BP 24: Systems Biology, Gene Expression, Signalling

Time: Thursday 10:30–12:30 Location: H16

Invited Talk BP 24.1 Thu 10:30 H16

Actin waves as building blocks of cellular function — •Carsten Beta — Institute of Physics and Astronomy, University of Potsdam, Potsdam, Germany

Many cellular functions, such was motility, phagocytosis, and cell division, are driven by coherent patterns of activity in the actin cytoskeleton. Among them, actin waves are a recurrent motive that is commonly observed across different cell types. Here, we present experimental results demonstrating the rich variety of wave patterns in the actin cortex of motile amoeboid cells. We show that ring-shaped actin waves, commonly acting as precursors of macropinocytic cups, can mediate switches between different modes of motility, a pseudopod-based amoeboid mode, and a more persistent, wave-driven migratory mode, reminiscent of keratocyte motility. In multinucleate, oversized amoeboid cells, the same waves may also trigger spontaneous, cell cycle-independent cytofission events, resulting in mononucleated daughter cells of a well-defined size. We also demonstrate that a second wave pattern can coexist with the ring-shaped macropinocytic waves. It emerges in a cell-size dependent manner and consists of rapidly moving planar pulses that show typical signatures of an excitable system. Our experimental findings demonstrate the functional versatility of cortical waves patterns. They can be rationalized based on minimal reaction-diffusion models that mimic the evolution of cortical wave patterns and are coupled to a dynamic phase field to take the cell shape evolution into account. In addition, bifurcation analysis provides a more detailed understanding of how regimes of pattern coexistence may emerge.

BP 24.2 Thu 11:00 H16

Quantifying Dynamic Information Transfer in Stochastic Biochemical Networks — •Anne-Lena Moor[1,2] and Christoph Zechner[1,2] — [1]Max-Planck Institute of Molecular Cell Biology and Genetics, Dresden Germany — [2]Center for Systems Biology, Dresden, Germany

Transmission and encoding of information are fundamental processes for the functioning of biochemical systems. Information theoretical concepts, such as the mutual information, provide a rigorous mathematical framework to study intracellular signal transmission. In many biological systems, information is encoded in the time-trajectory of signalling components as opposed to instantaneous levels. However, performing information theoretical analysis on the trajectory-level is computationally demanding. In this work, we present an effective approach to calculate mutual information between complete trajectories of biochemical components. The resulting measure provides useful insights into the dynamic information transfer through networks of chemical reactions.

BP 24.3 Thu 11:15 H16

Optimal ligand discrimination by asymmetric dimerization of interferon receptors — •Patrick Binder[1,2,3], Nikolas D. Schnellbächer[1,2], Thomas Höfer[2,3], Nils B. Becker[2,3], and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, 69120 Heidelberg, Germany — [2]BioQuant Center for Quantitative Biology, Heidelberg University, 69120 Heidelberg, Germany — [3]Theoretical Systems Biology, German Cancer Research Center, 69120 Heidelberg, Germany

In multicellular organisms, antiviral defense is mediated by ligands. These signaling molecules are usually characterized by highly inhomogeneous distributions due to scarcity of producer cells, diffusion and localized degradation. And yet, a molecular hub of the antiviral response, the interferon I receptor (IFNAR), discriminates between ligand types by their affinity regardless of concentration. In my talk, I address the long-standing question of how a single receptor can decode robustly ligand type. I frame ligand discrimination as an information-theoretic problem and systematically compare the major classes of receptor architectures: allosteric, homodimerizing, and heterodimerizing. As a result, asymmetric heterodimers achieve the best discrimination power over the entire physiological range of local ligand concentrations, enabling sensing of ligand presence and type. IFNAR exhibits this optimal architecture, suggesting that it has evolved the optimal design to detect and separate the presence of different ligand types in a noisy environment.

15 min. break

BP 24.4 Thu 11:45 H16

Rationalizing the optimality of the Drosophila gap gene system by ab-initio derivation of optimal solutions for morphogenetic patterns — •Thomas R. Sokolowski[1,2], Thomas Gregor[3,4], William Bialek[3], and Gašper Tkačik[1] — [1]IST Austria, Am Campus 1, A-4300 Klosterneuburg, Austria — [2]Present Address: Frankfurt Institute for Advanced Studies, Ruth-Moufang-Str. 1, D-60438 Frankfurt, Germany — [3]Department of Physics, Princeton University, Princeton, NJ 08540, U.S.A. — [4]Insitut Pasteur, Department of Developmental and Stem Cell Biology, 25 Rue du Dr. Roux, F-75015, Paris, France

Early fruit fly development is outstandingly precise in spite of the high level of stochasticity in the underlying biochemical processes. While the gap gene system driving fly embryo patterning has been shown to encode positional information optimally, the precise mechanisms that enable this remain elusive. We show that optimal solutions for the gap gene regulatory network can be obtained by optimizing a biophysically realistic spatial-stochastic embryo model, without inferring from data. Firstly, our predictions mechanistically explain how the observed developmental precision can be attained. Secondly, by exploring rich sets of optimal solutions, we elucidate the role of key components controlling early fly patterning. To our knowledge our work provides the first successful ab-initio derivation of a nontrivial biological network in a biophysically realistic setting. Our results suggest that even though real biological networks are hard to intuit, they may represent optimal solutions to optimization problems which evolution can find.

BP 24.5 Thu 12:00 H16

Stability of gene expression patterns in developmental systems with dynamic morphogen sources — •Maciej Majka — Jagiellonian University, Krakow, Poland

In developmental systems cells determine their fate by decoding chemical signals, called morphogens. In this presentation I will address the problem of gene expression patterns stability in the systems where two diffusible morphogens affect each other production and control the growth of their own source regions. Such systems are encountered in e.g. spinal cord development, limb formation and many others. The reaction-diffusion equation with bi-stable production term is employed as a generic model for this problem. The phase transition is found, between the phase of indeterminate patterning, where region of mixed gene expression is ever growing, and the phase of travelling gene expression patterns, where two expression domains form and preserve a well-defined contact zone. A sub-class of genuinely stationary patterns is then identified, alongside the exact conditions ensuring this stability. This allows me to classify the pattern stability for all possible two-gene regulatory motifs.

BP 24.6 Thu 12:15 H16

Conditions and trade-offs to enhance protein production in synthetic bacterial communities — •Marco Mauri[1,3], Jean-Luc Gouzé[2], Hidde de Jong[3], and Eugenio Cinquemani[3] — [1]Friedrich Schiller University, Jena, Germany — [2]University Côte d'Azur, Sophia-Antipolis, France — [3]Univ. Grenoble Alpes Inria, Grenoble, France

In nature, microorganisms occur in communities comprising a variety of mutually interacting species. To overcome the complexity of natural communities, a rapidly growing research field concerns the rational design and engineering of synthetic microbial consortia.

Here, based on a quantitative model of a prototypical synthetic microbial consortium, we discuss the precise conditions under which a consortium outperforms individual species in the production of a recombinant protein. Moreover, we identify the inherent trade-offs between productivity and efficiency of substrate utilization [1].

[1] Mauri M, Gouze' JL, de Jong H, Cinquemani E (2020) Enhanced production of heterologous proteins by a synthetic microbial community: Conditions and trade-offs. PLOS Computational Biology 16(4): e1007795. https://doi.org/10.1371/journal.pcbi.1007795