DY 52: Statistical Physics of Biological Systems II (joint session BP/DY)

Time: Friday 9:30–12:00 Location: BAR Schö

DY 52.1 Fri 9:30 BAR Schö

Evolutionary optimization of multicomponent phase separation — •David Zwicker[1] and Liedewij Laan[2] — [1]MPI-DS, Göttingen, Germany — [2]TU Delft, The Netherlands

Biological cells use passive phase separation to segregate different biomolecules into various condensates. Since the molecular interactions determine the number of distinct condensates and their composition, they have likely been optimized evolutionarily for robust segregation. To study this, I will present a numerical method that efficiently determines coexisting phases in multicomponent liquids and use it in evolutionary optimization experiments. I will demonstrate that the optimized interactions lead to a precise number of different condensates, even if the overall composition varies. Consequently, adjusting microscopic interactions leads to stable emergent behaviors in these complex systems.

DY 52.2 Fri 9:45 BAR Schö

Kinetics of droplet sizes in non-conserved emulsions — •Jacqueline Janssen[1], Frank Jülicher[1], and Christoph A. Weber[2] — [1]Max Planck Institute for the Physics of Complex Systems — [2]University of Augsburg

Droplets form via phase separation and coexist with a dilute phase that is composed of droplet material of lower concentration. Many droplets in an emulsion undergo coarsening to the thermal equilibrium state that corresponds to a single droplet in a finite system. In passive emulsions, where the total amount of droplet material is conserved, the average radius grows as a function $t^{1/3}$ in time, and the droplet size distribution function broadens. Here we consider emulsions for which the total droplet material is not conserved, e.g. material is supplied by a chemical reaction or external reservoirs. We calculate the kinetics of droplet sizes and show that there is a switch from coarsening to narrowing of the size distribution upon material supply. Regulation of droplet sizes by material supply could be relevant for biomolecular condensates in living cells.

DY 52.3 Fri 10:00 BAR Schö

Dynamics of vesicle clusters studied by passive x-ray microrheology — •Titus Czajka[1], Charlotte Neuhaus[1], Jette Alfken[1], Moritz Stammer[1], Yuriy Chushkin[2], Diego Pontoni[2], Christian Hoffmann[3], Dragomir Milovanovic[3], and Tim Salditt[1] — [1]Institut for X-ray Physics, Georg-August-Universität Göttingen, Germany — [2]ESRF, Grenoble, France — [3]Laboratory of Molecular Neuroscience, DZNE, Berlin, Germany

Inferring the viscoelastic properties of a complex fluid from the dynamics of suspended tracer particles is a common method to perform rheological measurements where a direct measurement of the constituents of the system is not possible or impractical. The previously observed pool formation of vesicles induced by divalent salts or the protein synapsin I is a case in point. One would like to know how the mobility of a single (tracer) particle changes in a dense pool as compared to a homogeneous vesicle suspension. Here we used x-ray correlation spectroscopy (XPCS) to measure silica nanoparticles immersed in a complex biomolecular fluid composed of small unilamellar vesicles and $CaCl_2$, or SUVs and Synapsin-Ia protein, both in buffer solution. While the former system leads to irregular clusters, the latter has been observed to form protein induced vesicle pools, suggesting a liquid-liquid phase separation. Analysis of the photon correlation functions reveals the presence of different timescales, which we attribute to the free diffusive motion of the tracer particles and the motion of the tracer particles that interact with the cluster.

DY 52.4 Fri 10:15 BAR Schö

A stereotypical sequence of condensation and dispersal of RNA polymerase II clusters during stem cell differentiation — •Tim Klingberg[1], Irina Wachter[2], Agnieszka Pancholi[2], Roshan Prizak[2], Priya Kumar[3], Yomna Gohar[3], Marcel Sobucki[2], Elisa Kämmer[2], Süheyla Eroğlu-Kayikçi[2], Sylvia Erhardt[2], Carmelo Ferrai[3], Vasily Zaburdaev[1], and Lennart Hilbert[2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]Karlsruher Institut für Technologie — [3]Universitätsmedizin Göttingen

Most eukaryotic genes are transcribed by RNA polymerase II (Pol II). In stem cells, recruited Pol II forms prominent, long-lived clusters, which gradually disappear during differentiation, so that only smaller clusters remain. Here, we ask whether the loss of large Pol II clusters is a stereotypical transition that can be explained by changes in the Pol II transcriptional state during differentiation. We assess clusters by super-resolution microscopy in three different experimental models of differentiation. In all cases, Pol II clusters first become larger and rounder, then unfold, and finally split into small clusters. These shape changes are accompanied by changes of transcriptional activity of Pol II. Previous work suggests a surface-condensate model, where enhancer regions support Pol II cluster formation, and transcriptional activity disperses clusters. Using this theoretical model, we propose that the developmental changes in enhancer marks and transcriptional activity during differentiation are sufficient to define a stereotyped trajectory through a cluster shape space.

