

BP 5: Statistical Physics of Biological Systems II (with DY)

Time: Monday 15:00–17:30

Location: H 1058

BP 5.1 Mon 15:00 H 1058

The probability of parallel evolution — ●JOACHIM KRUG¹, IVAN G. SZENDRO¹, MARTIJN F. SCHENK^{2,3}, and J. ARJAN G.M. DE VISSER³ — ¹Institut für Theoretische Physik, Universität zu Köln, Germany — ²Institut für Genetik, Universität zu Köln, Germany — ³Laboratory for Genetics, Wageningen University, Netherlands

The question whether evolutionary processes are repeatable is of central importance in evolutionary biology and continues to be vigorously debated. In a simple version of this problem introduced by Orr, one considers a situation where n beneficial mutations are available to an organism and asks for the probability P that the same mutation is fixed in two replicate populations. When the fitness values are drawn from a distribution that belongs to the Gumbel domain of attraction, Orr showed that $P = 2/(n+1)$, about twice the neutral expectation $1/n$ that would apply if all mutations were equally likely to fix. Motivated by recent experiments that observed a heavy-tailed distribution of fitness effects in an antibiotic resistance gene, we extend Orr's analysis to distributions of selection coefficients s of Pareto form, $f(s) \sim s^{-(\alpha+1)}$. Using an approach from the statistical physics of disordered systems, we show that the probability of parallel evolution is dramatically enhanced when $\alpha < 2$, with $P \sim n^{-(2-\alpha)}$ for $1 < \alpha < 2$ and $P = \text{const.}$ for $\alpha < 1$. We also briefly address the influence of population size on the probability of parallel evolution.

BP 5.2 Mon 15:15 H 1058

Evolution of cooperation in microbial biofilms - A stochastic model for the growth and survival of bacterial mats — ●JOHANNES KNEBEL, ANNA MELBINGER, JONAS CREMER, and ERWIN FREY — LMU Muenchen, Deutschland

Cooperating microbes are widespread in nature despite running the risk of being exploited by free-riders. This so-called dilemma of cooperation is especially important for microbial biofilms where diverse different strains interact in a complex community. The structure and composition of such a biofilm change over time and thereby influence the evolution of cooperation within the system. In turn, the level of cooperation affects the growth dynamics of the biofilm.

Here, we investigate this coupling for an experimentally well-defined situation in which mutants of the *Pseudomonas fluorescens* strain form a mat at the liquid-air interface by the production of an extra-cellular matrix [1]. We model the occurrence of cooperation in this bacterial population by taking into account the formation of the mat. The presence of cooperators enhances the growth of the mat, but at the same time cheaters can infiltrate the population and put the viability of the mat at risk. We find that the survival time of the mat crucially depends on its initial dynamics which is subject to demographic fluctuations [2]. More generally, our work provides conceptual insights into the requirements and mechanisms for the evolution of cooperation.

[1] P. Rainey et al., *Nature* 425, 72 (2003).[2] A. Melbinger et al., *PRL* 105, 178101 (2010).

BP 5.3 Mon 15:30 H 1058

Meso-scale symmetries explain dynamical equivalence of food webs — ●HELGE AUFDERHEIDE^{1,2}, LARS RUDOLF², and THILO GROSS² — ¹MPI für Physik komplexer Systeme, Dresden — ²University of Bristol, Bristol

In complex networks much of the dynamics emerges from the complex interactions between its constituents. However, connecting the interaction topology with the final dynamics remains a hard and largely unsolved problem. Inspired by a recent result on the dynamical equivalence of food webs differing only by local symmetries in their trophic graph, we investigate the effects of such symmetries on the dynamics of food webs. Using generalized modeling to establish the food web Jacobian matrix near the steady states we can study entire classes of food web models instead of fixing specific functional dependencies between the interacting species. Thereby we find that food webs differing by local symmetries indeed carry identical dynamics up to effects localized inside the symmetric part. On one hand this result for equivalent dynamics provides a link between the topology and the dynamical properties of a food web. On the other hand the formalism should be applicable to identify classes of equivalent dynamics hidden to empirical observation in more complicated systems.

