BP 28: Statistical physics of biological systems II (joint session BP/DY)

Time: Thursday 15:00–17:30 Location: H11

BP 28.1 Thu 15:00 H11

Experimental evidence of symmetry breaking of transition-path times — •Jannes Gladrow[1], Marco Ribezzi-Crivellari[2,3], Felix Ritort[3,4], and Ulrich F. Keyser[1] — [1]Cavendish Laboratory, University of Cambridge, Cambridge CB3 0HE, UK — [2]Laboratoire de Biochimie (LBC), ESPCI Paris, PSL Research University, CNRS UMR8231 Chimie Biologie Innovation, Paris, France — [3]Condensed Matter Physics Department, University of Barcelona, 08028 Barcelona, Spain — [4]CIBER-BBN de Bioingenieria, Biomateriales y Nanomedicina, 28029 Madrid, Spain

While thermal rates of state transitions in classical systems have been studied for almost a century, associated transition-path times have only recently received attention. Uphill and downhill transition paths between states at different free energies should be statistically indistinguishable. Here, we systematically investigate transition-path-time symmetry and report evidence of its breakdown on the molecular- and meso-scale out of equilibrium. In automated Brownian dynamics experiments, we establish first-passage-time symmetries of colloids driven by femtoNewton forces in holographically-created optical landscapes confined within microchannels. Conversely, we show that transitions which couple in a path-dependent manner to fluctuating forces exhibit asymmetry. We reproduce this asymmetry in folding transitions of DNA-hairpins driven out of equilibrium and suggest a topological mechanism of symmetry breakdown. Our results are relevant to electrophysiology and single-molecule fluorescence experiments.

BP 28.2 Thu 15:15 H11

Unveiling lineage decisions in zebrafish neurogenesis — Emmanuel Than-Trong[1,2], •Bahareh Kiani[3], Alessandro Alunni[1,2], Benjamin D. Simons[4,5,6], Laure Bally-Cuif[1,2], and Steffen Rulands[3] — [1]Institut Pasteur, Unit Zebrafish Neurogenetics, Department of Developmental & Stem Cell Biology, 25 rue du Dr Roux, 75015 Paris, France — [2]CNRS, UMR3738, 25 rue du Dr Roux, 75015 Paris, France — [3]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden, Deutschland — [4]Cavendish Laboratory, Department of Physics, University of Cambridge, Cambridge CB3 0HE, UK — [5]The Wellcome Trust/Cancer Research UK Gurdon Institute, University of Cambridge, Cambridge CB2 1QN, UK — [6]The Wellcome Trust/Medical Research Council Stem Cell Institute, University of Cambridge, Cambridge CB2 1QN, UK

Zebrafish neural tissue hosts specialised precursor cells which fuel the ongoing production of neurons into discrete brain regions. To understand how neural maintenance is achieved in this system, we performed a quantitative clonal analysis of the fate of precursor cells. Lineage tracing in growing tissues is complicated by the fact that labelled clones fragment into disconnected clusters, rendering the retrospective analysis of cell fate highly ambiguous. Combining statistical inference with biophysical modelling we reconstructed the clonal origin of labelled cells, revealing that progenitor containing clones persist over the lifetime of the animal. Using stochastic modelling, we unveiled lineage relationships and proliferation kinetics in the adult zebrafish pallium.

BP 28.3 Thu 15:30 H11

Revealing chromosome organization from Hi-C data using a maximum entropy approach — •Joris Messelink[1], Jacqueline Janssen[2], and Chase Broedersz[1] — [1]Arnold Sommerfeld Centre for Theoretical Physics, LMU Munich — [2]Max Planck Institute for the Physics of Complex Systems, Dresden

The bacterial DNA outsizes the cell by roughly a factor of a thousand. The DNA must not only be highly condensed to fit inside the cell, but this condensed DNA must be organized inside the cell to facilitate functional processes of the chromosome. Thus, understanding the three-dimensional spatial organization of the bacterial chromosome is important to understand how the core biological processes are regulated inside of the cell. Recent chromosome conformation capture experiments provide genome-wide data on chromosome folding. In particular, the Hi-C method provides contact frequency maps of the chromosome, revealing its highly organized structure. We develop a maximum entropy approach to extract the three-dimensional structure of the bacterial chromosome from such data. The aim of our method is to develop a coarse-grained model for the statistical mechanics of the folding of the whole bacterial chromosome. From this model, we obtain the full distribution of chromosome configurations in the cell.

