

BP 53: Posters - Statistical Physics of Biological Systems

Time: Wednesday 17:00–19:00

Location: Poster C

BP 53.1 Wed 17:00 Poster C

The stability of predator-prey systems on multiple patches coupled by migration — ●PHILIPP GRAMLICH¹, SEBASTIAN PLITZKO¹, LARS RUDOLF², BARBARA DROSSEL¹, and THILO GROSS² — ¹Institut für Festkörperphysik, TU Darmstadt, Deutschland — ²Faculty of Engineering, University of Bristol, United Kingdoms

Dispersal between different habitats influences the dynamics and stability of populations considerably. Furthermore, these effects depend on the local interactions of a population with other species. Using a generalized modelling approach that is based on a linear stability analysis, we perform a comprehensive study of the simplest possible system that includes dispersal and local interactions, namely a 2-patch 2-species system. We evaluate the impact of dispersal on stability and on the occurrence of bifurcations, including pattern forming bifurcations that lead to spatial heterogeneity, in several different classes of models. We find that dispersal often destabilizes equilibria, but it can stabilize them if it increases population losses. If dispersal is nonrandom, i.e. if emigration or immigration rates depend on population densities, the correlation of stability with dispersal rates is positive in part of the models. We then extend the model to include many patches that are connected as a Random Geometric Graph and investigate the effect of the topological features of the patch network on the stability of the system.

BP 53.2 Wed 17:00 Poster C

Stochastic thermodynamics of learning in neural networks — ●SEBASTIAN GOLDT and UDO SEIFERT — II. Institut für Theoretische Physik, Universität Stuttgart, 70550 Stuttgart, Germany

Over the past decade, stochastic thermodynamics has emerged as a powerful framework to understand the role of information in physical systems and the thermodynamic costs of manipulating it. A particularly intriguing application of these ideas is biology: every organism first gathers information about its noisy environment and then builds models from that data, at the expense of energy dissipation. Here, we focus on the second part of this process: learning.

Biologically, learning is implemented in neural networks where neurons receive and send signals from and to many other neurons via synapses. The strength of these synapses determines whether an incoming signal will make the neuron trigger an action potential, the electric pulse that is the basic token of communication in neural systems. The adaptation of synapses is the physiological mechanism for memory formation, e.g. in Hebbian learning.

Here, we use stochastic thermodynamics to analyse the learning of a classification rule by a feedforward neural network, whose synapses we endow with stochastic dynamics. Starting from the total entropy production of the network, we identify the rate of learning in a thermodynamically consistent way and introduce a measure for the thermodynamic efficiency of learning, which we compute for different learning algorithms.

BP 53.3 Wed 17:00 Poster C

Inference of chemotactic strategies of *E. coli* and *Pseudomonas putida* using Kramers-Moyal coefficients — ●MAXIMILIAN SEYRICH¹, OLIVER POHL¹, MARIUS HINTSCHE², CARSTEN BETA², and HOLGER STARK¹ — ¹Institut für Theoretische Physik, Technische Universität Berlin, 10623 Berlin, Germany — ²Institut für Physik und Astronomie, Universität Potsdam, 14476 Potsdam, Germany

Bacteria like *E. coli* and *Pseudomonas putida* move with alternating runs and tumbles that occur with a mean tumble rate. In the presence of gradients of a chemoattractant, they both perform chemotaxis. We set up a random-walk model that describes runs and tumbles as a stochastic process of the bacterium's swimming direction and speed. The dynamics includes rotational Brownian motion and shot noise, which initiates tumbling events with rates based on chemical gradients.

By analyzing experimental data of swimming trajectories, we infer the parameters of our model. For this purpose generalized Kramers-Moyal coefficients are calculated of our shot-noise model and matched to the ones determined from experimental trajectories. In contrast to common tumbling recognition algorithms no free parameters need to be preset. We first show that our method identifies the classical bacterial chemotaxis strategy for *E. coli* and *P. putida*, i.e., bacteria adapt

their tumble rate to the chemical gradients. Second, we find evidence that a subpopulation of *E. coli*, unlike *P. putida*, uses an additional turning bias during tumble events. We provide statistics which distinguish tumble rate chemotaxis and angle bias chemotaxis using scaling arguments for the Kramers-Moyal coefficients.

