BP 34: Statistical Physics of Biological Systems II (joint BP/DY/CPP)

Time: Wednesday 9:30–13:15 Location: H 1028

BP 34.1 Wed 9:30 H 1028

Pinned polymer loops in external field: how to align chromosomes for recombination? — Yen Ting Lin[1], Daniela Frömberg[1], Wenwen Huang[1], Petrina Delivani[2], Mariola Chacón[2], Iva Tolic[2], Frank Jülicher[1], and •Vasily Zaburdaev[1] — [1]MPI for the Physics of Complex Systems, Dresden, Germany — [2]MPI of Molecular Cell Biology and Genetics

Chromatin movement and structure are central to many processes in cells such as mitosis, replication, and transcription, where physical properties of the chromatin fiber play an essential role. Motivated by the problem of chromosome alignment and recombination during meiosis we solve for the statistics of a pinned polymer ring in an external force field. We predict how the contact probability between two rings depends on the ratio of the force to the intrinsic noise level and how it changes upon addition of new recombination spots. Due to the underlying loop topology, our theoretical results are readily applicable to the description of bacterial DNA and polymer brushes.

BP 34.2 Wed 9:45 H 1028

Statistical Inference of E.Coli's tumbling behavior and chemotaxis strategy using Kramers-Moyal coefficients — •Oliver Pohl[1], Marius Hintsche[2], Carsten Beta[2], and Holger Stark[1] — [1]Institut für Theoretische Physik, Technische Universität Berlin, 10623 Berlin — [2]Institut für Physik und Astronomie, Universität Potsdam, 14476 Potsdam

The bacterium Escherichia coli moves with alternating runs and tumbles that occur with a mean tumble rate. In the presence of gradients of a chemoattractant, E. coli performs chemotaxis. We set up a time-continuous model that describes runs and tumbles as a stochastic process of the bacterium's swimming direction and speed. The swimming direction updates according to rotational Brownian motion and additional shot noise, which initiates tumbling events. The speed is not constant as in previous models but decreases during the tumbling events.

By analyzing experimental data on swimming trajectories, we infer the parameters of our model. To this purpose generalized Kramers-Moyal coefficients are calculated for our shot-noise model and matched to the ones obtained from the trajectories. In contrast to common tumbling recognition algorithms no free parameters need to be predetermined. Furthermore, we can identify the bacteria's chemotaxis strategy by exploiting the Kramers-Moyal coefficients.

BP 34.3 Wed 10:00 H 1028

In vitro Min protein patterns arise from self-controlled chaos — •Jacob Halatek and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians-Universität, München, Germany

The mass-conserving reaction-diffusion dynamics of Min proteins act as spatial regulator for the assembly of the cell division machinery. A plethora of experiments has demonstrated a remarkable adaptability of oscillatory Min proteins patterns to variations of system geometry. As such, the Min system serves as ideal basis to study the theoretical concepts underlying a real pattern-forming system that can be found in nature. The classical picture for pattern-forming reaction-diffusion systems is rooted in two distinct concepts: The diffusion driven instability proposed by Turing, and the concept of diffusively coupled, self-sustained oscillators proposed by Kuramoto. Here, we investigate the spatio-temporal instabilities of Min protein dynamics that lead to characteristic patterns observed in vivo and in vitro. We find that the in vitro instability cannot be ascribed to any of the two classical concepts but gives rise to a new one. We find transient Turing patterns at onset that loose stability to a chaotic attractor. Further from onset this chaotic attractor condenses into a global limit cycle, passing a regime with transient chimera states. As such, Min protein patterns arise in vitro from a state of self-controlled chaos, rather than from destabilization of uniform states. We find that such dynamics stem from generic properties of mass-conserved reaction-diffusion dynamics and are not specific to the Min system.

BP 34.4 Wed 10:15 H 1028

Stochastic Dynamics of IFN Type I Signaling — •Nikolas Schnellbächer[1,2], Nils Becker[3], Thomas Höfer[3], and Ulrich Schwarz[1,2] — [1]Institute for Theoretical Physics, University of Heidelberg, Heidelberg, Germany — [2]BioQuant, University of Heidelberg, Heidelberg, Germany — [3]German Cancer Research Center, Heidelberg, Germany

The signaling molecules interferon (IFN) of type I are secreted by many nucleated cells to signal the presence of an intracellular viral infection to their environment and to inhibit viral replication. Once in the extracellular environment, they bind to a heterodimeric cell surface receptor (IFNAR = Interferon Alpha Receptor) to form an active ternary signaling complex, which then triggers an intracellular response. The most prominent pathway activated by interferons is the canonical JAK/STAT signaling pathway, where STAT molecules dock at the receptor associated Janus kinases (JAKs) at their cytoplasmic domains.

A central question of this system is to explain the differential information processing of different interferons through the same transmembrane receptor system. Moreover notoriously low copy numbers of the receptors on the cell surface are a typical cause for a high degree of intrinsic stochasticity. We use stochastic computer simulations to analyze the activation dynamics in space and time. In particular we investigate spatial effects on the dose response behavior of the IFN type I signaling system.

