BP 25: Statistical Physics in Biological Systems III (joint DY, BP)

Time: Thursday 10:15–13:00 Location: ZEU 260

Invited Talk BP 25.1 Thu 10:15 ZEU 260

Bacterial Games — •Erwin Frey — Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universitaet Muenchen, Theresienstrasse 37, D-80333 Muenchen

Microbial laboratory communities have become model systems for studying the complex interplay between nonlinear dynamics of evolutionary selection forces, stochastic fluctuations arising from the probabilistic nature of interactions, and spatial organization. Major research goals are to identify and understand mechanisms that ensures viability of microbial colonies by allowing for species diversity, cooperative behavior and other kinds of social behavior. A synthesis of evolutionary game theory, nonlinear dynamics, and the theory of stochastic processes provides the conceptual framework for a deeper understanding of these ecological systems. In this talk, we give an introduction into the modern formulation of these theories and illustrate their effectiveness focussing on selected examples of microbial systems. We also discuss current challenges and future perspectives in quantifying bacterial population dynamics, and how this might have an impact on research in non-equilibrium physics.

BP 25.2 Thu 10:45 ZEU 260

Transport efficiency governs the morphology of the plasmodial arterial network in slime moulds — •Werner Baumgarten and Marcus Hauser — Abteilung Biophysik, Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg, Universitätsplatz 2, 39106 Magdeburg, Germany

The plasmodium of the slime mould Physarum polycephalum is a single multi-nucleate giant amoeboid cell. It forms a characteristic two-dimensional arterial network, where the apical end of the plasmodium extends to search for new food sources, while the dense network of tubular arteries is in charge of transport of protoplasm throughout the giant cell. The tubular network forms a regular graph [1,2] and displays characteristic distributions of the lengths, widths, and surface area of the tubes [2]. With time, the originally dense network coarsens as tiny arterial segments are deleted. Taking into account the laminar flow inside the arterial network [3], the conductivity and drag inside the arteries are estimated. From these data it will be shown that the evolution of the network strongly depends on the efficiency of the protoplasmic transport in the arteries.

[1] W. Baumgarten, M.J.B. Hauser, J. Comp. Interdisc. Sci. 2010, 1, 241-249.

[2] W. Baumgarten, T. Ueda, M.J.B. Hauser, Phys. Rev. E 2010, 82, 046113.

[3] N. Kamiya, Protoplasma 1950, 39, 344-357.

BP 25.3 Thu 11:00 ZEU 260

A Thermal Trap for DNA Replication — •Christof B. Mast and Dieter Braun — Systems Biophysics, Physics Department, Center for Nanoscience, Ludwig Maximilians Universität München, Amalienstr. 54, 80799 München, Germany

The hallmark of living matter is the replication of genetic molecules and their active storage against diffusion. We implement both in the simple non-equilibrium environment of a temperature gradient. Convective flow both drives the DNA replicating polymerase chain reaction (PCR) while concurrent thermophoresis accumulates the replicated 143 base pair DNA in bulk solution. The time constant for accumulation is 92 s while DNA is doubled every 50 s. The length of the amplified DNA is checked with thermophoresis. Finite element simulations confirm the findings. The experiments explore conditions in pores of hydrothermal rock which can serve as a model environment for the origin of life.

BP 25.4 Thu 11:15 ZEU 260

Negative design in protein folding: The role of correlations — •Jonas Minning[1], Ugo Bastolla[2], and Markus Porto[3] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Germany — [2]Centro di Biología Molecular 'Severo Ochoa', Madrid, Spain — [3]Institut für Theoretische Physik, Universität zu Köln, Germany

Assessing the stability of a protein sequence folded into its native structure is a crucial aspect of protein design and of understanding protein evolution. Folding stability has two sides: (i) stability against the unfolded ensemble, which is usually achieved by evolution providing the native state with native contacts that are attractive enough to compensate for the loss of conformational entropy (positive design), and (ii) stability against incorrectly folded (misfolded) structures with low free energy, which is achieved through negative design.

A simple approximation based on the Random Energy Model (REM) and hence on the neglect of correlations predicts that negative design can be achieved by reducing the variance of the contact interaction energies of all possible residue-residue contacts. We verify that this approximation provides a good fit of the minimum free energy of misfolded structures. Nevertheless, our results suggest that negative design in protein evolution follows actually a completely different strategy, namely utilizing structural correlations between pairs of positions in the misfolded ensemble, which are neglected in the REM approach. We discuss how the REM approach might be generalized to include these correlations.

