BP 22: Physics of Cells I

Time: Wednesday 15:00–17:45 Location: ZEU 250

Invited Talk BP 22.1 Wed 15:00 ZEU 250

The interplay between actin dynamics and membrane tension determines the shape of moving cells — •Kinneret Keren — Department of Physics, Technion- Israel Institute of Technology, Haifa, Israel.

A central challenge in cell motility research is to quantitatively understand how numerous molecular building blocks self-organize to achieve coherent shape and movement on cellular scales. We focus on one of the classic examples of such self-organization, namely lamellipodial motility, in which forward translocation is driven by a treadmilling actin network. We combine detailed measurements of lamellipodial morphology, spatio-temporal actin dynamics and membrane tension, with mathematical modeling to explain how global shape and speed of the lamellipodium emerge from the underlying assembly and disassembly dynamics of the actin network within an inextensible membrane bag.

BP 22.2 Wed 15:30 ZEU 250

A common mechanism connects diverse reaction-diffusion models of cellular symmetry breaking — •Ernesto M. Nicola[1], Philipp Khuc Trong[2,3], Nathan W. Goehring[2], and Stephan W. Grill[2,3] — [1]IFISC, Institute for Cross-Disciplinary Physics and Complex Systems (CSIC-UIB), Campus Universitat Illes Balears, E-07122 Palma de Mallorca, Spain. — [2]Max-Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstrasse 108, 01307 Dresden, Germany. — [3]Max-Planck Institute for the Physics of Complex Systems, Noethnitzer Strasse 38, 01187 Dresden, Germany.

Polarity, the asymmetry in shape present in many cells, is a common feature of many different cell types and is a important mechanism to achieve functional specialization. The initial establishment of cell polarity can be considered as a symmetry-breaking process and has attracted much attention during the last years.

We study a minimal mathematical model for polarization in mass-conserved systems. We find that the symmetry-breaking mechanism leading to cell polarization is similar to a Turing instability and typically divides the system in two regions as observed in experiments. We also find that the topology of the bifurcations present in the parameter-space of our minimal model is equivalent to the parameter-spaces of a number of more realistic mass-conserved reaction-diffusion models proposed in the literature. This equivalence suggests that the conservation of mass, a rapid cytoplasmic diffusion and bistability are sufficient and necessary conditions to generate cell polarity.

BP 22.3 Wed 15:45 ZEU 250

Influence of cell shape on organelle organization — •Nina Malchus[1] and Matthias Weiss[1,2] — [1]DKFZ c/o BIOQUANT, Heidelberg, Germany — [2]University of Bayreuth, Bayreuth, Germany

Cells within a tissue often display a well-defined geometry in contrast to culture cells that adopt a wide variety of phenotypes. Using patterned substrates, we have forced cells into distinct geometries and examined the subcellular organization of organelles. To this end, we quantified the positions and shapes of organelles like the nucleus and the Golgi apparatus and determined correlations of these features within an ensemble of cells and in single cells as a function of time. In particular, we find that positions and sizes of organelles show fairly large varitions in an ensemble of cells despite a common geometry and symmetry-dependent correlations between features of different organelles.

BP 22.4 Wed 16:00 ZEU 250

Single cell motility in flow: how parasites invade tissue — •Sravanti Uppaluri[1], Niko Heddergott[2], Eric Stellamanns[1], Stephan Herminghaus[1], Markus Engstler[2], and Thomas Pfohl[1,3] — [1]Max Planck Institute for Dynamics and Self Organization, Göttingen, Germany — [2]University of Würzburg, Germany — [3]University of Basel, Switzerland

Foreign cells in the mammalian blood stream have to navigate through a dense and rapid stream of red blood cells to invade host tissue. Trypanosomes, parasites responsible for devastating disease in Africa, are found in the mammalian bloodstream and penetrate the central nervous system during late stages of African Sleeping Sickness. Using microfluidics as a tool to mimic blood vessels, we investigate single cell trypanosome motility. In flow, trypanosomes experience a velocity dependent lift force away from vessel walls and migrate to the centre. Purely hydrodynamic effects arising from the trypanosome's shape and density are distinguished from effects of cell motility by comparing with immobilised trypanosome behaviour. While immobilised trypanosomes are aligned parallel to the vessel walls in flow, self propelling cells orient themselves perpendicular to the wall. Typical blood vessels have a cell free layer near the channel walls due to the migration of red blood cells toward the centre of the vessel. We confirm that in high flow velocities active trypanosomes are found in the depletion layer near the . Our studies show that despite relatively high flow velocities both hydrodynamic interactions and cell motility play a strong role in the overall swimming behaviour of parasites.

15 min. break

BP 22.5 Wed 16:30 ZEU 250

High-Precision Dynamics of Membrane Protrusions and Dorsal Ruffles in Mouse Fibroblasts — •Erik Bernitt[1], Pritpal Singh[2], Christina Oettmeier[1], Cheng-Gee Koh[2], and Hans-Günther Döbereiner[1] — [1]Institut für Biophysik, Universität Bremen, Germany — [2]School of Biological Sciences, Nanyang Technological University, Singapore

High-contrast microscopy techniques like total internal reflection fluorescence microscopy allow to accurately locate cellular structures. Cell dynamics can thus be precisely described using advanced localization algorithms in combination with an appropriate tracking method. We implemented a novel velocity chart method and applied it to spreading NIH 3T3 fibroblast cells. We could clearly identify a difference in cell spreading velocities of wildtype cells and cells that overexpress the PAK phosphatase POPX2. The precision of the method is thereby only limited by spatial and temporal resolution of the micrographs and thus superior to the traditional method of kymographs that relies on a preserved direction of structure propagation. We give a detailed analysis of experimental error in measuring membrane protrusion speeds. Further, we report on our latest advances in the quantification of the dynamics of dorsal ruffles that are a characteristic feature of POPX2-overexpressing cells. Function and mechanism of dorsal ruffles are still under discussion and quantitative dynamic data is missing. Therefore our data provides the basis for the establishment of models describing dorsal ruffle dynamics.

