LMU-UT Joint Workshop on Statistical and Biological Physics
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Abstracts

Erwin Frey - Emergence and Self-Organisation in Biological Systems

Abstract:
Isolated systems tend to evolve towards thermal equilibrium, a special state that has been a research focus in physics for more than a century. By contrast, most processes studied in biological systems are far from equilibrium. A fundamental overarching hallmark of all these processes is the emergence of structure, order, and information, and we are facing the major challenge to identify the underlying physical principles. Two particular exciting problems are the self-organised formation of spatio-temporal patterns and the robust self-assembly of complex structures. In both fields there are recent advances in understanding the underlying physics that will be reviewed in this talk.

Shuji Ishihara - From cells to tissue: a continuum model for passive and active tissue deformation

Abstract: Morphogenesis is a process in which both chemical and mechanical interactions among cells play an essential role for determining shape of tissue and bodies. We have developed methods to quantify mechanical force and deformation in a growing epithelial tissue in terms of stress and deformation tensors. To relate these quantities, we also developed a continuum model for two-dimensional epithelial tissue, where a field variable representing coarse-grained cellular shape is included. Employing formalism developed in active gel theory, active terms were included into the model, by which new mechanism for cotraction-elongation, a typical morohogenetic process, was identified.

Fridtjof Brauns - Phase space geometry of reaction–diffusion systems

Abstract:
The dynamics of any physical system are encoded in the (flow) structure of the system's phase space. Phase space flow for low dimensional ODE dynamics can be studied in terms of geometric structures like nullclines and fixed points in phase space. This approach is at the core of Nonlinear Dynamics. Recent advances suggest that a general phase space geometric framework can be developed for mass-conserving reaction--diffusion systems.
Here we develop a comprehensive theory for pattern formation in two-component mass-conserving reaction--diffusion systems. These systems serve as paradigmatic class of systems able to form (stationary) patterns --- a prominent application is intracellular polarization. Based on the core concepts of mass redistribution and local chemical equilibria, we introduce geometric structures in phase space that explicitly reveal the interplay between reaction- and diffusion-processes. The nonlinear chemical interactions are captured by a line of chemical equilibria. We show that all aspects of pattern formation --- ranging from linear instability and excitability to the characteristics and bifurcations of stationary patterns --- can be extracted from the geometric features of the line of chemical equilibria. In particular, we find that a mass-redistribution instability is at the core of pattern formation. Furthermore, our analysis points towards a deep connection to equilibrium phase separation as described by Model~B dynamics. Challenges for future research will be to systematically work out this connection, to generalize the framework to mass-conserving systems

with more components and more conserved quantities, and to tackle issues like non-linear wavelength selection in such systems.

Taihei Fujimori - Tissue self-organization based on collective cell migration in Dictyostelium development

Abstract:

Although directional cell migration often has a crucial role in tissue patterning, the molecular and developmental complexity of higher animals hinders the exact identification of navigational rules of individual cell movement. We focused on a simple form of multicellular organization present in the development of Dictyostelium discoideum, one of the social amoeba. Upon starvation, Dictyostelium cells aggregate, differentiate into prestalk or prespore cells, and form segregated pattern where prestalk cell cluster sits on prespore cell mass. Despite the system being well-studied, the exact navigational rules underlying their morphogenesis remain elusive. By spatiotemporal manipulation of the chemoattractant and the cell-cell contact signal using microfluidics and purified adhesion protein, here we show that there is contact-dependent navigation in addition to their well known chemotaxis toward cAMP. Our analysis revealed that cell-cell adhesion promotes constitutive F-actin formation which gives rise to contact following motion, and the polarity induced by cell-cell contact competes with those induced by chemotaxis. Surprisingly, the mechanism is an inversion of the so-called contact inhibition of locomotion – a canonical scheme of collective cell migration in metazoans. Furthermore, we demonstrate that both signals are required for pattern formation. Isolated prestalk and prespore cells can protrude towards the contact signal as well as chemotax towards cAMP, however when given both signals, prestalk cells orient towards the chemoattractant whereas prespore cells choose the contact signal. We propose that the difference in prioritization to navigational cues works as an efficient and rapid means of cell segregation and that a similar mechanism may underlie tissue patterning in other systems.

