BP 8: Posters: Active cell and tissue mechanics

Time: Monday 17:30–19:30 Location: P3

BP 8.1 Mon 17:30 P3

The 3D Vertex Model for Epithelial Mechanics — •Silvanus Alt, Frank Jülicher, and Guillaume Salbreux — Max-Planck-Institut für Physik komplexer Systeme, Dresden, Deutschland

Understanding how mechanical forces drive epithelia deformations is crucial to shed light on processes involved in morphogenesis. Here we introduce a 3D vertex model, which represents cells in epithelia in three dimensions by a network of vertices joined by triangulated surfaces. Surface and line tensions, arising from forces generated in the actomyosin cytoskeleton, and the cells* intracellular elasticity act on the vertices to generate cellular deformations. Using this framework, we are interested in understanding the 3D cell shape in epithelia as well as the 3D deformations of epithelia, such as folding, formation of furrows, and invagination of structures.

In my talk, I focus on the physical mechanism for the formation of cysts, out-of-plane bulges which form in the Drosophila wing discs as a result of ectopic expression of a wide range of transcription factors. The 3D vertex model quantitatively captures the observed tissue deformations by considering an increase in line tension at the boundary of the cyst. The increase in tension at the boundary results in a planar pressure driving out of plane deformations. We propose that this constitutes a general mechanism for both invagination and evagination of epithelia.

BP 8.2 Mon 17:30 P3

Mechanical cues during early embryogenesis of *C. elegans* — •Philipp Struntz, Rolf Fickentscher, and Matthias Weiss — Experimental Physics I, University of Bayreuth, Bayreuth, Germany

The impact of biochemical signaling on developmental processes has been studied intensively during the last decades. However, the role of mechanical cues during embryogenesis has received much less attention. To elucidate the latter in the developmental model organism *C. elegans*, we have used a custom-made selective plane illumination microscope (SPIM) [1]. SPIM allowed us to quantitatively follow cell divisions and subsequent cell migration in three dimensions with a high spatiotemporal resolution. Comparison of different individuals showed only small deviations of cell trajectories, hence indicating a robust cellular arrangement process. A simple mechanical model revealed that cell organisation until gastrulation is determined by the cells' quest for a position with least repulsive interactions imposed by surrounding cells and the engulfing eggshell of the embryo. The model also predicts key features of the developing tissue that are in favorable agreement with experimental observations.

[1] Rolf Fickentscher, Philipp Struntz & Matthias Weiss: *Mechanical cues in the early embryogenesis of Caenorhabditis elegans*. Biophys. J, 105:1805 – 1811 (2013)

BP 8.3 Mon 17:30 P3

Broken detailed balance: A tool for identifying non-equilibrium dynamics — •Christopher Battle[1,4], Nikta Fakhri[1,4], Chase Broedersz[2,4], Fred C. MacKintosh[3], and Christoph F. Schmidt[1] — [1]Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Göttingen, Germany — [2]Lewis-Sigler Institute for Integrative Genomics and Department of Physics, Princeton University, Princeton, NJ, USA — [3]Dept. of Physics & Astronomy, Vrije Universiteit, Amsterdam, Netherlands — [4]These authors contributed equally to this work

Living systems exist far from thermal equilibrium, with active processes undergirding many of their functions. While some cellular processes show unmistakable non-equilibrium characteristics, e.g. persistent directed motion, others are more subtle, exhibiting non-thermal, random motion which is similar in appearance to Brownian motion, e.g. cortical stress fluctuations or active cellular mixing. Some techniques such as combined active and passive microrheology can quantify the non-equilibrium component of such processes, but they require comparisons between different measurement modalities. We here present an alternative and very general technique to identify non-equilibrium processes, searching for violations of detailed balance in an appropriately chosen phase space of the system. Our approach has the advantage of not requiring comparisons between different measurement techniques, and also allows us to determine a lower limit on the work dissipated by an active system.

