SYED 1: Physics of Embryonic Development Across Scales: From DNA to Organisms

Time: Monday 9:30–12:15 Location: H1

Invited Talk SYED 1.1 Mon 9:30 H1

Emergent crystalline order in a developing epithelium — Kartik Chhajed[1], Natalie Dye[2], Marko Popović[1], and •Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzerstrasse 38, 01187 Dresden, Germany — [2]Cluster of Excellence Physics of Life, TU Dresden, Arnoldstrasse 18, 01307 Dresden, Germany

A fundamental question in Biology is to understand how patterns and shapes emerge from the collective interplay of large numbers of cells. Cells forming two-dimensional epithelial tissues behave as active materials that can undergo remodeling and spontaneous shape changes. Focussing on the fly wing as a model system, we will discuss the physics underlying the emergence of crystalline order in the wing epithelium during the pupal phase of morphogenesis. Using a vertex model of epithelial tissue, we demonstrate that when cell size heterogeneity exceeds a critical value, cellular packing remains disordered, whereas reducing heterogeneity below this value induces a phase transition to crystalline packing. Combining these results with analysis of experimental data reveals that cell size heterogeneity controls crystallization in the developing fly wing. Shear flows facilitate this process but are not the main driver of the disorder-to-order transition. Our work reveals how order can emerge during morphogenesis by the dynamic remodeling of tissues.

Invited Talk SYED 1.2 Mon 10:00 H1

A tissue rigidity phase transition shapes morphogen gradients — Camilla Autorino[1], Diana Khoromskaia[2], Bernat Corominas-Murtra[3], Zena Hadjivasiliou[2], and •Nicoletta Petridou[1] — [1]EMBL Heidelberg, Germany — [2]Francis Crick Institute, UK — [3]University of Graz, Austria

Transitions between solid-like and fluid-like tissue material states are essential for morphogenesis. However, if phase transitions instruct cell function is still unknown. Here, we show that tissue rigidification impacts cell signalling by regulating the length-scales and time-scales of morphogen gradients. By combining rigidity percolation theory, reaction-diffusion modelling, quantitative imaging, genetics and optogenetics in zebrafish germ layer formation we uncover that a tissue rigidity phase transition defines the dynamics of fate specification by restricting Nodal morphogen transport and facilitating its signalling dynamics. This is a self-generated mechanism where Nodal, besides triggering cell fate specification, increases cell adhesion via regulating planar cell polarity genes. Once adhesion strength reaches a critical point it triggers a rigidity transition which sharply minimises tissue porosity and induces the formation of tricellular contacts. The resulted tissue reorganisation negatively feeds back to Nodal signalling by sealing the interstitial paths of Nodal diffusion and restricting it close to the source, and by speeding up its degradation. This leads to prompt expression of its inhibitor resulting in robust pattern formation. Overall, we reveal how phase transitions shape morphogen gradients and uncover macroscopic mechanisms of positional information.

Invited Talk SYED 1.3 Mon 10:30 H1

Building quantitative dynamical landscapes of developmental cell fate decisions — •David Rand — University of Warwick, Coventry CV4 7AL, UK

I will discuss the dynamics of decision-making in the early embryo. As cells proliferate and assemble into tissues, their molecular identity changes in discrete step-like transitions to produce diverging sequences of distinct cell states that culminate in the differentiation of specific functional cell types. Hence, cellular development can be viewed as sets of branching cell lineages generating increasing diversity and comprising increasingly specialised cell types. I will outline an approach to understanding this that relies on geometry and dynamics, and I will illustrate this with recent work on the early development of the nervous system. New methods for the analysis of single-cell temporal data combined with ideas from dynamical systems can be used to deduce the topology of the branching network, the dynamical nature of the branching transitions and a quantitative model of the underlying dynamics that reproduces the data.

15 min. break

Invited Talk SYED 1.4 Mon 11:15 H1

Control of lumen geometry and topology by the interplay between pressure and cell proliferation rate — •Anne Grapin-Botton[1], Byung Ho Lee[1], Masaki Sano[2,5], Daniel Riveline[3], Kana Fuji[2], and Tetsuya Hiraiwa[2,4] — [1]Max Planck Institute of Molecular Cell Biology and Genetics Dresden — [2]The University of Tokyo — [3]IGBMC, Strasbourg — [4]Academia Sinica, Taipei — [5]Shanghai Jiao Tong University

Many organs in multicellular organisms comprise epithelia which enclose fluid-filled cavities referred to as lumens. Their formation is regulated by a wide range of processes, including polarization, secretion, exocytosis and actomyosin contractility. While these mechanisms have shed light on lumen growth, what controls lumen morphology remains enigmatic. Here we use organoids to explore how lumens acquire either a spherical shape or a branched topology. We develop a multicellular phase field model with the following basic components: conditions for the timing and volume of cell division, lumen nucleation rules, and lumenal pressure. Combining computational simulations with experimental measurements we reveal that lumen morphology arises from the balance between the cell cycle duration and lumen pressure, with more complex lumen at low pressure and fast proliferation rates. Moreover, the perturbation of proliferation and lumen pressure in silico and in vitro is sufficient to alter and reverse the morphological trajectories of the lumens. We further show that low pressure depends on epithelial permeability enabling complex lumen shapes.

Invited Talk SYED 1.5 Mon 11:45 H1

Chromosomes as active communication and memory machines — •Leonid A. Mirny — Institute for Medical Engineering and Science, and Department of Physics, Massachusetts Institute of Technology, Cambridge, MA, USA

Chromosomes are long polymers of genomic DNA decorated by myriads of proteins. We are interested in understanding how cells fold them to read, write, and process genetic and epigenetic information. Can the way chromosomes are folded carry information itself?

Recent work from my group and others has shown that chromosomes are active polymers. First, we found that chromosomes are folded by the active (ATP-dependent) process of loop extrusion, where molecular motors form progressively larger loops. The collective action of these nanometer-sized motors shapes micron-sized chromosomes. This active mechanism also enables long-range communication between the *regulatory genome* and protein-coding genes.

Second, we found that chromosome folding can help store *epigenetic memory* patterns of chemical marks along the genome. Such marks are lost and spread by enzymes, yet when marks influence genome folding, the pattern of marks can be preserved for hundreds of cell divisions. We further identified a parallel between this mechanism of epigenetic memory and associative memory in a neural network, suggesting that this system may perform more complex information processing tasks.