Nen Saito - Self-organization via membrane deformation and reaction diffusion: 3D modeling for macropinocytosis of ameboid cell

Abstract:

Ameboid cell shows drastic deformation of cell shapes. Sometimes topology of cell shape can change (e.g. endocytosis). Macropinocytosis is clathrin-independent endocytosis and allows internalization of large volume of extracellular fluid. D. discoideum and tumor cells show constitutive macropinocytosis for uptake of nutrients from extracellular fluid. The mechanism of it remains still unclear.

We introduce a mathematical model based on 3D phase-field method, which enables to simulate reaction-diffusion process on the cell membrane and large membrane deformation simultaneously. Simulation results indicate that simple chemical reactions lead to drastic membrane deformation, which results in an engulfment of extracellular fluid. This study provides a new insight for macropinocytosis as a self-organization phenomenon via feedback between drastic deformation of membrane and reaction-diffusion on it.

Felix Kempf - Active Matter Invasion into Capillaries

Abstract:

Biological active materials such as bacterial biofilms and eukaryotic cells thrive in confined micro-spaces. Here, we numerically show that combining growth dynamics with their intrinsic activity cells can use confinement as a mechanical guidance to achieve distinct modes of collective invasion. We assess the dynamics of the growing interface and classify these collective modes of invasion based on the activity of the cells. While at small and moderate activities the active material

grows as a coherent unit, we find blobs of active materials collectively detaching from the cohort above an activity threshold in a process reminiscent of the intravasation in cancer cells. We further characterise the mechanical mechanisms of transition between different modes of invasion.

Tetsuya Hiraiwa - Theory on dynamics and stress generation in an actomyosin cytoskeleton

Abstract:

This talk focuses on active mechanics of a cortical cytoskeleton, which is a network structure consisting of actin and myosin filaments and crosslinker proteins located underneath the cell membrane. Mechanical properties of a cortical cytoskeleton govern not only cell's resistances to deformation but also contractility induced by the motor protein, myosin. Motor-induced contractile stress in a cortical cytoskeleton plays crucial roles in dynamic cellular behaviors, such as cytokinesis and cell migration.

In this talk, I would like to explain our theoretical work on dynamics and stress generation in a cortical cytoskeleton. I will propose a mechanical model of motor-induced stress in an isotropic actomyosin network with crosslinkers and share the results of the model about motor-induced¬¬ contractility. In particular, since a cortical cytoskeleton in a living cell should be flowable, we study the case of fluidic networks, in which there are only few amount of crosslinkers and/or network elements can undergo stochastic turnover processes. We found that a finite amount of crosslinkers is significant for motor-induced contractility. We also investigated how turnover of crosslinkers and actin filaments influences motor-induced stress. Furthermore, we looked at the dynamic local density inhomogeneity of the network with such contractility.

Manon Wigbers - A Cascade of Protein Patterns Senses Cell Shape in Starfish Oocyte during Meiosis

Abstract:

Cells are constantly subject to mechanical stresses, for example during migration, cell division and development. These mechanical stresses generate shape deformations and cytoplasmic flows, modulating the reaction diffusion dynamics of biochemical processes inside these cells. The general mechanisms of such mechanochemical feedback, underlying the formation of self-organized spatiotemporal patterns that are important during development, have remained largely unexplored. Here, we study how the Rho GTPase signaling pathway drives mechanical contraction waves post anaphase in starfish oocytes. We can modulate the speed of the contraction waves by manipulating the cell shape of the oocytes in micro-fabricated PDMS chambers of defined geometry. We combine our experimental results with a reaction-diffusion model and show how a cascade of protein patterns allows the RhoGTPase pathway to sense cell shape, giving rise to a close interplay between cell geometry and biochemical regulation in biological pattern formation.

Tomohiro Shima - Kinesin-binding–triggered conformation switching of microtubules contributes to polarized transport

Abstract:

Kinesin-1, the founding member of the kinesin superfamily of proteins, is known to use only a subset of microtubules for transport in living cells. This biased use of microtubules is proposed as the guidance cue for polarized transport in neurons, but the underlying mechanisms are still poorly understood. Here, we report that kinesin-1 binding on microtubules promotes additional kinesin-1 binding by inducing conformational switching of the microtubules. Our data demonstrate that this positive feedback spontaneously provide a subset of high affinity microtubules from other low affinity microtubules, shedding light on the mechanism behind polarized transport in cells.