BP 28.4 Thu 15:45 H11

Control of droplet coarsening in active emulsions — •Christoph Weber[1], Marta Tena-Solsona[2], Jacqueline Janssen[1], Caren Wanzke[2], Fabian Schnitter[2], and Job Boekhoven[2] — [1]MPIPKS, Dresden — [2]TUM, Munich

Spatial-temporal regulation of liquid phase separation is crucial inside living cells. While spatial control can be achieved through concentration gradients, temporal control is often limited by the slow coarsening processes of droplet fusion and Ostwald ripening. Here we present a new class of active emulsions where the rate of coarsening can be dramatically accelerated in a controlled manner. This class of active emulsions involves a fuel that drives a chemical reaction from thermodynamically stable precursor molecules to metastable building blocks. At large enough concentrations of building blocks liquid droplets can form. We show by experimental studies of various active emulsions and a theory which quantitively coincides with the experimental measurements, how the metastable building blocks actually accelerate the coarsening kinetics in this novel class of phase separated systems. This class of active emulsions indicates novel possibilities to control sizes of assemblies in chemical engineering and may also rely on a mechanism used for the size regulation of membrane-less organelles in living cells.

BP 28.5 Thu 16:00 H11

Immune Repertoire Dynamics out of Steady State — •Mario Udo Gaimann[1], Jonathan Desponds[2], and Andreas Mayer[3] — [1]Ludwig-Maximilians-Universität München, Faculty of Physics, Munich, Germany — [2]University of California San Diego, Department of Physics, La Jolla, CA, USA — [3]Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ, USA

Over the last ten years high-throughput sequencing of lymphocyte receptor repertoires has provided an increasingly precise view of how immune defenses are organized. A highly reproducible finding of these sequencing efforts has been that the clone sizes of lymphocytes which share the same receptor are heavy-tail distributed. Here, we present a simple neutral birth-death model kept out of steady-state by the arrival of new clones in which competition between cells for a global resource couples the birth rate to the total size of the immune repertoire. We show that this model produces transient, but long-lived power-law scaling of clone sizes through a rich-get-richer mechanism resembling preferential attachment. Our model predicts an onset of power-law scaling early in life, which should persist throughout the human lifespan in the biologically relevant parameter regime. We verify both predictions by reanalyzing previously published T cell receptor sequencing data from a human aging study. Furthermore, we demonstrate that our mechanism is robust to relaxations of the model assumptions including when competition is based on the lymphocyte receptor specificity. Overall, our work suggests that early life has a strong influence on the long-term structure of the immune repertoire.

BP 28.6 Thu 16:15 H11

Topological dynamics of small degree networks: percolation, rate equation, and stochastic network growth — •Adrian Fessel and Hans-Günther Döbereiner — Universität Bremen, Bremen, Deutschland

In self-organizing networks, topology and dynamic processes interact in a unique way: the network adapts its structure based on local activity, enabling the emergence of global dynamic properties on an optimized topology.
Working with *Physarum polycephalum* as an experimentally accessible model for an adaptive transportation system, we seek to formalize topological development into a sequence of discrete events intended to serve as basis for studying the interaction of flow and topology. We focus on reorganization of *P. polycephalum* networks after fragmentation, a process occurring in a prominent percolation transition in a system where system size is not fixed.
The theoretical description follows a master equation with parameters obtained from statistical analysis of experimental data. Computational investigation of the model recreates the dynamics of the topological phase transition and enables characterization of finite size effects and

critical exponents. Comparing the influences of system growth and fusion within the system reveals a significant shift of the transition when system growth dominates.