DY 52.5 Fri 10:30 BAR Schö

Anomalous dynamics of differentiated droplets — •Xi Chen[1], Frank Jülicher[2], Jens-Uwe Sommer[1], and Tyler Harmon[1] — [1]Leibniz-Institut für Polymerforschung Dresden, Institut Theory der Polymere 01069 Dsden — [2]Max-Planck-Institut für Physik komplexer Systeme, 01187 Dresden

Membraneless compartments formed by liquid-liquid phase separation in cells behave like droplets and take part in various biological processes. The function of these droplets are largely dependent on their components. We previously showed with a theoretical model that droplets can undergo a differentiation process where a homogeneous population of droplets converts into two coexisting types of droplets. We proposed this allows droplet specialization similar to cell differentiation.

These differentiated droplets exhibit new features and anomalous dynamics. Like a normal droplet system where droplets ripen and merge into one big droplet, this differentiation can significantly accelerate this Ostwald ripening. This happens with the caveat that instead of ripening into one droplet, it ripens into two droplets of different types with a competing reverse Ostwald ripening process. Unexpectedly, these differentiated droplets divide and repel each other over long distances.

15 min. break

DY 52.6 Fri 11:00 BAR Schö

Microrheology of red blood cell cytosol — •Thomas John and Christian Wagner — Universität des Saarlandes, Saarbrücken

Tracking of small particles undergoing a Brownian motion is a widespread method in passive microrheology. Washed human red blood cells (RBC) are destroyed by ultrasound treatment to extract the cytosol, the hemoglobin and protein solution inside the cells. We use microrheology with sub-micrometer-sized particles to determine the viscosity of the cytosol. Since the cytosol is always diluted with an unknown amount of water due to the treatment, this small dilution has a huge impact on the viscosity. To circumvent this problem, we measured very accurately the mass density of every sample. However, the resulting density-viscosity relation is a strong monotonic increasing relation. In a separate experiment we determined the mass density distribution of individual intact RBCs in a continuous density gradient by centrifugation. Finally, we can present the probability density distribution of the viscosity in naturally distributed human RBCs.

DY 52.7 Fri 11:15 BAR Schö

Clonal dynamics at tissue interfaces — •Ruslan Mukhamadiarov[1,2], Matteo Ciarchi[1,2], Fabrizio Olmeda[1,2], and Steffen Rulands[1,2] — [1]Ludwig Maximilian University of Munich, München, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Tissue morphogenesis relies on the spatial separation of different cell types. Understanding how cells regulate the positions of such interfaces is key to understanding the processes that occur during dysregulation, such as in cancer. Genetic tracing has become an important experimental tool in studying the regulation of cell behaviour. However, its use in both homeostatic and growing tissues is limited by the emergence of universal size distributions. Here, we show that the mechanisms of tissues interface regulation is reflected in cell-fate specific

size distributions of genetically labelled cells, termed clones. Specifically, we show how interface fluctuations affect the size distributions of labelled clones and derive theoretical predictions for a range of biologically relevant scenarios that can be tested experimentally. We test our theoretical framework by stochastic simulations and analysis of live imaging experiments. By relating interface fluctuations to clone size distributions our work paves the way for using genetic tracing experiments to understand the mechanisms underlying tissue compartmentalization.

DY 52.8 Fri 11:30 BAR Schö

Multivalent binding proteins can drive collapse and reswelling of chromatin in confinement — •Sougata Guha and Mithun K. Mitra — Department of Physics, IIT Bombay, India

Collapsed conformations of chromatin have been long suspected of being mediated by interactions with multivalent binding proteins, which can bring together distant sections of the chromatin fiber. In this study, we use Langevin dynamics simulation of a coarse grained chromatin polymer to show that the role of binding proteins can be more nuanced than previously suspected. In particular, for chromatin polymer in confinement, entropic forces can drive reswelling of collapsed chromatin with increasing binder concentrations, and this reswelling transition happens at physiologically relevant binder concentrations. Both the extent of collapse, and also of reswelling depends on the strength of confinement. We also study the kinetics of collapse and reswelling and show that both processes occur in similar timescales. We characterise this reswelling of chromatin in biologically relevant regimes and discuss the non-trivial role of multivalent binding proteins in mediating the spatial organisation of the genome.

DY 52.9 Fri 11:45 BAR Schö

A possible application of the Physics of topological defects to oncology — •Andy Manapany, Leïla Moueddenne, Sébastien Fumeron, Bertrand Berche, and Loriane Didier — Université de Lorraine

We propose a numerical study of the thermal diffusion process in non-Euclidian geometry applied to biological active matter. Thanks to the similarities displayed by both nematic and cells in biological tissue, we aim to apply results derived from the study of diffusion processes around topological defects found in liquid crystals, in order to highlight the thermal response in the vicinity of certain disclination defects found in epithelial tissues. This work is motivated by the fact that these types of disclination defects, mainly "comet" and "trefoil" systematically appear during metastatic phases in some forms of aggressive cancers. Thus, a study of the thermal footprint in such mediums may give us information on the most efficient ways to perform thermal ablation targeted towards aforementioned cells while preserving healthy surrounding tissue.