Philipp Geiger - Topologically Robust Zero-Sum Games
Abstract:
To explore how the topology of interaction networks determines the robustness of dynamical systems, we study the antisymmetric Lotka-Volterra equation (ALVE). The ALVE is the replicator equation of zero-sum games in evolutionary game theory, in which the strengths of pairwise interactions between strategies are defined by an antisymmetric matrix such that typically some strategies go extinct over time. Here we show that there also exist topologically robust zero-sum games, such as the rock-paper-scissors game, for which all strategies coexist for all choices of interaction strengths. We refer to such zero-sum games as coexistence networks and construct coexistence networks with an arbitrary number of strategies. By mapping the long-time dynamics of the ALVE to the algebra of antisymmetric matrices, we identify simple graph-theoretical rules by which coexistence networks are constructed. In particular, we characterize the kernel of an antisymmetric matrix in terms of Pfaffians and their relation to near-perfect matchings. Our results show that the topology of interaction networks alone can determine the long-time behavior of nonlinear dynamical systems, and may help to identify robust network motifs arising, for example, in ecology.

Yuma Fujimoto - Evolution of Intention through mutual recognition in Game Theory
Abstract:
Intention recognition is an important characteristic of intelligent agents. In their interactions with others, they try to read others' intentions and make an image of others to choose their actions accordingly. While the way in which players choose their actions depending on such intentions has been investigated in game theory, how dynamic changes in intentions by mutually reading others' intentions are incorporated into game theory has not been explored. We present a novel formulation of game theory in which players read others' intentions and change their own through an iterated game. Here, intention is given as a function of the other's action and the own action to be taken accordingly as the dependent variable, while the mutual recognition of intention is represented as the functional dynamics. It is shown that a player suffers no disadvantage when he/she recognizes the other's intention, whereas the functional dynamics reach equilibria in which both players' intentions are optimized. These cover a classical Nash and Stackelberg equilibria but we extend them in this study: Novel equilibria exist depending on the degree of mutual recognition. Moreover, the degree to which each player recognizes the other can also differ. This formulation is applied to resource competition, duopoly, and prisoner's dilemma games. For example, in the resource competition game with player-dependent capacity on gaining the resource, the superior player's recognition leads to the exploitation of the other, while the inferior player's recognition leads to cooperation through which both players' payoffs increase.

David Muramatsu - Range Expansions in a Stochastic Metapopulation Model
Abstract:
In range expansions, the colonization of a territory by an invading species, the front between invaded and new territory roughens due to stochastic fluctuations.
To investigate the growth laws describing the front width of a given system, large sized systems have to be considered, since finite size effects may otherwise obscure the dynamics that govern the interface.
Naive implementations of exact simulation algorithms like the Gillespie algorithm scale unfavorably in the system size such that the simulation of ensembles of large systems with complex interactions quickly becomes unfeasible.

We address this problem by implementing a parallelized version of the Gillespie algorithm, which scales linearly in the system size, suited for lattice based systems that display local fast dynamics while having a low rate of particle exchange between lattice sites.
We employ this algorithm to determine the growth law governing the front width of a system which has been inaccessible to previously used simulation methods.

Tetsuhiro Hatakeyama - Reciprocity between Robustness and Plasticity as a Universal Law in Biology

Abstract:
Robustness and plasticity are important characteristics in biological systems and have therefore attracted much attention from not only biologists but also physicists. Whereas robustness concerns insensitivity to perturbations, plasticity concerns the variability of external inputs. How the two phenomena are compatible with each other is an important question to be addressed.
We investigate the compatibility of the two distinguishable properties in some biological systems, e.g., circadian clocks and reaction-diffusion systems, and we found the reciprocity between robustness and plasticity as a quantitative relationship. For example, the robustness of period and plasticity of phase against environmental changes such as temperature and nutrient conditions are compatible in circadian clocks. We found a quantitative relationship between them: higher robustness in the period implies higher plasticity in the phase, where changes in period and phase follow a linear relationship with a negative coefficient.

Yongtae Hwang - Collective behaviors of cardiac myosin molecules for effective cardiac function

Abstract:
For effective heart contractions, it is extremely important to maintain high and stable ventricular pressure during systole and release the pressure immediately during the following relaxation. However, myosin and actin filaments are distributed in a complex 3D arrangement in heart and thus, one can imagine that contractile forces are somehow coordinated among myosins and there must be a key molecular property of cardiac myosin for such functional demands in heart. In this study, in order to reveal molecular properties of cardiac myosins for functional demands in heart, forces generated by synthetic cardiac myosin filaments were measured by optical tweezers at high spatiotemporal resolution. Back and forth stepwise force curves were frequently observed at high ATP and ADP concentrations. Combined with simulation results, one key feature for back and forth force generations is the ADP state of myosin, which remains bound to actin and causes the reverse strokes and subsequent detachments more frequently at higher loads. These molecular properties appeared to be suitable to maintain high systolic pressure and achieve pressure release quickly during the following relaxation.

