DY 12: Joint focus session (with BP): Statistics of Cellular Motion

This topical session brings together theoretical and experimental researchers working on statistical descriptions of cell motility, which is an emerging theme in the rapidly growing field of cell motility. (Organizers Carsten Beta, Peter Dieterich, Rainer Klages and Lutz Schimansky-Geier)

Time: Tuesday 9:30–13:30 Location: H 1028

Topical Talk DY 12.1 Tue 9:30 H 1028

Data-driven modeling of cell trajectories: a do-it-yourself kit — •Henrik Flyvbjerg — DTU Nanotech, Kongens Lyngby, Denmark

Resent results in data-driven modeling of cell trajectories are reviewed. A do-it-yourself toolkit is presented. Technical points are discussed, such as how to glean mathematical properties of a model-to-be-found from appropriate model-independent experimental statistics, and how such statistics are affected by finite sampling frequency of time-lapse recordings and experimental errors on recorded positions.

Topical Talk DY 12.2 Tue 10:00 H 1028

The statistics of eukaryotic chemotaxis — •Eberhard Bodenschatz — MPI Dynamics and Self-Organization, Goettingen, Germany

The directed motion of eukaryotic cells in a chemoattractant gradient depends on the the steepness of the gradient as well as the average concentration surrounding the cell. It was recently theoretically predicted that for a given situation the chemotactic efficacy is determined by the stochastic fluctuations of a two step process: first the binding of the signaling molecule to the transmembrane receptor and second the intracellular unbinding of a second messenger. It was suggested that the signal to noise ratio of this two stage process is sufficient to explain the chemotactic behavior. In this talk we will first introduce eukaryotic chemotaxis and the experimental micro-fluidic system for controlled chemical signals. Then we shall present the data on the random directed motion of cells and will describe it with a 2D Langevin equation. Then we show that the stochasticity of the two step process can indeed describe the experimentally observed behavior.

Topical Talk DY 12.3 Tue 10:30 H 1028

Dynamics of directed cell migration — •Albrecht Schwab[1], Otto Lindemann[1], and Peter Dieterich[2] — [1]University of Münster, Germany — [2]University of Dresden, Germany

Directed migration (chemotaxis) is the prerequisite for an efficient immune defense. The chemical signal is transduced to the cell migration machinery via complex intracellular signaling cascades that also include the activation of plasma membrane Ca2+ channels of the TRPC family. Chemotaxis involves a cellular motor for migration and a steering mechanism. Here, we aim to determine which of these two components are controlled by TRPC channels. Their contribution is assessed with time-lapse video microscopy of single neutrophils from wildtype and TRPC knockout mice exposed to chemoattractants. Since raw velocities or straightness indices calculated from the experimental cell paths provide only a coarse interpretation of the migratory behavior, we analyze all data within the concept of stochastic processes. The cell is regarded as an object driven by internally correlated stochastic forces and external fields generated by chemoattractants. Anomalous properties that we previously identified in cells migrating without external stimuli and described with a fractional Klein-Kramers equation are maintained during chemotaxis. This enables a modeling based quantification of correlations and allows to disentangle the influence of the chemoattractants on the motor strength (thermal velocity) and directed migration (drift) of the cells under different conditions. Our statistical analyses show that TRPC channels are primarily involved in controlling the steering mechanism of chemotacting neutrophils.

Topical Talk DY 12.4 Tue 11:00 H 1028

Medley swimming of sleeping sickness parasites — •Vasily Zaburdaev[1], Sravanti Uppaluri[2], Thomas Pfohl[3], Markus Engstler[4], Rudolf Friedrich[5], and Holger Stark[6] — [1]Harvard University, Cambridge, USA — [2]Max-Planck-Institute for Dynamics and Self-Organization, Göttingen, Germany — [3]University of Basel, Basel, Switzerland — [4]University of Würzburg, Würzburg, Germany — [5]University of Münster, Münster, Germany — [6]Technical University of Berlin, Berlin, Germany

Though cell locomotion has been examined almost since the discovery of the cell itself, advances in microscopy and biochemical studies have paved the way to a more fundamental understanding of cell motility. This work is a detailed, quantitative characterization of trypanosome motility. Trypanosomes, parasites responsible for deadly disease in humans and cattle, swim with the aid of an appendage called a flagellum. The flagellum, produces rapid undulatory movements that result in cell locomotion. We followed single trypanosomes in a homogeneous environment and found that cells that swim faster also exhibit stronger fluctuations in velocity. Statistical analysis allowed us to develop a mathematical model that could reproduce the diverse trajectories followed by the trypanosomes. Finally, we were able to show that the rapid movements of the body (with time scales on the order of 0.1s) are a result of an active process and thus cannot be described as simple thermal fluctuations. On the whole, such studies provide insight into basic mechanisms of motility, allow for modeling of cell movement, and may eventually even provide design ideas for artificial microswimmers.

