DY 10: Cell Mechanics (Joint Session BP/DY)

Time: Monday 15:00–16:45 Location: SCH A251

Invited Talk DY 10.1 Mon 15:00 SCH A251

Quantifying and modelling active motion in biological systems — •Timo Betz — Institute of Cell Biology, ZMBE, University Münster, Germany

Living biological systems are continuously reorganizing their structure to perform their function. The mechanical activity plays here an important role, as the constant generation of forces drives fluctuations as well as controlled motion of intracellular particles, membranes and cells. From a physical point of view, this active motion drives the system far away from thermodynamic equilibrium, which can be measured as a violation of equilibrium quantities such as the fluctuation dissipation theorem.

Quantifying the out-of-equilibrium components provides the possibility to model the active molecular processes. We measure the energy and the forces actively applied on membranes as well as cellular granules and model these with an active Langevin approach. By comparing the predictions of forces and mechanics with the measurement of the fluctuations and viscoelastic properties we can extract molecular parameters from mesoscopic measurements. This gives timescales and chemical reaction parameters such as forces, binding states and velocities of the underlying proteins using a simple average measurement of the active motion.

DY 10.2 Mon 15:30 SCH A251

Feeling for Phenotype: Real-Time Deformability Cytometry for Label-Free Cell Functional Assays — •Oliver Otto[1,2,3], Philipp Rosendahl[1,3], Maik Herbig[1], Angela Jacobi[1,4], Martin Kräter[1,4], Nicole Töpfner[1], Marta Urbanska[1], Maria Winzi[1], Katarzyna Plak[1], Alexander Mietke[5], Christoph Herold[3], Daniel Klaue[3], Edwin Chilvers[6], Reinhard Berner[4], Martin Bornhäuser[4], and Jochen Guck[1] — [1]Technische Universität Dresden, Dresden, Germany — [2]Universität Greifswald, Greifswald, Germany — [3]Zellmechanik Dresden, Dresden, Germany — [4]Universitätsklinikum Dresden, Dresden, Germany — [5]Max-Planck-Institut für Molekulare Zellbiologie und Genetik, Dresden, Germany — [6]University of Cambridge, Cambridge, United Kingdom

By real-time deformability cytometry (RT-DC), we have introduced a high-throughput method for continuous mechanical single-cell classification of heterogeneous cell populations at rates of several hundred cells per second. Here, we demonstrate the extension of this method towards a multi-parameter biological assay where phenotyping is based on quantitative image analysis. Performing RT-DC on whole blood we highlight its potential to identify subsets in heterogeneous cell populations without any labelling and extensive sample preparation. We also demonstrate its capability to detect lineage-, source- and disease-specific mechanical phenotypes in primary human hematopoietic stem cells and mature blood cells. In summary, RT-DC enables marker-free, quantitative phenotyping of heterogeneous cell populations with a throughput comparable to standard flow cytometry.

DY 10.3 Mon 15:45 SCH A251

Light-driven intracellular flow perturbations to unravel transport processes in cells and developing embryos — •Matthäus Mittasch[1,4], Peter Gross[2], Michael Nestler[3], Mathias Munder[1], Axel Voigt[3,4], Simon Alberti[1], Stephan Grill[2,4], and Moritz Kreysing[1,4] — [1]MPI-CBG, Dresden — [2]Biotechnology Center, Technische Universität Dresden — [3]Department of Mathematics, TU Dresden — [4]Center for Systems Biology Dresden

Throughout the last decades, advances in molecular and cell biology have allowed for a precise control of molecular reactions inside cells. The complex interplay of molecular reactions with physical transport processes was suggested to control the spatiotemporal organization of cells and developing embryos. However, unravelling the function of physical transport during morphogenesis and cellular homeostasis remains a challenge due to the lack of suitable perturbation methods for in vivo systems. Here, we exploit thermoviscous pumping (Weinert & Braun) to perform light-driven intracellular flow perturbations. Thereby, we show the causal implications of intracellular flows during PAR polarization of the C. elegans zygote. Finite element simulations in 3D of the Stokes equation with time-dependent source terms recapitulated the experimental findings nearly identical. Furthermore, we utilize flow perturbations for active and probe-free micro-rheology measurements in yeast cells. Hence, we revealed a fluid-to-solid transition of the cytoplasm in energy-depleted cells. Light-driven intracellular flow perturbations lay the foundation to dissect the design principles of transport-dependent organization of living systems.

