BP 22: Focus Phase Separation in Biological Systems II (joint session BP/CPP)

Time: Tuesday 14:00–16:00 Location: BPb

BP 22.1 Tue 14:00 BPb

Phase separation provides a mechanism to reduce noise in cells — •Florian Oltsch[1,2], Adam Klosin[1], Tyler Harmon[1,3], Alf Honigmann[1,4], Frank Jülicher[2,3,4], Anthony Hyman[1,2,4], and Christoph Zechner[1,2,4] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany — [2]Center for Systems Biology Dresden, 01307 Dresden, Germany — [3]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [4]Cluster of Excellence Physics of Life, TU Dresden, 01062 Dresden, Germany

Noise in gene expression can cause significant variability in protein concentration. How cells buffer variation in protein concentration is an important question in biology. In this talk, I will show that liquid-liquid phase separation provides an effective mechanism to reduce variability in protein concentration. First, I will introduce our theoretical framework that discusses phase separation in the presence of active protein production and turnover. This stochastic non-equilibrium model allows us to study how fluctuations in protein concentration are affected by phase separation. I will then present under which physical conditions noise buffering by phase separation can be effective. Subsequently, I will show experimental data to test our theoretical predictions.

BP 22.2 Tue 14:20 BPb

Parasitic Behavior in Competing Dissipative Reaction Cycles — •Patrick Schwarz[1], Sudarshana Laha[3,4], Jacqueline Janssen[3,4], Tabea Huss[1], Christoph A. Weber[3,4], and Job Boekhoven[1,2] — [1]Department of Chemistry, Technische Universitat München, Lichtenbergstrasse 4, 85748 Garching, Germany — [2]Institute for Advanced Study, Technische Universität München, Lichtenbergstrasse 2a, 85748 Garching, Germany — [3]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden, Germany — [4]Center for Systems Biology Dresden, CSBD, Dresden, Germany

Fuel-driven reaction cycles serve as model systems of the intricate reaction network of life. Rich and dynamic behavior is observed when such reaction cycles regulate phase separation or assembly. However, it remains unclear how the interplay between multiple reaction cycles affects their fate. To tackle this question, we created a library of precursor molecules that compete for a common fuel to transiently activate products. Generally, the competition for fuel means that a competitor decreases the success of the cycle. However, in cases where the transient competitor product can phase separate, this relation can be inverted. The presence of assemblies formed by such a competitor can increase the survival time of one product, analogous to how the presence of a host can increase the survival time of a parasite. Our study of such a parasitic behavior in multiple fuel-driven reaction cycles represents a lifelike trait, paving the way for bottom-up design of synthetic life.

BP 22.3 Tue 14:50 BPb

Surface condensation of a pioneer transcription factor on DNA — •Jose A. Morin[1,2], Sina Wittmann[1], Sandeep Choubey[1,3], Adam Klosin[1], Stefan Golfier[1,3], Anthony A. Hyman[1,5], Frank Julicher[3,4,5], and Stephan W. Grill[1,2,5] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany. — [2]Biotechnologisches Zentrum, Technische Universitat Dresden,Dresden, Germany. — [3]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [4]Center for Systems Biology Dresden, Dresden, Germany. — [5]Cluster of Excellence Physics of Life, Technische Universitat Dresden, Dresden, Germany.

Transcription factors cluster into sub-micrometer sized condensates while initiating transcription of their target genes. How cells achieve liquid-like clusters of constrained size at specific locations on DNA is not known. Here we investigate the role of DNA in the nucleation of condensates, using the pioneer transcription factor KLF-4. We show that KLF-4 forms liquid-like condensates on the DNA surface at physiological concentrations, below the one required for Klf4 phase separation. Through a dialogue between theory and experiments, we demonstrate that condensation occurs via a switch-like transition from a thin adsorbed layer to a thick condensed layer on DNA that is well described as a prewetting transition on a heterogeneous substrate. This phenomenon is thus a form of surface condensation mediated by and limited to the DNA surface.

BP 22.4 Tue 15:10 BPb

Slowing down protein aggregation in liquid compartments — •Wojciech P. Lipiński[1], Brent Visser[1], Mireille Claessens[2], Mohammad A. A. Fakhree[2], Saskia Lindhoud[3], and Evan Spruijt[1] — [1]Institute for Molecules and Materials, Radboud University, Nijmegen, the Netherlands — [2]Nanobiophysics, Faculty of Science and Technology, University of Twente, Enschede, the Netherlands — [3]Molecular Nanofabrication, Faculty of Science and Technology, University of Twente, Enschede, the Netherlands

With increasing life expectancy in modern societies, amyloid-related diseases are becoming alarmingly common. Extensive work has been done to investigate the kinetics of amyloid formation and the structure of aggregates. Recently it has been suggested that protein aggregation can be influenced by the presence of membraneless organelles. Aggregation-prone proteins may be sequestered by liquid compartments, leading to significant changes in concentration and altered aggregation kinetics.

Here, we present a combined computational and experimental study of the fate of aggregation-prone proteins that are sequestered by liquid droplets. We investigated computationally the influence of varying parameters describing aggregation and transport processes and showed that aggregation process can be either accelerated or inhibited by the presence of liquid compartments. Motivated by these findings we have undertaken efforts to develop experimental systems exhibiting diversified influence of the phase-separated environment on the protein aggregation process.

30 min. Meet the Speaker