip velocity. The optimal shapes again resemble those of different ciliates. If we combine the results of our optimization with experimental efficiency estimates we can show that Paramecium has a propulsion efficiency that is within a factor of 2 of the theoretical optimum.

[1] N. Osterman and A. Vilfan, *PNAS* 108, 15727 (2011) [2] A. Vilfan, *Phys. Rev. Lett.* 109, 128105 (2012)

DY 11.3 Tue 10:00 ZEU 146

**Hydrodynamics of spherical microswimmers in a quasi-2D geometry** — ●ANDREAS ZÖTTL and HOLGER STARK — TU Berlin

Microorganisms like bacteria, sperm cells or algae live in aqueous environments and their motion is therefore governed by low-Reynolds-number hydrodynamics, but also influenced by thermal and biological noise. Experiments with artificial microswimmers, which are used to study collective motion of self-driven particles out of equilibrium, are often performed in a quasi-2D geometry or in thin films, where dynamic clustering and motility-induced phase separation is observed.

Motivated by recent experiments of active colloids and emulsion droplets in confinement, we also study the collective motion of spherical squirmers moving in a quasi-2D geometry by means of multi-particle collision dynamics. Hydrodynamic near-field interactions between swimmers lead to hydrodynamic rotational diffusion, while hydrodynamic interactions between the channel walls and swimmers strongly influence the preferred swimmer orientations and therefore the formation of hexagonal clusters. Neutral squirmers in particular separate

into a gas-like and a crystalline phase which we characterize by a structural order parameter. Varying the density of the swimmers from low to high area fraction results in a steep increase of the order parameter at the critical density, accompanied by strong fluctuations indicating a non-equilibrium phase transition which is absent for strong pullers and pushers.

DY 11.4 Tue 10:15 ZEU 146

**Optimization of bead-spring micro-swimmers and study of dense swimmer solutions** — ●JAYANT PANDE<sup>1,2</sup> and ANA-SUNČANA SMITH<sup>1,2</sup> — <sup>1</sup>Institute for Theoretical Physics, Friedrich-Alexander University, Erlangen, Germany — <sup>2</sup>EAM: Cluster of Excellence, Friedrich-Alexander University, Erlangen, Germany

With the increasing need to understand and predict the locomotion of natural organisms and machines at the micro-scale, the theoretical modelling of micro-swimmers has become an important field of study. Contributing to its development, we present analytical results on the geometric and kinematic optimization of three-ellipsoid micro-swimmers, based on the three-sphere model of Najafi and Golestanian. Assuming a sinusoidal driving protocol, we identify different drag-related regimes and determine the exact shapes which maximise the swimming velocity and efficiency in each regime. Conditions on the optimal forcing parameters as well as the push/pull nature of the swimmer are elucidated. The analytical work is supported by simulations using an in-house framework based on the lattice-Boltzmann method. Its versatility and massively-parallel capabilities allow us to explore near-field effects as well as those arising from asymmetry in the swimmer design. We show that these effects, while inaccessible to an exact theoretical treatment, are nevertheless amenable to an approximate description. In the last part of our contribution, we employ our simulation system to study large populations of passive and active particles in fluids. For different concentrations, we observe previously-known effects as well as departures from theory.

DY 11.5 Tue 10:30 ZEU 146

**Statistical properties of tracer positions, sedimenting in an active fluid** — ●THOMAS JOHN, MATTHIAS MUSSLER, and CHRISTIAN WAGNER — Experimentalphysik, Universität des Saarlandes

Fluid dynamics on  $\mu\text{m}$  scale at velocities in  $\mu\text{m/s}$  is characterized by very low Reynolds numbers. Therefore no turbulent behavior and characteristics is expected. Nevertheless, a spatial-temporal random flow field can be present in a media if the fluid contains a lot of active, irregular moving micro-swimmers. We consider trajectories of passive sedimenting beads in such fluids. This trajectories are strongly influenced from the random flow field if the passive particle (tracer) diameter comparable or less than the diameter of the micro-swimmers. We measured such trajectories in suspensions of the green alga *Chlamydomonas reinhardtii*. The alga has two flagella, a diameter of  $10\ \mu\text{m}$  and swims as a puller with  $50\ \mu\text{m/s}$ . We extract statistical properties of the passive bead positions, e.g. the mean square displacement or the probability density function. Our results are compared with the Brownian motion characteristics of sedimenting particles in very dilute systems and the known non-Brownian characteristics in passive sedimenting particles at higher volume concentrations where the hydrodynamic interactions becomes important.

DY 11.6 Tue 10:45 ZEU 146

**Propulsion of droplets by rigidly tethered traction forces** — ●P. SEKHAR BURADA, REINER KREE, and ANNETTE ZIPPELIUS — Institute for Theoretical Physics, University of Göttingen, Germany

We study the dynamics of an active droplet, with both translational- and rotational degrees of freedom. A field of interfacial traction forces, which is time independent in a body-fixed reference frame drives the system. Using the general solution of the Stokes equation, with the appropriate boundary conditions, we are able to calculate the hydrodynamic flow pattern both inside and outside of the droplet. Also, using force- and torque balance conditions the translational- and rotational velocities of the droplet are calculated. We derive the conditions, in terms of mode amplitudes of the traction force, which need to be satisfied in order to preserve the shape of the droplet.