15 min break

DY 12.5 Tue 11:45 H 1028

Describing Run and Tumble Motion with Alternating Random Walks — •Felix Thiel, Lutz Schimansky-Geier, and Igor M. Sokolov — Institut für Physik der Humboldt-Universität zu Berlin, Newtonstr. 15, 12489 Berlin

Run and tumble motion is the motile behaviour of flagellated bacteria like E.Coli. Much effort has been made in order to understand and describe such motion. Continuous time random walks (CTRW) are a common tool for description, but lack the possibility of incorporating different kinds of motion. In order to fill this gap, we present a modification of the usually considered CTRW: the alternating random walk. We explicitly distinguish between the run and the tumble phase. By using the techniques of CTRW – integral transforms and asymptotic analysis – we are able to obtain the short-time as well as the long-time behaviour of the mean squared displacement of the process. The main free parameters of the process governing the diffusive behaviour are the waiting-time-PDFs describing the dwelling time in run resp. tumble mode. It is shown that models constructed as above may exhibit a transition in diffusive behaviour from normal to superdiffusion and a change of the effective diffusion coefficient. They may thus be suitable to describe other situations which are known for those phenomena.

DY 12.6 Tue 12:00 H 1028

Swimming of microorganisms in a microchannel flow. — •Adam Wysocki, Roland G. Winkler, and Gerhard Gompper — Theoretical Soft Matter and Biophysics, Institute of Complex Systems and Institute for Advanced Simulation, Forschungszentrum Jülich

We consider an active suspension – motile microorganisms dispersed in a fluid – under flow in a microchannel. We use a coarse-grained model of an active suspension, where the microorganisms are modeled as spherical particles with a prescribed tangential surface velocity, and the fluid is described by multiparticle collision dynamics approach, a particle-based, mesoscopic simulation method, which includes thermal fluctuations. Our model of a swimmer can easly be tuned to be a puller or a pusher, which generate thrust in the front or at the back of the body, respectively. At low swimmer concentrations, far from the walls and for external flow fields u small compared to the propulsion velocity U_0, puller and pusher swim upstream following on average a sinusoidal trajectory. Near the walls, where hydrodynamic interactions are significant, pullers and pushers show a qualitatively different behaviour. Individual pushers swim upstream near the wall for $U_0/u > 1$, while pullers swim downstream for $U_0/u \gg 1$ and change to upstream swimming with increasing flow field u. The collective behaviour at higher concentrations of microorganisms will be discussed.

DY 12.7 Tue 12:15 H 1028

Self-propelled rod-like microswimmers near surfaces — •Kristian Marx and Gerhard Gompper — Theoretical Soft Matter and Biophysics, Institute of Complex Systems, Forschungszentrum Jülich

Self-propelled microswimmers (e.g. sperm, E. coli and the alga Chlamydomonas) are biological organisms that propel themselves through fluid. In future applications, microswimmers may also be used as biosensors on lab-on-a-chip devices. They can be classified as having *pusher* or *puller polarity*, which are driven from the rear or the front, respectively. We study the behavior of a general polar rod model at high swimmer densities in three dimensions, in particular close to walls, including hydrodynamics and volume-exclusion interactions. We employ hydrodynamics simulations using a mesoscale particle based technique (*multi-particle collision dynamics*) implemented on GPU hardware. The swimmer behavior is found to strongly depend on the swimmer polarity: Pushers experience parallel alignment with the walls and strongly aggregate near them. Due to mutual hydrodynamic attraction the rods form motile clusters at the walls. Interacting clusters can form swirls, destroying long-range nematic order. Pullers aggregate into giant immotile clusters that span the entire system at high densities. While they are overall isotropic, the puller clusters show a typical hedgehog structure at the walls, with most of the swimmers pointing towards the walls. Finally, *unpolar driven* rods interact only weakly via hydrodynamics and show an isotropic-nematic phase transition at critical densities much lower than passive rod systems.