Invited Talk BP 28.7 Thu 16:30 H11

Spontaneous buckling of active matter — •Karsten Kruse — NCCR Chemical Biology, Departments of Biochemistry and Theoretical Physics, University of Geneva, 1211 Geneva, Switzerland

Active matter in living systems is often organized in the form of quasi two-dimensional sheets. Examples are the actin cortex of animal cells or epithelial cell monolayers in organisms. In many processes, these sheets fold, for instance, during cell division or gastrulation, which is the developmental process of inward folding of a single-cell layered sphere in early embryogenesis. The molecular players and signaling cascades involved in these processes have been studied in detail. In contrast, the underlying mechanics remains poorly characterized. This is in large part due to technical difficulties in measuring the material properties of these systems as well as the forces acting on them. Theoretical analysis can shed light on the mechanics governing the spontaneous buckling of active matter as I will illustrate by two model systems: One system consists of an initially homogenous actomyosin sheet reconstituted *in vitro* that can buckle spontaneously into states of positive and negative Gaussian curvature upon contraction. The other example is provided by a cell monolayer growing on the inside of an elastic sphere. It buckles spontaneously as cells continue to proliferate beyond the state when the whole inner surface of the sphere is covered with cells. In both cases, theoretical analysis allows to extract mechanical properties of the active materials that are difficult to assess otherwise.

BP 28.8 Thu 17:00 H11

Phase separation in the ensemble of fixed pH — •Omar Adame-Arana[1], Christoph A. Weber[1], Vasily Zavurdaev[1,2], Jacques Prost[3], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]Friedrich-Alexander Universität Erlangen-Nürnberg, Cauerstr. 11, 91058 Erlangen, Germany — [3]Institut Curie, 26 rue d'Ulm, 75248 Paris Cedex 05, France

Recent developments at the interface of biology and physics brought to light the importance of phase separation in explaining biological processes in the cell. It has been shown that some proteins are able to phase separate in solution and form liquid-like droplets in the cytoplasm that carry out a distinct biological function. Particularly, a drop in the cytosolic pH leads to a widespread protein assembly in the cytoplasm, this phenomenon triggered our interest to the mechanism of protein phase separation as a function of pH. In order to study this mechanism, we define a model of a solution composed of macromolecules which can exist in three different charge states and have a tendency to phase separate. The pH dependence is introduced in terms of chemical reactions which control the charge state of the macromolecules. Using conservation laws and chemical equilibrium, we identify the conjugate variables of the system. We then perform a Legendre transform which defines the free energy corresponding to a fixed pH ensemble. We conclude by showing phase diagrams as a function of pH, where we find that under most conditions, phase separation is most pronounced near the isolectric point.

BP 28.9 Thu 17:15 H11

Kleiber's law scaling of the metabolic rate in planarians — Albert Thommen[1,2], Steffen Werner[2,3], Olga Frank[1], Jenny Philipp[4], Oskar Knittelfelder[1], Yihui Quek[2,5], Karim Fahmy[4], Andrej Shevchenko[1], •Benjamin M. Friedrich[2,6], Frank Jülicher[2], and Jochen C. Rink[1] — [1]MPI CBG, Dresden. Germany — [2]MPI PKS, Dresden, Germany — [3]AMOLF, Amsterdam, Netherlands — [4]HZDR, Dresden, Germany — [5]MIT, Cambridge, USA — [6]cfaed, TU Dresden, Germany

Kleiber's law states that the metabolic rate of animals scales with the 3/4 power of their body mass. It is considered one of the few quantitative laws in biology, yet its mechanistic basis remains unknown. Here, we take advantage of the reversible changes in body size by 2 orders of magnitude as function of food abundance in the planarian *Schmidtea mediterranea*. Using microcalometry, we show that Kleiber's law applies to adult organisms of this flatworm species. Intriguingly, the metabolic rate per cell is independent of organism size. Instead, Kleiber's law in planarians results from a size-dependent increase in mass per cell, reflecting a higher proportion of energy stores in large animals. Using a minimal energy balance model, we relate energy currents to growth and degrowth rates, in quantitative agreement with experiment. Our study is a first step to link energy fluxes, metabolism, and pattern formation in living matter.

[1] Thommen et al. BioRxiv; doi: https://doi.org/10.1101/332916 (accepted in eLife)