DY 42: Statistical Physics of Biological Systems 2 (joint session BP/DY)

Time: Thursday 15:00–16:30 Location: H16

DY 42.1 Thu 15:00 H16

Sensing and making sense of fluctuating cellular states — •Felix J. Meigel[1], Lina Hellwig[2], Philipp Mergenthaler[2], and Steffen Rulands[1,3] — [1]Max Planck Institute for Physics of Complex Systems, Dresden — [2]Neurology Department, Charité University Medicine Berlin — [3]Center for Systems Biology Dresden

The self-organisation of cells into complex tissue relies on the tight regulation of cellular responses to fluctuating cues. Typically, the regulation of cell decisions is attributed to pathways controlling the concentration of molecular species in response to intrinsic or extrinsic signal. Here, by contrast, we show in the paradigmatic example of cell death that cells manipulate how fluctuations propagate across spatial scales to regulate cellular behavior. Specifically, we find that the feedback between molecular and mesoscopic organelle fluctuations gives rise to a quasi-particle degree of freedom whose intriguing kinetic properties construct a kinetic low-pass filter of time-dependent concentrations of signaling molecules. We show that the collective dynamics of the quasi-particle degree of freedom exhibits different kinetics on different temporal scales. This allows cells to distinguish between fast fluctuations and slow, biologically relevant changes in environmental signals. We demonstrate an order of magnitude effect of this phenomenon on the quality of the cell death decision and validate our predictions experimentally by dynamically perturbing the intrinsic apoptosis pathway. Our work reveals a new mechanism of cell fate decision making.

DY 42.2 Thu 15:15 H16

Guidance and optimization in branching morphogenesis — •Mehmet Can Ucar and Edouard Hannezo — Institute of Science and Technology Austria, Am Campus 1, 3400 Klosterneuburg, Austria

The development of branched, tree-like biological structures such as lung, kidney, or the neurovascular system has been a pivotal question in biology, physics and mathematics. Recently, many studies based on combinatorial, mechanical, or stochastic models explored local, selforganizing rules leading to branched morphologies in specific systems. However, in addition to local interactions, the growth of branched structures is also regulated globally by external chemical or mechanical guidance cues. In this talk, we present our recent theoretical framework that integrates local and global regulatory mechanisms of branching morphogenesis. Combining analytical theory and numerical simulations, we show that branch orientations follow a generic scaling law that depends on the strength of global guidance. Local interactions such as self-avoidance of branches, on the other hand, lead to denser, efficiently space-filling networks, with a minimal influence on the overall shape and territory. These quantitative predictions of the model are corroborated by experimental data on sensory neurons in the zebrafish caudal fin. Finally, we discuss effects of local interactions on optimal tiling of space in branched distribution networks such as in lymphatic vasculature.

DY 42.3 Thu 15:30 H16

Random force yielding transition in spherical epithelia — Aboutaleb Amiri[1], Charlie Duclut[2], Frank Jülicher[1], and •Marko Popović[1] — [1]Max Planck Institute for Physics of Complex Systems, Dresden — [2]Université Paris Diderot, Paris

Developing biological tissues are often described as active viscoelastic fluids on long time-scales, due to fluidization by cell division and apoptosis. However, on shorter time-scales they can behave as amorphous solids with a finite yield stress [Mongera et al., Nature, 2018]. Under shear stress beyond the yield stress value amorphous solids begin to flow. This yielding transition is a dynamical phase transition characterized by a diverging correlation length and a set of critical exponents. Developing tissues are active matter systems whose constitutive cells can propel themselves by exerting traction forces. Recently, a remarkable correspondence has been proposed between uniformly sheared amorphous solids and dense self-propelled particle systems [Morse et al., PNAS, 2021] based on the identical scaling of non-linear properties of their energy landscapes. Here, we use a vertex model of epithelial tissues to study how randomly oriented traction forces fluidize a spherical epithelial tissue. In particular, we identify a sharp transition between quiescent and randomly flowing states separated by the critical value of the traction force magnitude, analogous to the yield stress. Moreover, we show that this transition is characterized by the same set of exponents as the classical yielding transition, and the corresponding scaling relations provide a non-trivial relation between cell geometry, cell rearrangement dynamics and tissue flow.