BP 8.4 Mon 17:30 P3

Morphological analysis of epithelial tissues — •Sara Kaliman[1], Damir Vurnek[1], Florian Rehfeldt[2], and Ana-Sunčana Smith[1] — [1]Institut für Theoretische Physik, Universität Erlangen-Nürnberg — [2]3rd Institute of Physics-Biophysics, University of Göttingen

Tissue growth is an inherently complex process, the details of which need to be understood not only from a biological standpoint but also in terms of the purely physical and geometrical aspects. In the most common scenario, epithelial tissue exhibits an increase in cell density during the growth of a colony until such time as a steady state is reached. Using the growth of MDCK II epithelial tissue as an example, we show that several millimeter-sized compartments organize radially, within the typically circular colony, over several days. To characterize these compartments, we study the intensity of the cell-cell and cell-substrate adhesion, as well as the structure of the cellular actin cortexes within each compartment. These data are correlated with information about the local cell density and division rate. Furthermore, we show that the cells within the colony divide the space according to a Voronoi tessellation, based on the shape of the cell nuclei. We use this realization to study the development of the morphological measures (the cell area, orientation, elongation and volume) in the process of densification. We find that as the cell density increases, the tissue structure approaches, but never reaches, a Centroidal Voronoi tessellation. This reorganization is achieved by positioning the nuclei closer to the centers of mass of the cell bodies and by decreasing the area associated with the intercellular contacts.

BP 8.5 Mon 17:30 P3

Cellular chirality derives from active torques generated in the actomyosin cytoskeleton — •Sundar Naganathan[1], Sebastian Fürthauer[2], Frank Jülicher[3], and Stephan Grill[1,3,4] — [1]MPI-CBG, Pfotenhauerstr. 108, 01307, Dresden — [2]Courant Institute of Mathematical Sciences, New York University, 251 Mercer Street, New York, N.Y. 10012 — [3]MPI-PKS, Nöthnitzerstr. 38, 01187, Dresden — [4]Biotechnology Center, TU Dresden, Tatzberg 47/49, 01307, Dresden

Many developmental processes break left/right (L/R) symmetry with a consistent handedness, which require cells to be chirally asymmetric. The mechanisms by which cell chirality is established remain unclear, but the actomyosin cytoskeleton appears to be involved. To address this problem, we investigated flows in the actomyosin cortex of the one-cell stage C. elegans embryo. In addition to anterior-directed cortical flow, we observe the cortex to break chiral symmetry by counter-rotating flow with a consistent handedness in the anterior and posterior halves. Using active chiral fluid theory, we demonstrate that this motion derives from an active torque-generation process of defined chirality in the actomyosin cortex. This torque generation depends on myosin activity and can be independently regulated from tension generation though mild changes in Rho pathway activity, which we show by weak perturbation RNAi experiments. Our experiments suggest that chirality and torque generation is an emergent network property of the cortex. Interestingly, genes that affect the establishment of the C. elegans L/R body axis also regulate active torques, setting the stage for a mechanistic understanding of chiral morphogenesis in development.

BP 8.6 Mon 17:30 P3

Uncovering the slow mode dynamics of migrating tumor cells — •Christoph Mark, Claus Metzner, Julian Steinwachs, and Ben Fabry — Biophysics Group, University of Erlangen

Cell migration is usually analyzed by statistical methods that assume temporal homogeneity of the random process. Using long-time migration data from MDA-MB-231 tumor cells on 2D surfaces and in 3D collagen matrices, we show that this random walk process is highly inhomogeneous in time and accross the ensemble. Analysing the cell trajectories with a Hidden Markov Model reveals distinct migration modes with small mode switching rates. We thus describe the measured velocity time series $\vec{v}_t$ as a first-order autoregressive process $\vec{v}_{t+1} = q_t\vec{v}_t + \sigma_t\vec{g}_t$, in which the correlation factor q_t and the noise amplitude σ_t are treated as slowly varying superstatistical parameters. We show that the joint distribution $p(q, \sigma)$ and the temporal correlations of these super-parameters provide a characteristic fingerprint of the cell's migration mechanisms in different environments, whereas

traditional time-averaging measures, such as the mean squared displacement, mask such differences almost entirely. An inhomogeneous model, based on the extracted superstatistics can reproduce a large set of characteristic data features quantitively.