DY 12.8 Tue 12:30 H 1028

Collective Dynamics of swimming bacteria and surface attached clusters during biofilm formation — •Matthias Theves and Carsten Beta — Universität Potsdam, Potsdam, Germany

Biofilms (BFs) are communities of sessile bacteria, embedded in an extracellular polymeric structure (EPS), which form at solid-liquid or liquid- air interfaces. We use biocompatible microfluidic channels and high speed time lapse microscopy to study the recruitment of cells from the bulk fluid to a glass surface. During this early stage of BF-formation, bacteria from the swimming phase coexist with surface attached cells that cluster together and form the cores of growing colonies. We analyze the growth dynamics of both populations. After a continuous increase in cell density and cluster size, we observe a sudden increase in the number of swimming cells. Furthermore, we analyze the random walk of isolated swimmers and perform a statistical analysis that allows us to identify changes in the migration patterns of swimming cells in the presence of different obstacles in the microchannel and during experiments with different medium availability.

DY 12.9 Tue 12:45 H 1028

Rotationally induced polymorphic transitions of a bacterial flagellum — A full model of swimming *Rhodobacter sphaeroides* — •Reinhard Vogel and Holger Stark — Institute of Theoretical Physics, TU Berlin

The bacterium *Rhodobacter sphaeroides* swims by rotating a helical filament also called flagellum. The filament is driven by a rotary motor. Depending on the speed of the motor, the flagellum assumes different configurations characterized by its pitch and radius (polymorphism). If the motor stops, the flagellum relaxes into a coiled form with large radius and small pitch, whereas if the motor runs it assumes a helical state with large pitch better suited for swimming. Due to the switch between running and stopping, the bacterium changes its direction randomly.

The bacterial flagellum consists of three parts; the rotary motor embedded in the cell membrane, a short proximal hook that acts as a universal joint and couples the motor to the third part, the long helical filament. The helical shape of the filament converts rotational motion into a thrust force that pushes a bacterium forward. We present our approach to mimic the rotary motor and hook within a continuum model of the flagellum. We use the elastic theory for flagellar polymorphism, developed in Ref. [1], to investigate how an applied motor torque induces a transition between two polymorphic configurations. We attach the bacterial flagellum to a load particle and thereby model the locomotion of the bacterium *Rhodobacter sphaeroides*.

[1] R. Vogel and H. Stark, Eur. Phys. J. E **33**, 259–271 (2010).

DY 12.10 Tue 13:00 H 1028

Hydrodynamic Simulation of Bacteria Swimming — •Shang Yik Reigh, Roland G. Winkler, and Gerhard Gompper — Theoretical Soft Matter and Biophysics, Institute of Complex Systems and Institute for Advanced Simulation, Forschungszentrum Juelich, 52425 Juelich

Locomotion of bacteria such as E. coli or Salmonella is achieved by rotation of helical flagella, which are randomly distributed on the cell body. A directional running motion is attained by bundle formation of multiple flagella, while tumbling motion is achieved by the reverse rotation of one of the flagella. Alternating running and tumbling phases allow the bacteria to perform a directed random walk, and play an important role in their chemotaxis. During bacterial swimming, the pitch and the radius of flagella are changed (polymorphic transformations) and the cell body counter-rotates against the flagella to conserve angular momentum. To gain insight into the bacterial swimming behavior, hybrid mesoscale simulations are performed, which combine molecular dynamics simulations for the bacterium with the multiparticle collision (MPC) method for the solvent. The flagella are constructed by a sequence of mass points interacting by bond, bending, and torsional potentials. Such a model can efficiently be coupled to the MPC fluids. Results are presented for the synchronization and the bundle formation of several flagella. The synchronization and bundling times are analyzed in terms of the applied torque, the separation distances, and the number of flagella. The role of counter-rotating cell body for synchronization and bundling will be discussed.

DY 12.11 Tue 13:15 H 1028

Pili-induced clustering of *Neisseria gonorrhoeae* bacteria — •Johannes Taktikos[1,2], Vasily Zaburdaev[2], Nicolas Biais[3], David A. Weitz[2], and Holger Stark[1] — [1]Technische Universität Berlin — [2]Harvard University, USA — [3]Columbia University, USA

The attachment of *Neisseria gonorrhoeae* bacteria, the causative agent of the gonorrhea disease, to human epithelial cells constitutes the first step of colonization. The attachment of *N. gonorrhoeae* to surfaces or other cells is primarily mediated by filamentous appendages, called type IV pili. Cycles of elongation and retraction of these pili are responsible for a common form of bacterial motility called twitching motility which allows the bacteria to crawl over surfaces. Experimentally, *N. gonorrhoeae* cells initially dispersed over a surface agglomerate into round microcolonies within hours. It is so far not known whether this clustering is driven entirely by the pili dynamics or if chemotactic interactions are needed. Thus, we investigate whether the agglomeration may stem solely from the pili-mediated attraction between cells. By developing a model for pili-taxis, we try to explain the experimental measurements of the mean cluster size, number of clusters, and area fraction covered by the cells.