BP 32: Tissue Mechanics II

Time: Thursday 15:00–17:45 Location: H 2032

BP 32.1 Thu 15:00 H 2032

Letting cells off the Hook: A non-mechanistic vertex model predicts inverse stress-strain relation in epithelial tissues by statistical inference. — •Zoë Lange and Franziska Matthäus — Frankfurt Institute for Advanced Studies, Goethe-Universität, Frankfurt am Main, Germany

Disordered epithelial cell packings are considered to be a result of cell mechanics, cell-cell interaction and proliferation (Farhadifar et al. 2007). A recent vertex model proposes remodeling of cell-cell junction length and tension as a proliferation-free alternative explanation (Pérez-Verdugo & Banerjee 2023). Despite the mechanical basis of vertex models it remains poorly understood how stress and strain in epithelial tissues relate to each other on the cell scale. We use a non-mechanistic vertex model to estimate effective forces in different epithelial tissues by statistical inference (Ishihara & Sugimura 2012). We obtain an inverse relation between tension and cell shape in both proliferating and non-proliferating epithelial tissues. We show that the modulus of the relation is exclusively negative even when tissue is not stretched. We find that the cell perimeter alone is not correlated with tension. Our work highlights how the power of statistical inference will contribute to unravelling different contributions of subcellular processes on macroscopic properties of tissues by extracting empirical laws from experimental data.

BP 32.2 Thu 15:15 H 2032

Agent-based model for active nematics of cellular tissues — •Mathieu Dedenon[1,2], Carles Blanch-Mercader[3], Karsten Kruse[1,2], and Jens Elgeti[4] — [1]Department of Biochemistry, University of Geneva, 1211 Geneva, Switzerland — [2]Department of Theoretical Physics, University of Geneva, 1211 Geneva, Switzerland — [3]Laboratoire Physico-Chimie Curie, Institut Curie, Université PSL, Sorbonne Université, CNRS UMR168, Paris, France — [4]Theoretical Soft Matter and Biophysics, Institute of Complex Systems, Forschungszentrum Jülich, D-52425 Jülich, Germany

Biological cellular tissues often exhibit domains of orientational order, separated by topological defects where orientation is ill-defined. Those regions concentrate active stresses generated by cell force dipoles and give rise to spontaneous flows. This interplay of nematic order and activity has been explored based on two-dimensional continuum theory, but more complex geometries remain unexplored theoretically.

Based on a two-particle agent-based model, we describe cells as multi-particle filaments with controllable aspect ratio. We incorporate mechanical activity in terms of individual cell force dipoles. This framework is designed to capture hydrodynamic modes at large scales.

In agreement with the continuum theory of active nematics, we recapitulate the active flow transition beyond a critical activity threshold for two-dimensional simulations. In addition, we confirm the influence of activity on the onset of nematic order and identify a fluidization effect. In the future, we plan to explore active nematic features in more complex geometries.

BP 32.3 Thu 15:30 H 2032

Cell divisions imprint long-lasting shear strain on epithelial tissue — •Ali Tahaei[1], Romina Pisticello-Gómez[2,3], Suganthan S[1], Greta Cwikla[3], Jana Fuhrmann[2,3], Natalie Dye[3], and Marko Popović[1,3] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max Planck Institute of Molecular Cell Biology and Genetics — [3]Cluster of Excellence Physics of Life, Technische Universität Dresden

Biological tissues exhibit complex dynamics, with mechanical behaviors that vary across different timescales. They flow on long timescales and exhibit more solid-like characteristics on short timescales. In this work, we use experiments and linear elasticity theory to show that fruit fly wing epithelial behave as two-dimensional linear elastic solids. To this end, we measure the strain field in the epithelium generated by a linear laser ablation and we find that we can describe them as a linear combination of elastic stress propagators. This allows us to determine the relative magnitudes of force dipoles generated by the laser ablation. Motivated by this discovery we next analyzed the strain patterns in the tissue generated by cell divisions. As before, by accounting for the observed strain using linear elasticity propagators, we find that cell divisions generate an isotropic force dipole transiently during the division process, which subsequently vanishes soon after the cell division. However, cell divisions exert a pure shear force dipole that imprints a long-lasting elastic strain pattern in the tissue. In summary, we have developed a method that allowed us to describe in detail the dynamics of forces generated during cell divisions.