BP 34.5 Wed 10:30 H 1028

Scaling Regimes for Confined Wormlike Chains under Tension — •Greg Morrison[1] and Dave Thirumalai[2] — [1]IMT Lucca Institute for Advanced Studies, Lucca Italy 55100 — [2]University of Maryland at College Park, College Park MD 20742

In this talk, we study the scaling behavior of a wormlike chain (WLC) with persistence length l_p confined to the surface of a cylinder of radius R under the application of an external tension. Inextensibility and confinement effects are treated on a mean field level, and we show that the stationary solution for the mean field parameters can be reduced simple equations that can be solved asymptotically. We are able to accurately recover the well known Odijk scaling of $F \sim L/l_d$, with the deflection length $l_d = (l_p R^2)^{1/3}$, for strongly confined chains and show that this scaling is robust to weak external forces. We show that the scaling regimes for both weakly and strongly confined polymers change drastically under application of large external tension, with $F \sim L/l_t$ for a tensile length scale $l_t \sim (l_p/\beta f)^{1/2}$. Our results may be relevant in the mechanical unbinding of histone-bound DNA as well as a variety of experimental situations involving DNA confined to nanochannels.

BP 34.6 Wed 10:45 H 1028

Single molecule measurement of the effective temperature in nonequilibrium steady states — •Eckhard Dieterich[1], Joan Camunas-Soler[2,3], Marco Ribezzi-Crivellari[2,3], Udo Seifert[1], and Felix Ritort[2,3] — [1]II. Institut für Theoretische Physik, Universität Stuttgart, Germany — [2]Departament de Física Fonamental, Universitat de Barcelona, Spain — [3]CIBER-BBN de Bioingeniería, Biomateriales y Nanomedicina, Instituto de Salud Carlos III, Madrid, Spain

Temperature is a crucial concept for equilibrium systems. For glassy systems, it has been extended to the nonequilibrium regime as an effective quantity showing up in the fluctuation-dissipation theorem. However, direct supporting experimental evidence remains scarce. Here, we present the first direct experimental demonstration of the effective temperature by measuring correlations and responses in single molecules in nonequilibrium steady states generated under external random forces. We combine experiment, analytical theory and simulations for systems with different levels of complexity ranging from a single bead in an optical trap to two-state and multiple-state DNA hairpins. From these data, we can extract a unifying picture for the existence of an effective temperature based on the relative order of various time-scales characterizing intrinsic relaxation and external driving. Our study thus introduces driven small systems as a fertile ground to address fundamental concepts in statistical physics, condensed matter physics and biophysics.

30 min break

Invited Talk BP 34.7 Wed 11:30 H 1028

Efficiently extracting thermodynamics and kinetics from molecular simulation data at multiple thermodynamic states — •Frank Noe — FU Berlin, Arnimallee 6, 14195 Berlin

I will present novel methods based on Markov modeling for extracting statistical information (thermodynamics and kinetics) from molecular simulation data that has been generated at multiple thermodynamic states. Such data may be obtained from enhanced sampling protocols, such as umbrella sampling or replica-exchange dynamics, and by mixing one of these protocols with direct molecular dynamics data. Here I will propose ways to optimally extract information from such data, including the reconstruction of the kinetics of rare events that are not directly sampled in the data. An application of our approach is the estimation of rare unbinding kinetics of protein-ligand complexes when only the more frequent binding process can be sampled in direct MD simulations.

BP 34.8 Wed 12:00 H 1028

Stochastic dynamics of adhesion bonds for a rod propelled by both force and torque — •Anna Battista and Ulrich Schwarz — Heidelberg University, Heidelberg, Germany

The stochastic dynamics of adhesion bonds has emerged as a powerful theoretical framework to explain many prominent features of sliding friction, including the stick-slip regimes often observed at intermediate driving velocity. Sliding friction occurs in a variety of physical contexts, ranging from tribology to cell motility. In particular, stochastic bonds have been employed to model the dynamics of adhesion between a cell and its substrate. Although much progress has been achieved with the help of stochastic bond models, up to now they have been restricted to sliding friction in one dimension. However, there are situations in which translation is coupled with rotation, as is the case of gliding cells with a shape asymmetry. Motivated by this observation, we develop a sliding friction model for a slider that is both translated and rotated, while being connected to the substrate by stochastic bonds. We find that torque enhances the tendency for stick-slip behaviour and that adhesive patches spontaneously form at the moving interface when the on-rate of the bonds has a velocity dependence. Interestingly, our results show an adhesion dynamics reminiscent of that observed during the migration of curved malaria parasites.