DY 10.4 Mon 16:00 SCH A251

Biophysics of neutrophil extracellular trap (NET) formation — •Daniel Meyer[1], Elsa Neubert[1,2], Anja Kwaczala-Tessmann[2], Susanne Senger-Sander[2], Michael P. Schön[2], Luise Erpenbeck[2], and Sebastian Kruss[1] — [1]Institute of Physical Chemistry, Göttingen University, Germany — [2]Dermatology, Venerology and Allergology, University Medical Center Göttingen, Germany

Neutrophils are the most abundant type of immune cells in the human blood system and central for immune defense. Recently, it was found that neutrophils and other cells are able to catch and kill pathogens by expelling a fibril network made from their own DNA (neutrophil extracellular traps, NETs). During this process (NETosis), a massive rearrangement of the materials inside the cell takes place which is still poorly understood. Our results show that NETosis can be divided into three distinct phases. The chromatin decondenses out of the disassembled nucleus until it fills the complete cell lumen. Simultaneously, the cytoskeleton decomposes and the cells become softer. In the final phase the cell body rounds up yet stays adherent to the surface, and the cytoplasmic membrane ruptures releasing the NET to the extracellular space. Using Atomic Force Microscopy (AFM) together with fluorescence microscopy methods, we demonstrate how the NETs-release is temporarily regulated by chromatin swelling, changes within the cytoskeletal components as well as the mechanical properties of the cell.

DY 10.5 Mon 16:15 SCH A251

Building up and force probing the microtubule cytoskeleton from scratch — •Matthias Koch[1,2] and Alexander Rohrbach[1] — [1]IMTEK, University of Freiburg, Germany — [2]Lewis-Sigler Institute, Princeton University, USA

Eukaryotic cells are exposed to and driven by a large variety of forces or mechanical stimuli on a brought range of times scales. Due to their mechanical rigidity, microtubules are able to transport such stimuli enabling instantaneous mechanical integration of distant regions of a cell. However, only equilibrium mechanical properties of single microtubules have been characterized so far. We fill this void by using an in vitro bottom-up approach to determine the frequency response of single microtubules and small networks thereof that mimic the basic cytoskeletal structure. We combine a new scanned darkfield imaging technique with multiple time-shared optical tweezers to flexibly construct and force probe such networks with a well-defined, user-selected geometry over a broad frequency range. We report on a length dependent stiffening of individual microtubules above a physiologically relevant transition frequency between 1-30Hz due to the excitation of higher order bending modes which displays a mechanical high-pass filter with a tunable cutoff frequency. Furthermore, we identify and relate different mechanical responses of different network geometries to different functions inside the cell. The mechanistic comparison of basic network geometries to the known cytoskeletal topologies and the general function of different cell lines will substantially strengthen our understanding of the function and structure of the cytoskeleton.

DY 10.6 Mon 16:30 SCH A251

Theory for forces that slide k-fibers and bridging microtubules to move chromosomes — •Agneza Bosilj[1], Kruno Vukusic[2], Renata Buda[2], Ana Milas[2], Iva Tolic[2], and Nenad Pavin[1] — [1]Department of Physics, Faculty of Science, University of Zagreb, Bijenicka cesta 32, 10000 Zagreb, Croatia — [2]Division of Molecular Biology, Ruder Boskovic Institute, Bijenicka cesta 54, 10000 Zagreb, Croatia

During cell division forces on chromosomes are exerted by k-fibers, bundles of microtubules which extend from the opposite spindle poles and attach to chromosomes. Recently we have shown that in metaphase microtubules which extend between sister chromatids, termed bridging fibers, bridge sister k-fibers and balance the tension between sister chromatids [Kajtez et al, Nat Commun 2016]. However, a theoretical description of forces driving chromosome segregation in anaphase is still missing. Here we introduce a theoretical model which

includes motor proteins that connect antiparallel microtubules, as well as passive cross-linkers that connect parallel microtubules. Our model shows that motor proteins generate forces that slide antiparallel bridging microtubules apart, thereby sliding sister k-fibers apart. This implies that forces at chromosomes are balanced by bridging fibers, which we confirmed experimentally by laser ablation of (i) k-fibers close to the spindle pole and (ii) bridging fibers. Our model also predicts that non-motor cross-linkers in regions of parallel overlap allow for movement of k-fibers and chromosomes together with the bridging fiber.