BP 32.4 Thu 15:45 H 2032

Topological Transformations in Graph Vertex Model — •Urban Železnik, Tanmoy Sarkar, and Matej Krajnc — Jožef Stefan Institute, Jamova cesta 39, SI-1000 Ljubljana, Slovenia

Vertex Model (VM) shows its reliability in modeling confluent biological tissues in two dimensions (2D). However, its application in three dimensions (3D) has been constrained by computational complexities, primarily stemming from managing topological changes during cell rearrangements. In the talk, I will demonstrate how the recently introduced Graph Vertex Model (GVM) successfully addresses the challenges posed by VM. GVM achieves this by exclusively storing topological data of cell networks within a Knowledge Graph (KG). The unique data structure of KG enables cell rearrangements and divisions to be equivalent to elementary graph transformations, which are also represented by graphs. Furthermore, cell rearrangements in 3D consist of graph transformations that correspond to more fundamental T1 transitions, thereby unifying topological transitions in both 2D and 3D space-filling packings. This implies that the GVM's graph data structure may be the most natural representation for cell aggregates and tissues.

BP 32.5 Thu 16:00 H 2032

Vertex Model Challenges Meet Knowledge Graph Solutions — •Tanmoy Sarkar and Matej Krajnc — Jožef Stefan Institute, Jamova 39, SI-1000 Ljubljana, Slovenia

Vertex model (VM) shows its credibility in modeling confluent biological tissues in two dimensions. However, due to computational complexities, only a few studies have been reported since the introduction of the first three-dimensional (3D) vertex model almost two decades ago. Most of the challenges lie in handling the changes in topology during dynamic cell rearrangements, which justifies the absence of a proper algorithmic form of topological transformations so far. This issue is often viewed in the community as a complex engineering problem. In the talk, I will demonstrate a possible solution to this outstanding problem using a new approach called the Graph Vertex Model (GVM). GVM is founded on the concept of representing the topology of the cell network using a Knowledge Graph (KG), effectively rendering topological transformations both intuitive and mathematically well-defined. Furthermore, I will highlight the enhanced credibility and utility of the KG by introducing the GRAPh Embryo project (GRAPE). GRAPE is an online database designed to facilitate interactive analyses of an entire fly embryo, showcasing the practical applications and benefits of this approach.

15 min. break

BP 32.6 Thu 16:30 H 2032

Growth arrest and scaling during axolotl limb regeneration — •Natalia Lyubaykina[1,2], Pietro Tardivo[3], Dunja Knapp[4], Tatiana Sandoval-Guzmán[4], Elly Tanaka[3], and Benjamin M Friedrich[1,2] — [1]Cluster of Excellence 'Physics of Life', Technical University Dresden, Dresden, Germany — [2]Center for Advancing Electronics, Technical University Dresden, Dresden, Germany — [3]Research Institute of Molecular Pathology, Vienna Biocenter (VBC), Vienna, Austria — [4]CRTD/Center for Regenerative Therapies, Technical University Dresden, Dresden, Germany

Axolotl can regenerate lost limbs even as adults, posing the question of how a regenerating limb matches animal size, which can differ up to five-fold between juvenile and adult axolotl. Two key morphogens, SHH and FGF8, are known to regulate proliferation and growth. Yet it remains unclear how these morphogens control growth arrest once a correct target size of the wound tissue (blastema) is reached. Inspired by this biological example, we theoretically investigate growth arrest during blastema growth and address the question of proportional growth matching animal size. Using a minimal reaction-diffusion model, we describe SHH and FGF8 dynamics during regeneration and

formulate French flag-like growth rules to discern conditions for robust growth arrest during tissue growth. We also explore how a putative scaling of SHH or FGF8 morphogen gradients with either blastema or animal size impacts growth arrest and proportional growth. Finally, we compare theory predictions to recent quantifications of SHH and FGF8 morphogen gradients.

BP 32.7 Thu 16:45 H 2032

A mechano-chemical model of Hydra regeneration — •Suganthan Senthilkumar[1], Yonit Maroudas-Sacks[2], Kinneret Keren[2], and Marko Popović[1] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden — [2]Technion University, Haifa, 3200003, Israel

Hydra is a freshwater animal with extraordinary regeneration properties making it an excellent model organism to study morphogenesis. It has a simple body plan, with a double layered epithelium enclosing a fluid-filled lumen. Hydra epithelia contain long actin muscle fibres that are highly organized with an aster point defect positioned at the head. Starting from an excised tissue fragment Hydra can fully regenerate, however, it is unclear how the fibre pattern self organizes. The regeneration of the fibre pattern is inhibited by perturbing either tissue strain or production of Wnt, which is a morphogen relevant for head regeneration. We propose a mechano-chemical feedback between tissue mechanics, nematic fibre pattern and morphogen dynamics, as a mechanism of Hydra regeneration. For this we have developed a vertex model of curved epithelia that incorporates the feedback mechanism. In the model, each cell contains a nematic, representing the orientation of actin fibres, that generate stress upon activation, and a morphogen concentration. We implement the mechano-chemical feedback such that the morphogen production depends on cellular strain, with morphogen gradients guiding nematic orientation, which in turn focusses the tissue strain. We find that this mechanism can robustly reproduce experimentally observed dynamics of Hydra tissue and nematic fibres.