BP 34.9 Wed 12:15 H 1028

High stress levels lead to transition from heterogeneous timing to synchronized cellular response of the *E.coli* Colicin E2 operon — •Andreas Mader[1], Benedikt von Bronk[1], Benedikt Ewald[1], Sara Kesel[1], Karin Schnetz[2], Erwin Frey[1], and Madeleine Opitz[1] — [1]Faculty of Physics, LMU München, Germany — [2]Institute for Genetics, Universität zu Köln, Germany

The production of bacteriocins, such as colicins, is one means of bacteria to outcompete other microorganisms. In a single cell study, we analyze the heterogeneous gene expression of Colicin E2, expressed from the SOS inducible *E.coli* Colicin E2 operon. We quantitatively study the expression dynamics of the Colicin E2 operon in *E.coli* using fluorescence time-lapse microscopy. Different fluorescence reporter proteins allow us to observe heterogeneity in Colicin production and Colicin release separately. At low exogenous stress levels all cells eventually respond after a given time (heterogeneous timing), high stress levels lead to a synchronized stress response of all cells about 75 min after induction via stress. A heterogeneous response in combination with heterogeneous timing can be biologically significant. It might enable a bacterial population to endure low stress levels, while at high stress levels an immediate and synchronized response may allow elimination of closely related bacteria competing for resources. Furthermore we could demonstrate that the amount of Colicin released is dependent on *cel* (lysis) gene expression. Future investigations will focus on transcriptional as well as post-transcriptional regulation affecting the dynamics of Colicin expression and release.

BP 34.10 Wed 12:30 H 1028

The fluidity of the cytoplasm is regulated by cytosolic pH — Matthias Munder[2], •Daniel Midtvedt[1], Elisabeth Nüske[2], Shovamayee Maharana[2], Sonja Kroschwald[2], Doris Richter[2], Vasily Zaburdaev[1], and Simon Alberti[2] — [1]Max Planck Institut für Physik komplexer Systeme — [2]Max Planck Institut für molekulare Zellbiologie und Genetik

Upon sub-optimal growth conditions, many cells enter a quiescent state characterized by lack of cell division, low metabolic activity and decreased intracellular pH. The mechanisms by which cells enter and leave quiescence are as of yet largely unknown.

Using single-particle tracking, we investigate the mobility of foreign tracer particles under different cytosolic pH conditions. We find a significant decrease in the mobility of the particles under acidic conditions.

Indicative of obstructed motion in a crowded solution, at short times the velocity autocorrelation function (VACF) of the tracer particles is negative. We relate these findings to a structural phase transition in the cytoplasm.

Our findings indicate that cells may use cytosolic pH to change the material properties of the cytoplasm. We are currently investigating possible consequences of these changes. Our findings could have broad implications for the understanding of alternative physiological states in cells, and promotes a view on the eukaryotic cytoplasm as a viscoelastic material with widely tunable properties.

BP 34.11 Wed 12:45 H 1028

Detailed balance violations in mesoscopic biological systems — •Christopher Battle[1], Chase P. Broedersz[2], Nikta Fakhri[1], Fred C. MacKintosh[3], and Christoph F. Schmidt[1] — [1]Drittes Physikalisches Institut, Georg-August Universitaet, Goettingen, Germany — [2]Lewis-Sigler Institute for Integrative Genomics and Department of Physics, Princeton University, Princeton, NJ, USA — [3]Dept. of Physics & Astronomy, Vrije Universiteit, Amsterdam, Netherlands

Living systems exist far from thermal equilibrium, with active processes powering many of their functions. As such, they are expected to violate fundamental tenets of equilibrium, such as the principle of detailed balance. While some cellular processes show unmistakable non-equilibrium characteristics, e.g. persistent directed motion, others are more subtle, exhibiting non-thermal, random motion which is similar in appearance to Brownian motion, e.g. cortical stress fluctuations or active cellular stirring. It is not a priori clear whether the active, random nature of the second class of motions will translate into observable violations of detailed balance on the mesoscopic, i.e. cellular, scale. Here we report experimental evidence of detailed balance violations for such a case. Such violations can be used to "fingerprint" non-equilibrium systems, and differentiate active processes from thermal ones without perturbing the system.

BP 34.12 Wed 13:00 H 1028

Genetic networks specifying the functional architecture of orientation domains in V1 — •Joscha Liedtke and Fred Wolf — Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, 37077 Goettingen (Germany)

Although genetic information is critically important for brain development and structure, it is widely believed that neocortical functional architecture is largely shaped by activity dependent mechanisms.

Here we show theoretically that mathematical models of genetic networks of principal neurons interacting by long range axonal morphogen transport can generate morphogen patterns that exactly prescribe the functional architecture of the primary visual cortex (V1) as experimentally observed. We analyze in detail an example genetic network that encodes the functional architecture of V1 by a dynamically generated morphogen pattern. We use analytical methods from weakly non-linear analysis [Cross & Hohenberg 1993] complemented by numerical simulations to obtain solutions of the model. In particular we find that the pinwheel statistics are in quantitative agreement with high precision experimental measurements [Kaschube et al. 2010].

This theory opens a novel perspective on the experimentally observed robustness of V1's architecture against radically abnormal developmental conditions such a dark rearing [White et al. 2001]. Furthermore, it provides for the first time a scheme how the pattern of a complex cortical architecture can be specified using only a small genetic bandwidth.