BP 9: Systems Biology II

Time: Monday 14:00–16:30 Location: BPc

Invited Talk BP 9.1 Mon 14:00 BPc

From individual to collective intermittent motion: from bacteria to sheep — •Fernando Peruani — CY Cergy Paris University, Cergy, France

Intermittent behavior is observed in biological systems at all scales, from bacterial systems to sheep herds. First, I will discuss how Escherichia coli explores surfaces by alternating stop and moving phases. Specifically, I will show that a stochastic three behavioral state model is consistent with the empirical data. The model reveals that the stop frequency of bacteria is tuned at the optimal value that maximizes the diffusion coefficient. These results provide a new perspective on how evolution may have reshaped the bacterial motility apparatus. Intermittent motion is also observed in Merino sheep, where again a stochastic three behavioral state model provides a quantitative understanding of the empirical data. However, in sheep, individual transition rates depend on the behavioral state of other individuals and collective behaviors emerge. Specifically, I will show that small sheep herds display highly synchronized intermittent collective motion, with the herd behaving as a self-excitable system. Based on the analysis of these two biological systems (bacteria and sheep), we will discuss the need of three behavioral states to describe intermittent motion in biological systems, providing a unified picture of such behavior across scales.

Refs.: Perez Ipina et al. Nature Physics 15, 610-615 (2019); Gascuel et al. Animal behavior (2021); Gomez Nava et al. (2021)

BP 9.2 Mon 14:30 BPc

Specialisation and plasticity in a primitive social insect — •Adolfo Alsina[1], Solenn Patalano[2], Martin Bachman[3], Irene Gonzalez-Navarrete[4], Stephanie Dreier[5], Shankar Balasubramanian[3], Seirian Sumner[5], Carlos Gregorio-Rodriguez[6], Wolf Reik[2], and Steffen Rulands[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]The Babraham Institute, Cambridge, UK — [3]University of Cambridge, Cambridge , UK — [4]Centre for Genomic Regulation (CRG), Barcelona , Spain — [5]Institute of Zoology, London , UK — [6]Universidad Complutense de Madrid (UCM), Madrid, Spain

Biological systems not only have the remarkable capacity to build and maintain complex spatio-temporal structures in noisy environments, they can also rapidly break up and rebuild such structures. How can such systems can simultaneously achieve both robust specialisation and plasticity is poorly understood. Here we use primitive societies of Polistes wasps as a model system where we experimentally perturb the social structure by removing the queen and follow the relaxation dynamics back to the social steady state over time. We combine a unique experimental strategy correlating measurements across vastly different spatial scales with a theoretical approach. We show that Polistes integrates antagonistic processes on multiple scales to distinguish between extrinsic and intrinsic perturbations and thereby achieve both robust specialisation and rapid plasticity. Such dynamics provide a general principle of how both specialization and plasticity can be achieved in biological systems.

BP 9.3 Mon 14:50 BPc

Plasticity in vertex model of epithelial tissues — •Marko Popović[1,2], Valentin Druelle[1,3], Natalie Dye[4,5], Frank Julicher[2,5], and Matthieu Wyart[1] — [1]Institue of Physics, École Polytechnique Fédérale de Lausanne (EPFL), CH-1015 Lausanne, Switzerland — [2]Max Planck Institute for Physics of Complex Systems, Nöthnitzer Strasse 38, 01187 Dresden, Germany — [3]Biozentrum, University of Basel, Klingelberstrasse 70, 4056 Basel, Switzerland — [4]Max Planck Institute for Molecular Cell Biology and Genetics, Pfotenhauerstrasse 108, 10307 Dresden, Germany — [5]Cluster of Excellence Physics of Life, TU Dresden, 01307 Dresden, Germany

Developing tissues are often described as viscoelastic liquids. However, tissues can also be plastic and respond elastically to stresses below the critical value, while flowing plastically at higher stresses. Plasticity is exhibited by a wide class of amorphous solids such as colloidal gels, emulsions, and foams where it corresponds to a yielding transition. Are features of yielding transition, such as dependence on system preparation and non-linear rheology, relevant in developing tissues? Motivated by similarities of disordered tissues and amorphous solids we study the plasticity of the vertex model of epithelial tissues, where the mechanical properties of cells are prescribed and tissue mechanics is obtained from their collective behavior. We describe the mechanics of T1 transitions, which are the elementary plastic events in epithelial tissues. We find that interactions between T1 transitions are analogous to those of particle rearrangements in amorphous solids and our simulations suggest that the vertex model belongs to the same class of universality.

BP 9.4 Mon 15:10 BPc

Selection via phase separation — •Giacomo Bartolucci[1,2], Adriana Serrao[3], Philipp Schwintek[3], Alexandra Kühnlein[3], Yash Rana[4], Dieter Braun[3], Christof Mast[3], and Christoph A. Weber[1,2] — [1]Max Planck for the Physics of Complex Systems, Dresden — [2]Center for Systems Biology Dresden — [3]Ludwig Maximilian University, München — [4]Harvard University, Cambridge, USA

Living cells and pre-biotic systems are complex aqueous mixtures composed of thousands of different heteropolymers. In such multicomponent mixtures, enrichment and selection of a small set of components are important to achieve biological function. However, when the number of components increases, each of them becomes more diluted impeding a significant enrichment of selected components. Here, we propose a selection mechanism relevant for prebiotic mixtures based on cycles of phase separation combined with material exchange of the dense phase with a reservoir. We find a selective enrichment of components up to two orders of magnitude coinciding with a growth of the dense phase up to the system volume. Such enrichment of selective components is robust also in mixtures composed of a large number of components. For a prebiotic soup, our findings indicate that cycles of phase separation and material exchange with a reservoir, e.g. the accumulation DNA gel in rock pores periodically filled with DNA rich aqueous solution, could provide a mechanism for the selection and enrichment of specific heteropolymers sequences in a multi-component mixture at the origin of life.

BP 9.5 Mon 15:30 BPc

Towards an alphabet of random matrix models for large biological networks — •Philipp Fleig[1] and Ilya Nemenman[2] — [1]University of Pennsylvania, Philadelphia, USA — [2]Emory University, Atlanta, USA

Biological interaction networks such as populations of neurons or amino acid sequences in proteins are critical to the functioning of any biological system. The trend of modern high-throughput experiments is to record data from a rapidly increasing number of simultaneously measured network units. Such data recorded from a biological network has characteristics of a large random matrix with hidden structures encoded in it. We present first steps towards the design of an alphabet of random matrix models to describe data of biological networks. Here, we focus on how to detect different random matrix structures in data from simple observable quantities such as pairwise correlations and the eigenvalue spectrum of the correlation matrix. Using random matrix theory we show analytically how properties of the data, such as a hidden dimensionality, are encoded in these observables. Finally, we use a neural network classifier with the observables as input to detect different types of random matrix structures in our alphabet and their hidden dimensionality in noisy data of finite size. Our approach can likely be used to model large and complex data of diverse types of biological networks.

40 min. Meet the Speaker