Sakurako Tanida - Self-organizations of microtubule filaments gliding on kinesin motors

Abstract:
Microtubules are the common substrates to eukaryotic cells and some bacteria.In those cells, the filamentous proteins micortubules interact with motor proteins, and show coordinated motion. Such motions play an important role in cell dynamics, for example, division, intraceller transportation, and migration.While other proteins are known to often help the self-organization process, the kinetics of microtubules itself also responsible for the self-organization process. In this study, we investigated the relation between dynamical self-organization and the microtubules' motion generated by motor proteins. By using a simple experimental system in which the microtubules glide on the carpet of the kinesin motor, we found that a subtle interaction difference whether microtubules overlap each other makes a big difference in the large-scale self-organization.

Patrick Wilke - Two-Species Active Transport along Cylindrical Biofilaments is Limited by Emergent Topological Hindrance

Abstract:

Active motion of molecules along filamentous structures is a crucial feature of cell biology and is often modeled with the paradigmatic asymmetric simple exclusion process. Motivated by recent experimental studies that have addressed the stepping behavior of kinesins on microtubules, we investigate a lattice gas model for simultaneous transport of two species of active particles on a cylinder. The species are distinguished by their different gaits: While the first species moves straight ahead, the second follows a helical path. We show that the collective properties of such systems critically differ from those of one-species transport in a way that cannot be accounted for by standard models. This is most evident in a jamming transition far below full occupation, as well as in non-equilibrium pattern formation. The altered behavior arises because -- unlike the case in single-species transport -- any given position may be targeted by two particles from different directions at the same time. However, a particle can leave a given position only in one direction. This simple change in connectivity significantly amplifies the impact of steric interactions and thus becomes a key determinant of mixed species transport. We computationally characterize this type of hindrance and develop a comprehensive theory for collective two-species transport along a cylinder. Our observations show high robustness against model extensions that account for additional biomolecular features and demonstrate that even small fractions of a second species can significantly alter transport. This suggests that our analysis is also relevant in a biological context.

Renan A. L. Almeida - Coarsening & percolation in twisted nematic liquid crystals Coarsening & percolation in twisted nematic liquid crystals

Abstract:

When the two-dimensional Ising-Glauber (2DIG) model is quenched from the paramagnetic to the ferromagnetic phase, locally equilibrated regions of spins up and down spontaneously form amid the system and coarsen over time. Some aspects of this coarsening dynamics can be described by phenomenological scaling theories that suggest universal behaviours out-of-equilibrium. However, these universal behaviours remain to be experimentally substantiated in many directions: functional forms of space-time scaling functions are just a few, but some of the notable examples. Beyond that, recent simulations of the 2DIG model surprisingly indicated that, along with the coarsening, the statistics of certain length scales might be in the universality class of the critical percolation model (a purely static model). In this seminar, I will address both of these universal aspects - coarsening and percolation - by analysing the two-dimensional ordering dynamics of twisted nematic liquid crystals quenched from a hydrodynamic turbulent state. The ordering is featured in this case by the disentangling and shrinking of topological defects that lie in between twisted domains. I will give experimental evidence that the celebrated Ohta-Jasnow-Kawasaki scaling theory well describes functional forms for space and for time scaling functions. Finally, but not least important, it will be argued that universal exponents related to the critical percolation model are indeed measured along the out-of-equilibrium ordering dynamics.

Kazumasa Takeuchi - Turbulent liquid crystal and competing bacteria: possible universal relaxation at criticality

Abstract:

On the basis of experiments on turbulent liquid crystal under a twist alignment and simulations on bacteria strains competing in a microfluidic channel, I argue that critical relaxation dynamics in those apparently different problems may be governed by a single universality class, namely the voter universality class. The voter class is theoretically believed to describe phase transitions into absorbing states in the presence of the Ising-like up-down symmetry, but so far remains experimentally elusive. Here I describe two possible situations, showing some experimental and numerical observations akin to the voter class dynamics, and discuss underlying mechanisms. The work on competing bacteria is due to collaboration with Takuro Shimaya (arXiv:1804.09895).