BP 53.4 Wed 17:00 Poster C

Species diversity in meta-foodwebs consisting of several patches coupled by stochastic migration — ●TATJANA THIEL and BARBARA DROSSEL — Institut für Festkörperphysik, TU Darmstadt, Germany

The structure of space has a considerable influence on the stability and diversity of ecosystems. So far, there are only few theoretical studies investigating the population dynamics of systems consisting of many species that can migrate between several patches, and most of these model migration as a continuous, deterministic process. However, when migration events are rare (for instance because the patches are far apart), migration is a stochastic process and should be modelled accordingly.

To this purpose, we place a foodweb model consisting of many species on a system of several patches and evaluate the stable configurations that arise due to the population dynamics. This dynamics has a deterministic contribution from the processes within a patch, and a stochastic contribution due to migration events, which are implemented using the Gillespie algorithm. We explore the different ways in which migration rates can depend on population sizes and body masses.

We will discuss how the local and regional species diversity depend on the mode and frequency of migration. Typically, local diversity is largest with intermediate migration rates, since migration is frequent enough that species can be rescued from extinction by immigration but not so frequent that all patches have an identical species composition.

BP 53.5 Wed 17:00 Poster C

Influence of heterogeneous habitat quality on meta-foodweb robustness — ●MICHAELA HAMM and BARBARA DROSSEL — Institut für Festkörperphysik, TU Darmstadt, Deutschland

Anthropogenic changes in ecosystems, e.g. habitat fragmentation due to agricultural land usage, have a large effect on the diversity and stability of ecosystems.

In order to better understand these effects, theoretical investigations are needed that take into account the complex foodweb structure as well as the distribution of the species over several habitats and the different quality of these habitats.

We therefore present a computer simulation study of the influence of the degree of habitat heterogeneity on the robustness (number of persisting species) and on the local and regional biodiversity of meta-foodwebs. Each habitat is randomly assigned a high or low quality (abundance of resources), and the total number of habitats as well as the fraction of high- and low-quality habitats are varied.

Among other results we find that heterogeneity promotes diversity, because predators cannot be supported by low-quality habitats, thus providing refuges for prey.

BP 53.6 Wed 17:00 Poster C

Maze runner: microbial swimming in hexagonal and squared arrays — ●MARCO BAHRS, MARIUS HINTSCHE, MICHAEL RAATZ, MATTHIAS THEVES, and CARSTEN BETA — Institut für Physik und Astronomie, Universität Potsdam, Potsdam, Germany

By randomly changing direction, bacteria effectively explore their surroundings. The natural habitat of many microbial swimmers is dominated by interfaces and narrow interstitial spacings. Thus, the organism's movement strategy cannot be understood without reference to its environment and to the close interactions with it. We examined the steric effects of a homogeneously distributed geometrical pattern on bacterial swimming behavior. Experiments were conducted in a microfabricated array of hexagonal and square obstacles. In these environments we recorded the flux of bacteria through the resulting system of channels. Results were compared to an environment comprised of an array of linear channels. Motility parameters like the effective diffusion coefficient and the mean square displacement serve to compare the different experimental surroundings.

BP 53.7 Wed 17:00 Poster C

Geometric hindrance in multi-species transport on microtubules — ●PATRICK WILKE, EMANUEL REITHMANN, and ERWIN FREY — Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität, Munich, Germany

Intracellular transport on microtubules is performed by molecular motors which have for a long time been thought to move exclusively longitudinally to the axis of the cylindrically shaped biopolymer. Recent experimental studies have revealed that, opposed to this standard hypothesis, motion on spiraling paths is observed for many kinesin such as kinesin-2 [1] and 8 [2]. Here, we study collective transport of multiple particle species which move along different, periodically intersecting spiraling paths on a cylinder. Based on a lattice gas description we find that these intersections provoke correlations in the exclusion process which significantly influence the particle flux. Opposed to classical transport models, our system is characterized by a vanishing particle current at densities far below full occupation. To account for such effects, we develop an analytic framework which allows us to compute the current reduction due to geometric hindrance and the underlying correlations. Surprisingly, the stationary particle-density profile exhibits spatially oscillating patterns which are unfeasible in classical single-species or one-dimensional models.

[1] M. Brunnbauer et al. *Molecular cell* 46.2 (2012): 147-158.

[2] V. Bormuth et al. *Biophysical journal* 103.1 (2012): L4-L6.