15 min break

DY 11.7 Tue 11:15 ZEU 146

**Transport powered by bacterial turbulence** — ●ANDREAS KAISER<sup>1</sup>, ANTON PESHKOV<sup>2</sup>, ANDREY SOKOLOV<sup>3</sup>, BORGE TEN HAGEN<sup>1</sup>, HARTMUT LÖWEN<sup>1</sup>, and IGOR S. ARANSON<sup>3</sup> — <sup>1</sup>Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf — <sup>2</sup>Service de Physique de l'Etat Condensé, Gif-sur-Yvette — <sup>3</sup>Materials Science Division, Argonne National Laboratory

We show that turbulence in a bacterial bath can be exploited to power and steer directed transport of mesoscopic carriers through the suspension. In our experiments and simulations, a microwedge-like "bulldozer" is exposed to a bacterial bath of varied concentration and obtains a maximal transport speed in the turbulent state of the bacterial suspension.

DY 11.8 Tue 11:30 ZEU 146

**Cell body rocking is dominant mechanism for flagellar synchronization in a swimming alga** — VEIKKO GEYER<sup>1</sup>, FRANK JULICHER<sup>2</sup>, JONATHAN HOWARD<sup>1</sup>, and ●BENJAMIN FRIEDRICH<sup>2</sup> — <sup>1</sup>Max Planck Institute for Cell Biology and Genetics — <sup>2</sup>Max Planck Institute for the Physics of Complex Systems

The eukaryotic flagellum is a best-seller of nature: These slender cell appendages propel sperm and many other microswimmers, including disease-causing protists. In mammalian airways and the oviduct, collections of flagella beat in synchrony to pump fluids efficiently. Here, we report on theory and experiment that elucidate a mechanism of flagellar synchronization in the model organism *Chlamydomonas*, a green algal cell that swims with two flagella like a breaststroke swimmer. Our analysis shows how synchronization arises by a coupling of swimming and flagellar beating and characterizes an exemplary force-velocity relationship of the flagellar beat. Any perturbation from the synchronized state causes the cell body to rock, which changes the hydrodynamic friction forces acting on the flagella and thus their speed, which restores their synchronization.

Geyer *et al.*: Proc. Natl. Acad. Sci. U.S.A. **110**, 2013.

DY 11.9 Tue 11:45 ZEU 146

**Direct Measurements of Active Flagellar Fluctuations** — ●BENJAMIN FRIEDRICH<sup>1</sup>, RUI MA<sup>2</sup>, GARY KLINDT<sup>1</sup>, FRANK JULICHER<sup>1</sup>, and INGMAR RIEDEL<sup>3</sup> — <sup>1</sup>Max Planck Institute for the Physics of Complex Systems — <sup>2</sup>Institute for Advanced Study, Tsinghua University, Beijing, China — <sup>3</sup>Department of Bioengineering, Stanford University, Stanford, CA, USA

The eukaryotic flagellum beats regularly, driven by the oscillatory dynamics of molecular motors, to propel cells and pump fluids. Small, but perceivable fluctuations in the beat of individual flagella have physiological implications for synchronization in collections of flagella as well as for hydrodynamic interactions between flagellated swimmers. Here, we characterize phase diffusion and amplitude fluctuations of sperm flagellar beat patterns. We employ shape mode analysis and limit cycle reconstruction for a low-dimensional representation of flagellar bending waves. We find that flagellar fluctuations are dominantly of

active origin. Using a minimal model of collective motor oscillations, we demonstrate how active fluctuations can naturally arise from the stochastic dynamics of individual motors.

DY 11.10 Tue 12:00 ZEU 146

**Synchronization of rigid microrotors by time-dependent hydrodynamic interactions** — ●MARIO THEERS and ROLAND WINKLER — Theoretical Soft Matter and Biophysics, Institute for Advanced Simulation and Institute of Complex Systems, Forschungszentrum Juelich, D-52425 Juelich, Germany

The synchronized beating of flagella is fundamental for the coordinated motion of microswimmers such as spermatozoa, bacteria, protozoa, or algae. It is a longstanding conjecture that this microscopic synchronization could be induced by hydrodynamic interactions. However, synchronization is not easily achieved for low Reynolds-number fluids, which are described by Stokes equations. The presence of kinematic reversibility combined with swimmer symmetries may prevent synchronization.

We provide an extension of previous low-Reynolds number studies by analyzing the linearized, time-dependent Navier-Stokes equations instead of the usually adopted Stokes equations. As a model system, we investigate the emergent dynamical behavior of hydrodynamically coupled microrotors and demonstrate that time-dependent hydrodynamic interactions inevitably lead to synchronization of their rotational motion, which is not achieved on the basis of Stokes equations. We show that the system can be described by coupled nonlinear integro-differential equations and derive analytical results for the phase difference. Additionally, results are compared to mesoscale hydrodynamic simulations. Our studies provide a deeper insight into the nature of hydrodynamic interactions between microswimmers.

DY 11.11 Tue 12:15 ZEU 146

**A close look at the tumbling of bacteria** — ●TAPAN CHANDRA ADHYAPAK and HOLGER STARK — Institut für Theoretische Physik, Technische Universität Berlin

Peritrichous bacteria such as *Escherichia coli* propel themselves by using multiple flagella, each rotated at the base by a rotary motor. Hydrodynamic interactions together with an intricate balance of elasticity of the flagella cause them to synchronize and form a single bundle leading to propulsion in a straight line. Such straight runs of a bacterium frequently terminate at relatively short lived tumbling events during which one or more of the flagella leave the bundle disrupting uniform motion and causing the bacterium to change its course. In addition to hydrodynamic interactions and elasticity, rotation-induced polymorphic transitions between different flagellar states [1] is observed to play an important role in re-orientating the bacterium. The detailed process however is complex and very little understood. We investigate the tumbling strategy of an *E. coli* modelling its propulsion using an extended continuum theory of elasticity in presence of hydrodynamic interactions. We examine, in particular, the effect of rotation-induced polymorphic transitions of flagella during such processes.

[1] R. Vogel and H. Stark, Phys. Rev. Lett. **110**, 158104 (2013).