BP 8.7 Mon 17:30 P3

Mobility of semi-flexible chains coupled with hydrodynamics — •Won Kyu Kim and Roland Netz — Freie Universität Berlin, Arnimallee 14, 14195 Berlin, Germany

We study the hydrodynamic coupling and the effect of fluctuations on semi-flexible chains propulsion dynamics, where the chains are externally driven by an oscillating force or torque. By use of the linear response theory and Brownian dynamics simulations, we find optimal conditions for the chain propulsive force which can be maximized by proper driving frequencies and chain flexibilities. And we discuss how can the chain dynamics attain the effective propulsion in a collective manner.

BP 8.8 Mon 17:30 P3

AFM-based indentation measurements of adult zebrafish spinal cord tissue — •Stephanie Möllmert[1], Veronika Kuscha[1,2], Anna V. Taubenberger[1], Michael Brand[1,2], and Jochen Guck[1,3] — [1]BIOTEC, TU Dresden, Germany — [2]CRTD, TU Dresden, Germany — [3]Cavendish Laboratory, Department of Physics, University of Cambridge, UK

Severe injury to the mammalian spinal cord triggers a complex cascade of biochemical signals that eventually lead to the formation of a glial scar. In addition to inhibiting neuronal regrowth and causing loss of motor function, the glial scar has been proposed to act as a mechanical barrier preventing successful axon regeneration. Studies on spinal cord regeneration in adult zebrafish have revealed that zebrafish - in contrast to mammals - are able to successfully regain motor function after complete spinal cord transection. Therefore, the mechanical description of live spinal cord tissue poses an intriguing addition to biochemical analysis and might shed light on previously unknown mechanisms involved in successful spinal cord regeneration or the failure thereof. To efficiently investigate inherent mechanical properties of live spinal cord tissue from adult zebrafish, we have established a reliable protocol to prepare viable transverse acute spinal cord sections. Indentation type atomic force microscopy (AFM) was then employed to determine apparent elastic moduli (Young's moduli) of these sections under near physiological conditions. The presented work serves as a basis to investigate mechanical properties of neuronal tissue in vivo and test their importance in addition to biochemical and genetic factors.

BP 8.9 Mon 17:30 P3

Coordinated actomyosin kinetics in generating pulsatory dynamics — •Masatoshi Nishikawa[1,2,3], Sundar Naganathan[1,2,3], Guillaume Salbreux[1], and Stephan Grill[1,2,3] — [1]Max Planck Institute for Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]BIOTEC, Dresden, Germany

The cell cortex, which consists of cross-linked actin filaments and non-muscle myosin and is located beneath the cell membrane, is responsible for driving cell mechanical events. The cortex has been shown to be inherently unstable, displaying pulsatory dynamics characterized by transient accumulations of myosin at μm length scales. We sought to identify the regulatory mechanism of coordinated actomyosin kinetics to generate pulsatory dynamics, and that ensures the robust cellular processes. To this end we develop a new method to characterize, in the comoving frame of reference, turnover timescales of cortical components as a function of the concentration of actin and myosin, which we term Comoving Mass Balance Imaging (CoMBI). We applied this method to the cortical flow in the one-cell stage *C. elegance* embryo, and succeeded to extract the actomyosin kinetics in spatially and temporally resolved manner. This method provides us with a detailed description of actomyosin mechanochemical dynamics, relevant for the cellular scale.

BP 8.10 Mon 17:30 P3

Simulation of force transmission in random fiber networks — •Arne Monsees, Julian Steinwachs, Claus Metzner, and Ben Fabry — Biophysics Group, University of Erlangen

Self-organizing random networks of biopolymers, such as collagen gels, are routinely used as three-dimensional matrices for cell migration experiments. Methods for reconstructing the cell's traction forces from displacement fields take into account nonlinear mechanical properties of the networks, but usually approximate it as a continuum material. In the close vicinity of the cell, this approximation fails, since there the transmission of a point force is not spherically symmetric but focused into a small set of individual fibers. We present first simulation results for networks of realistic fibers with built-in curvature and cross-links. The fibers are represented as chains of straight segments, and the discrete chain units have a stiffness with respect to streching, bending and torsional deformations. The response to a static perturbation is found by minimizing the potential energy of the system. By comparing the results to a mean field theory, we map out the limits of applicability of both approaches and explore the combined effects of nonlinearity and inhomogeneity.