BP 5.4 Mon 15:45 H 1058

Geometrical trajectories of a Listeria-type actin-driven particle in 2D — ●FU-LAI WEN¹, KWAN-TAI LEUNG^{1,3}, and HSUAN-YI CHEN^{1,2,3} — ¹National Central University, Jhongli, Taiwan 32001, Republic of China — ²Physics Division, National Center for Theoretical Sciences, Hsinchu, Taiwan 30113, Republic of China — ³Institute of Physics, Academia Sinica, Taipei, Taiwan 11529, Republic of China

Self-propulsions have been a focus of the non-equilibrium statistical physics where an input energy is converted into the kinetic energy of motion. It is interesting that a deformable self-propelled domain is shown to generate a series of geometrical trajectories like circles, wiggles, etc. A similar result is also found in the motion of a bacterium *Listeria* which, although not deformable, moves in a geometrical trajectory by the polymerization of protein actin on its surface. Similar actin-driven motility was also shown in vitro studies on functionalized beads or disks. Here, a phenomenological model is constructed for the generation of geometrical trajectories of a *Listeria*-type actin-driven spherical particle in two dimensions. In our model, the evolutions of actin filament density and force on surface are coupled to the translation and rotation of the particle which in turn are determined by those densities. It is shown that this feedback can destabilize the straight trajectories and lead to the geometrical trajectories observed in experiments. It further shows that a straight trajectory transits to a circular one through a pitchfork bifurcation or to a wiggled one through a Hopf bifurcation on the distributions of those densities. This transition mechanism is generic and robust as indicated in our studies.

BP 5.5 Mon 16:00 H 1058

Mean Exit Time of a Brownian Particle from a Spherical Domain with Multiple Exit Sites on the Boundary — ●RONNY STRAUBE¹, MICHAEL J. WARD², and ALEXEI F. CHEVIAKOV³ — ¹Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg — ²University of British Columbia, Vancouver, Canada — ³University of Saskatchewan, Saskatoon, Canada

In biological signal transduction a target molecule often has to find a small exit site on an otherwise impermeable boundary. Important examples of such **narrow escape** processes include diffusion through ion channels and trafficking through pores of the nuclear membrane. We have recently extended the calculation of the mean exit time (MET) from the case of a Brownian particle exiting from a spherical domain with a single exit site [1] to the case of multiple exit sites [2]. Using the method of matched asymptotic expansions we provide a three-term approximation of the MET which explicitly depends on the spatial configuration of the exit sites. We show that for a fixed surface fraction of exit sites the MET reaches a value close to its minimum already for 30-40 exit sites which suggests, for example, that cell nuclei have many more pores than would be needed if nuclear export was a purely diffusion-limited process.

[1] Singer A, Schuss Z, Holcman D, Eisenberg RS. Narrow escape, part I. *J. Stat. Phys.* 122, 437-463 (2006).[2] Cheviakov AF, Ward MJ, Straube R. An asymptotic analysis of the mean first passage time for narrow escape problems: part II: The sphere. *SIAM Multiscale Model. Simul.* 8, 836-870 (2010).

BP 5.6 Mon 16:15 H 1058

Fractional Brownian Motion in Crowded Fluids — DOMINIQUE ERNST¹, MARCEL HELLMANN², JÜRGEN KÖHLER¹, and ●MATTHIAS WEISS² — ¹Experimental Physics IV, University of Bayreuth, D-95440 Bayreuth — ²Experimental Physics I, University of Bayreuth, D-95440 Bayreuth

Diffusion in crowded fluids, e.g. in the cytoplasm of living cells, has frequently been reported to show an anomalous characteristics ('subdiffusion'). Several random walk models have been proposed to explain these observations, yet so far an experimentally supported decision in favor of one of these models has been lacking. Here, we show that experimentally obtained trajectories in a prototypical crowded fluid show an ergodic behavior and an asphericity that is most consistent with the predictions of fractional Brownian motion, i.e. an anti-correlated, anti-persistent generalization of normal Brownian motion that is related to the fluid's viscoelasticity.

BP 5.7 Mon 16:30 H 1058

Time domain representation of active nonlinear cochlear waves — ●FLORIAN FRUTH^{1,2}, FRANK JÜLICHER¹, and BENJAMIN LINDNER² — ¹Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, 01187 Dresden — ²Bernstein Center for Computational Neuroscience, Philipstr. 13, Haus 2, 10115 Berlin

The inner ear, the so called cochlea, can be modeled generically in terms of coupled critical oscillators, which has been done previously in the frequency (Fourier) domain. This one-dimensional model describes a nonlinear cochlear wave that is pumped by active oscillators. We extend and generalize this model by constructing a similar version in time domain, in order to include dynamical noise (originating, e.g. in the stochastic activity of outer hair cells) and static disorder (resulting from inhomogeneities of system parameters along the cochlea). We discuss the spontaneous oscillations in the model and also investigate its response to external stimuli such as clicks or pure tones.