BP 53.8 Wed 17:00 Poster C

Stuttering of Min oscillations is induced by stochastic effects — ●LUKAS WETTMANN and KARSTEN KRUSE — Theoretische Physik, Universität des Saarlandes, Postfach 151150, 66041 Saarbrücken, Germany

The site of cell division in wild type *E. coli* bacteria is determined through pole-to-pole oscillations of the Min proteins. Although the oscillations are fairly stable across a wide variety of cell shapes and protein concentrations the emerging patterns are subject to molecular noise, due to the small copy number of proteins in a single cell. This causes the oscillations to sometimes "stutter" and remain in the same polar configuration. We used a model based on transient binding of MinE to the cytoplasmic membrane to describe the dynamics of the Min system and analyzed the stochastic dynamics in the limit of weak noise.

BP 53.9 Wed 17:00 Poster C

Micro-swimming with inertia — ●OLEG TROSMAN^{1,2}, JAYANT PANDE^{1,2}, and ANA-SUNČANA SMITH^{1,2,3} — ¹PULS group, Department of Physics, Friedrich-Alexander-University of Erlangen-Nuremberg, Germany — ²Cluster of Excellence: Engineering of Advanced Materials, Department of Physics, Friedrich-Alexander-University of Erlangen-Nuremberg, Germany — ³Division of Physical Chemistry, Ruđer Bošković Institute, Zagreb, Croatia

Increased theoretical study in the past few decades has enabled scientists to gain a good understanding of the motion of micro-swimmers, yet this has focused on the world of inertia-free swimming. While this is a good approximation for many micro-swimmers as the Reynolds numbers of their flow are typically negligible, for some micro-swimmers

inertia can have observable effects on the motion, such as affecting the swimming gait and the velocity. In this talk we present a theoretical study of a micro-swimmer where inertial effects are taken into account to the lowest non-zero order. For this we employ the popular Golestanian model of the swimmer, with three beads attached in series in a fluid and the motion along the axis of the swimmer. By combining the Oseen-Stokes equations for the coupled motion of distant spheres in a fluid with Newton's force-mass relations, we obtain a coupled system of second-order differential equations for the sphere positions. Solutions of these equations numerically and analytically allow us to discuss interesting deviations from inertia-less swimming.

BP 53.10 Wed 17:00 Poster C

Correlated fluctuations in strongly-coupled binary networks beyond equilibrium — ●DAVID DAHMEN¹, HANNAH BOS¹, and MORITZ HELIAS^{1,2} — ¹Inst. of Neurosci. and Medicine (INM-6) and Inst for Advanced Simulation (IAS-6) and JARA BRAIN Institute I, Jülich Research Centre — ²Dept. of Physics, Faculty 1, RWTH Aachen University

Randomly coupled Ising spins constitute the classical model of collective phenomena in disordered systems. Their phase diagram is obtained by averaging over the quenched random couplings, but many applications require the activity statistics for a single realization of the possibly asymmetric couplings in finite-sized networks: the reconstruction of couplings from the observed dynamics, learning in the central nervous system by correlation-sensitive synaptic plasticity, and representation of probability distributions for sampling-based inference. We present a systematic cumulant expansion for kinetic binary (Ising) threshold units with strong, random and asymmetric couplings that goes beyond mean-field theory and is applicable outside thermodynamic equilibrium; a system of approximate non-linear equations predicts average activities and pairwise covariances in quantitative agreement with full simulations down to hundreds of units [Dahmen et al. 2015, arXiv]. The linearized theory yields an expansion of the correlation- and response functions in collective eigenmodes, leads to an efficient algorithm solving the inverse problem, and shows that correlations are invariant under scaling of the interaction strengths. Partly supported by Helmholtz association: VH-NG-1028 and SMHB; EU Grant 604102 (HBP).

BP 53.11 Wed 17:00 Poster C

Coarse-Grained Interacting Particle Models for Chromatin Remodeling — ●MICHAEL WOLFF, JOHANNES NÜBLER, and ULRICH GERLAND — Physik-Department TU München, James-Frank-Straße 1, 85748 Garching

To explore the action of remodeling mechanisms on nucleosome patterns, we are studying physical models for one-dimensional interacting particle systems under the influence of additional agents actively displacing or evicting the particles. We characterize the connections between the mechanics of remodelers and the arising patterns, including non-equilibrium steady states with non-zero entropy production. We compare our modeling results, for example the formation of clusters, to nucleosome patterns obtained under varying experimental conditions with the aim to identify biologically relevant mechanisms.