BP 32.8 Thu 17:00 H 2032

Continuum mechanics of apical constriction — •Chandraniva Guha Ray[1,2,3], Marija Krstic[2,3], and Pierre Haas[1,2,3] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max Planck Institute of Molecular Cell Biology and Genetics — [3]Center for Systems Biology Dresden

Apical constriction, the contraction of apical cell sides, is a common mechanism driving deformations of biological tissues during development. It is associated with the geometric singularity in which cell cross-sections become triangular and hence the cell sides are maximally bent, splaying the cells and thus bending the cell sheet.

Here, we explore the mechanical consequences of this geometric singularity in what is perhaps the simplest problem of tissue buckling: Under external compression, a monolayer of cells buckles, and, as the compression is increased further, fans of triangular cells expand from the crests and troughs of the buckled shape. Taking a continuum limit of a "differential-tension model" describing the cell mechanics [1], we show how these expanding fans lead to a strong increase of the resistance of the tissue to further compression. We reveal an intriguing secondary bifurcation beyond the onset of triangular cells: The buckling amplitude of a thin monolayer increases with increasing compression until the cells touch sterically, but, surprisingly, the buckling amplitude of a thick monolayer decreases with increasing compression. We develop a scaling argument to describe this bifurcation, and discuss its consequences for tissue development.

[1] P. A. Haas and R. E. Goldstein, Phys. Rev. E 99, 022411 (2019)

BP 32.9 Thu 17:15 H 2032

Mechanotransduction in Lateral Root Initiation: A Model Integrating Growth Mechanics and Auxin Signaling — •João R. D. Ramos[1], Karen Alim[1], and Alexis Maizel[2] — [1]School of Natural Sciences, Technical University of Munich, Germany — [2]Centre for Organismal Studies, University of Heidelberg, Germany

Plant development relies on the precise coordination of cell growth, which is influenced by the mechanical constraints imposed by rigid cell walls. The hormone auxin plays a crucial role in regulating this growth by altering the mechanical properties of cell walls. During the post-embryonic formation of lateral roots, pericycle cells deep within the main root are triggered by auxin to resume growth and divide to form a new root. This growth involves a complex interplay between auxin, growth, and the resolution of mechanical conflicts, that is still not well understood. We propose a model that integrates tissue mechanics and auxin transport, revealing a connection between the auxin-induced relaxation of mechanical stress in the pericycle and auxin signalling in the endodermis. We show that the growth of pericycle cells is initially limited by the endodermis. However, the resulting modest growth is sufficient to redirect auxin to the overlying endodermis, which then actively accommodates the growth, allowing for the subsequent development of the lateral root. Our model uncovers the mechanical parameters that underlie endodermal accommodation and how the structure and shape of the endodermis influence the formation of the new root. These findings emphasize the vital role of the endodermis in shaping root development through mechanotransduction and auxin signalling.

BP 32.10 Thu 17:30 H 2032

Cytoplasmic streaming induces nuclear trafficking and signalling in Physarum polycephalum — •Johnny Tong[1], Kaspar Wachinger[1], Siyu Chen[1], Nico Schramma[2], and Karen Alim[1] — [1]School of Natural Sciences, Technical University of Munich, Germany — [2]University of Amsterdam, The Netherlands

Syncytial organisms and organs house hundreds of thousands of nuclei within a single cell, are often shaped into a complex network architecture. How are nuclei able to efficiently exchange signals over long distances? To understand how syncytia coordinate gene expression, intracellular transport within these networks is key. Here, we investigate how communication is achieved by flow-driven behaviours of nuclei functionally different regions of the network in Physarum polycephalum. Using microinjection of fluorescent dsDNA markers, followed by image-based methods such as tracking and velocimetry, we analyze the dynamics of nuclei and cytoplasm flow.

This dynamics of nuclei allows us to formulate a potential framework of how Physarum utilizes the two-phase flow profile and distribution of nuclei, which it enables a relay-like model for long-range signal propagation, where flowing nuclei act as carriers and trapped nuclei act as waypoints. Our findings could lead to a better understanding of the mechanisms of long-range genetic communication within network-shaped systems like fungi and placenta.