BP 5.8 Mon 16:45 H 1058

The effects of temperature changes on the timing of cell division — ●FEDERICO VAZQUEZ^{1,2}, ABIGAIL KLOPPER³, MARIA BEGASSE², and STEPHAN GRILL^{1,2} — ¹Max Planck Institute for the Physics of Complex Systems — ²Max Planck Institute for Molecular Cell Biology and Genetics — ³Nature Publishing Group

Accurate timing of early embryogenesis is crucial for the development of an organism, and is subject to sensitive dependence on fluctuations in temperature. We investigate how timing is affected by temperature using *C. elegans* as a model organism, which benefits from rapid early cell divisions and an inability to maintain a constant body temperature, independent of ambient conditions. Experiments show that cell division rates have an Arrhenius dependence on temperature in an intermediate range, but they continuously deviate from this law outside this range, that is, for high and low temperatures. We propose a simple model for cell division, in which the state of the cell performs a Brownian motion on a complex network with temperature-dependent hopping rates, and associate division rates to mean first-passage times. We obtain analytical expressions for simple topologies that fit the experimental data very well, showing that the fundamental mechanism behind the temperature dependence rates can be captured by a very low dimensional system. By comparing timings between different phases as a function of temperature, we are able to relate the lack of event coordination to the malfunction of the cell cycle at extreme temperatures. We also compare rates of *C. elegans* and *C. briggsae*, two closely related organisms known to differ in their optimal temperature range.

BP 5.9 Mon 17:00 H 1058

Spatial organization of the cell cytoplasm: Amplifying protein concentration gradient by phase separation — ●CHIU FAN LEE¹, CLIFFORD P. BRANGWYNNE², JÖBIN GHARAKHANI¹, ZDENĚK PETRÁŠEK³, PETRA SCHWILLE³, ANTHONY A. HYMAN⁴, and FRANK JÜLICHER¹ — ¹Max Planck Institute for the Physics of Complex Sys-

tems, Dresden, Germany — ²Department of Chemical and Biological Engineering, Princeton University, USA — ³Biotechnologisches Zentrum, Dresden, Germany — ⁴Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Pattern formation in the cell cytoplasm plays an important role in a number of biological processes. During cell division, the cell cytoplasm undergoes dramatic spatial reorganization. In the case of asymmetric cell division, cytoplasmic components are segregated spatially. An intriguing example is the spatial organization of the cytoplasm during asymmetric cell division in the *C. elegans* embryo, which involves the generation of a concentration gradient of the protein Mex-5 that in turn localizes P granules to the posterior side. P granules are liquid droplets consisting of RNA and proteins that are important for germline specification. Combining theory and quantitative experiments, we propose a simple scenario that describes how the Mex-5 concentration gradient controls the spatial profile of P granule formation and the localization of P-granules to the posterior of the cell. Furthermore, we demonstrate that with the help of phase separation based on the Flory-Huggins formalism, the P granule concentration gradient can be drastically amplified in comparison to the Mex-5 concentration gradient.

BP 5.10 Mon 17:15 H 1058

Molecular Force Response Characteristics from Power Spectral Analysis of Optical Tweezer Experiments — ●YANN VON HANSEN^{1,2}, ALEXANDER MEHLICH¹, BENJAMIN PELZ¹, MICHAEL HINCZEWSKI^{1,3}, MATTHIAS RIEF¹, and ROLAND R. NETZ^{1,2} — ¹Physik Department, TU München — ²Fachbereich Physik, FU Berlin — ³IPST, University of Maryland, USA

The thermal fluctuations of micron-sized beads in dual trap optical tweezer experiments contain a wealth of dynamic information about the viscoelastic properties of the experimental object of study. Dynamic deconvolution theory relates the beads' power spectral densities (PSDs) and the mechanic force response of individual components in the mechanic network [1]. For the quantitative evaluation of the measured signals, a detailed understanding of instrumental characteristics and an accurate calibration of the setup are required. For a simple model system, a pair of unconnected, but hydrodynamically interacting spheres, we obtain excellent agreement between theoretical and measured self- and cross-PSDs over a wide range of inter-bead distances and frequencies, for motion parallel and perpendicular to the inter-bead axis. A comparison to theoretical predictions based on instantaneous hydrodynamics emphasizes the importance of hydrodynamic retardation effects. The viscoelastic response of the force-transducing element between the beads in more complex experimental constructs can be obtained applying a maximum likelihood method [2].

[1] M. Hinczewski et al., Proc. Natl. Acad. Sci. USA 107, 21493 (2010)

[2] Y. von Hansen et al., manuscript in preparation