BP 22.6 Wed 16:45 ZEU 250

Spatio-Temporally Controlled Cues Mediating Cell Migration — Börn Meier and •Doris Heinrich — Faculty of Physics and Center for NanoScience (CeNS), Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, 80539 München, Germany

Cell migration relies on iterative pseudopod extension, which is based on internally controlled actin polymerization. In the chemotactic model organism Dictyostelium discoideum, robust intracellular feedback systems of complex protein interactions ensure directed cell migration towards an external chemotactic stimulus. Here, we investigate how external, spatiotemporally varying cues influence pseudopod generation and intracellular actin distribution in living cells. To relate the dynamics of pseudopod formation to the spatial distribution of chemotactic key players, we developed a microfluidic chamber with three independently tunable inlets to generate large scale spatiotemporally controlled gradient fields. For a quantitative description of cellular repolarization dynamics, we reverse the chemotactic gradient direction on freely tunable timescales. In response, we observe the time-resolved spatial distribution of actin polymerization in the evolving external gradient field. We can control cell migration by increasing the switching frequency of the gradient direction up to the point, where we chemically trap the cells.

BP 22.7 Wed 17:00 ZEU 250

Actin network growth in the tail of small propelled particles — •Julian Weichsel and Ulrich S. Schwarz — ITP and Bioquant, University of Heidelberg

In the lamellipodium of migrating animal cells, the growth of the actin network against the plasma membrane generates the work required to push the cell envelope forward. The same mechanism is exploited by

pathogens like the Listeria bacterium and the Vaccinia virus as they propel themselves forward in the cytoplasm of the infected host cell. In fact even plastic beads, vesicles or oil droplets can be propelled in this way in in-vitro assays. We have shown before with stochastic network simulations and a rate equation theory that the steady state structure of the growing actin network in the lamellipodium can dramatically change as a function of network growth velocity [1]. Here we extend this description to curved obstacles in a piecewise-linear approximation in two dimensions. By using adequately rotated reference frames, we again find similar transitions in the actin network behind small propelled particles.

[1] Weichsel, J., and Schwarz, U. S. Two competing orientation patterns explain experimentally observed anomalies in growing actin networks. PNAS 107, 14 (2010), 6304–6309.

BP 22.8 Wed 17:15 ZEU 250

Cell-substrate impedance analysis of cellular motility — •Helmar Leonhardt, Matthias Gerhardt, and Carsten Beta — Institute of Physics and Astronomy, University of Potsdam, Germany

Electric cell-substrate impedance sensing (ECIS) measures the frequency dependent impedance of a small disc-shaped electrode to ac current in the presence of cells. Cells on the electrode restrict the current path, forcing it to pass through the gaps between neighboring cells or through the cell membranes. We have applied ECIS to motile cells of the social amoebae Dictyostelium discoideum. During starvation, Dictyostelium forms multicellular aggregates, which eventually turn into a migrating slug and later into a fruiting body to facilitate spore dispersal. The chemotactic motility of Dictyostelium cells requires the formation and retraction of pseudopodia, resulting in cyclic changes of cell shape and size, which lead to distinct periodicities in the impedance signal. Thus, while shape oscillations of single cells and small ensembles are often difficult to detect by optical microscopy, ECIS can serve as a biosensor for detection of spatiotemporal changes on the nanometer scale such as shape, size, junctional resistance, or cell-substrate separation.

BP 22.9 Wed 17:30 ZEU 250

Mechanical energetics of helical bacteria trapped in a light tube — Matthias Koch and •Alexander Rohrbach — University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

The wall-less, helical bacterium spiroplasma melliferum has an extreme structural simplicity and is among the smallest cells in size (˜200nm thin, 3-5μm long). However, they infect various plants and insects and thereby do tremendous harm to agriculture industry. It has been hypothesized only recently that spiroplasms are responsible for mad cow disease and Creutzfeldt-Jakob-disease. Their motility, defined by helicity changes, kinking and propelling is very complex, and enables propagation in complex environments.

However, it is unclear how this ˜500 gene machine works. Which molecular machines work at which forces on which time scales? What are the energetic of this apparatus and how do they change during external disturbances. We try to answer these questions by optically trapping the whole bacterium in a light tube, which consists of a high speed scanning line optical trap. Although propelling and kinking, the bacterium remains in the focal plane and can thereby be observed with video microscopy. In addition, trapping light scattered at the slopes of the helix gives precise 3D information about its dynamics, which is analyzed and modelled with Fourier-techniques. We show experimental results, including energies and forces involved in its motility, and compare them to simulation data. Further, we present a first model of how this minimal machine could work and which amount of power it needs for self-propulsion.