DY 42.4 Thu 15:45 H16

Biological tissues as living amorphous solids — •Ali Tahaei and Marko Popović — Max Planck Institute for Physics of Complex Systems, Dresden

Biological tissues are often described as viscoelastic fluids on long timescales. However, on shorter times-scales, tissues can behave as amorphous solids, such as clay, changing shape only when exposed to a shear stress above the material yield stress Σ_c. Amorphous solids near Σ_c display critical behaviour with a diverging correlation length-scale characterising dynamics of plastic activity. Here, we ask how would this critical behaviour be affected by active processes present in biological tissues, such as cell divisions.

In order to model yielding of biological tissues we employ the mesoscopic elasto-plastic model, commonly used to describe yielding of amorphous solids. Here, we extend the classical elasto-plastic model by introducing cell divisions as an additional source of plastic activity. We find that cell divisions strongly fluidise the solid phase of the system at stresses lower than Σ_c, consistent with literature. Furthermore, we find that critical behaviour is strongly suppressed, leading to localised dynamics of plastic activity nucleated by cell divisions. Finally, in our model we can describe how well is the cell division orientation aligned with local shear stress. We find that low alignment strength leads to less mechanically stable tissues where, consequently, most of the plastic flow arises from cell rearrangements, and vice versa.

DY 42.5 Thu 16:00 H16

Order-disorder transition in epithelial tissues — •Kartik Chhajed, Marko Popović, and Frank Jülicher — Max Planck Institute for Physics of Complex Systems, Dresden

Two dimensional packings of cells in developing epithelial tissues are commonly found to be disordered. However, highly organised packings can emerge during development, such as hexagonal pattern of ommatidia in the eye epithelium of the fruit fly. Here, we observe a disorder to order transition in the packing of the fruit fly pupal wing epithelium. In particular, we find a sudden increase in the hexatic order parameter ψ_6, which suggests a presence of hexatic and crystalline phases in two dimensional systems, as described by the classical KTHNY theory. The melting transition scenario with the intermediate hexatic phase has been reproduced in a model of epithelial tissues [Pashupalak et al. Soft Matter, 2020] where the stochastic active forces generated by the cells play the role of an effective temperature. However, both KTHNY theory and recent literature on packings of epithelial tissues assume uniform properties of particles and cells, respectively. In a proliferating tissue cells grow and divide, which inevitably leads to a heterogeneity of cell sizes. Here, we use the vertex model of epithelial tissues to study how the disorder to order transition is affected by the heterogeneity of cell sizes. We find that reducing cell heterogeneity as a control parameter drives the system through an ordering transition. We compare our results with the experimental data of the fruit fly wing to identify the role of cell size heterogeneity in the observed disorder to order transition.

DY 42.6 Thu 16:15 H16

The Influence of Contact Maps on RNA Structure Prediction — •Christian Faber[1] and Alexander Schug[1,2] — [1]Jülich Supercomputing Centre, FZ Jülich — [2]Steinbuch Centre for Computing, KIT

The 3d structure of Proteins and non coding RNA are essential for their function, but hard to determine via NMR or x-ray crystallography. Therefore an effective way of simulation with the knowledge of the sequence only would be a huge improvement. Impressive progress has been made in recent years, most notably AlphaFold2 for protein structure prediction using Machine Learning techniques. Such a break through is still missing for RNA.

For RNA, there are folding programs such as SimRNA, that simulate the structure with a physical force field [1]. The outcome can

be improved by incorporating evolutionary data from homologous sequences. From the evolutionary data, we can make predictions about possible contacts in the form of contact maps [2].

We investigate how contact maps can influence prediction quality and what are particularly valuable contacts. From these insights we develop new measures for machine learning algorithms.

[1] Boniecki, M. J. et al. *SimRNA: a coarse-grained method for RNA folding simulations and 3D structure prediction.* Nucleic Acids Research 44, e63 (2016).

[2] Weigt, M., White, R. A., Szurmant, H., Hoch, J. A., Hwa, T. *Identification of direct residue contacts in protein-protein interaction by message passing.* PNAS 106, 67-72 (2009).