15 min. break

BP 25.5 Thu 11:45 ZEU 260

Assessing the asymptotic fitness distribution of beneficial mutations from incomplete data sets — •Ivan G. Szendro[1], Martijn Schenk[2], J. Arjan G.M. de Visser[2], and Joachim Krug[1] — [1]Institut für Theoretische Physik, Universität zu Köln — [2]Laboratory of Genetics, Wageningen University

Since seminal work by Gillespie [1] and Orr [2] it is expected that the distributions of fitness effects of beneficial mutations are determined by the universality classes of extreme value theory. More specifically, it is commonly assumed that the distributions of fitness fall into the Gumbel class, implying an exponential decay at large values. However, there have been recent claims that for some viruses the distribution belongs to the Weibull class [3].

In this contribution, we assess the effect of not observing existing beneficial mutations on the assignment of fitness distributions to one of the three extreme value classes. We assume that the probability to observe a specific mutant depends on its selective disadvantage with respect to the fittest observed mutants. In the light of our considerations, we analyze data collected in an experimental evolution study of the TEM-1 β-lactamase enzyme, which confers antibiotic resistance to *Escherichia coli*.

[1] J.H. Gillespie, Theor. Popul. Biol. 23, 202 [2] H.A. Orr, Genetics 163, 1519 [3] D.R. Rokyta et al., J. Mol. Evol. 67, 368

BP 25.6 Thu 12:00 ZEU 260

Stochastic tunneling in a two-locus system with recombination — •Andrej Fischer, Ivan Szendro, Joachim Krug, and Alexander Altland — Institut für Theoretische Physik, Universität zu Köln, D-50973 Köln, Germany

The analysis of minimal models in population genetics is an important conceptual task. The effects of mutation, selection and drift (finite population size) on evolution are captured by Kimura's well-known one-locus model with two alleles. Here, we analyze a model that includes additionally the effects of epistasis and recombination in a two-locus setting. For sign epistasis, i.e. the over-compensation of an initial deleterious point mutation by a beneficial secondary mutation at the other locus, the fixation of the fittest genotype is dominated by the presence of several bottlenecks. The interplay of both finite size effects and meta-stability induced by recombination make for intricate fixation dynamics in this paradigmatic model system. Both analytical and numerical results are presented.

BP 25.7 Thu 12:15 ZEU 260

How to cross a fitness valley - A network approach — •Hinrich Kielblock[1], Marc Timme[1,2], and Stefan Grosskinsky[3] — [1]Network Dynamics Group, Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Bernstein Center for Computational Neuroscience Göttingen, Germany — [3]Centre for Complexity Science, University of Warwick, Conventry, UK

How fast does a population evolve from one fitness peak to another in a fitness landscape? This question has recently received much attention as the answer may strongly affect the speed of evolution.

Here we analyze the problem in the stochastic tunneling regime,

where almost always almost all individuals are found near one fitness peak but once in a while the population switches to another peak. We derive an analytical expression for this switching time considering finite polulation sizes. We first analyze the dynamics of a population existing in only two different genotypes. The results of such a simple system enable us to derive a formula for an effective mutation rate between the peaks of a fitness valley. This effective rate makes it possible to determine the mean switching times in more complex setups, as e.g. multiple fitness valleys or other structures.

BP 25.8 Thu 12:30 ZEU 260

A dynamical phase transition in a model for evolution with migration — •Bartlomiej Waclaw, Rosalind Allen, and Martin Evans — Department of Physics & Astronomy, University of Edinburgh, JCMB, The King's Buildings, Mayfield Road, Edinburgh EH9 3JZ, United Kingdom

Migration between different habitats is ubiquitous among biological populations. Here I will discuss a simple model for evolution of asexual organisms in two different habitats coupled by one-way migration as well as mutations. This gives rise to clusters of closely related genotypes (quasispecies). The habitats are assumed to have different fitness landscapes, i.e., organisms which are well-adapted in the primary habitat are likely to be maladapted in the secondary habitat. The model undergoes a dynamical phase transition: at a critical value of the migration rate, the time to reach the steady state diverges. Above the transition, the population is dominated by immigrants from the primary habitat. Below the transition, the genetic composition of the population is highly non-trivial, with multiple coexisting "quasispecies" which are not native to either habitat. Using results from localization theory, I will show that the critical migration rate may be very small — demonstrating that evolutionary outcomes can be very sensitive to even a small amount of migration.

BP 25.9 Thu 12:45 ZEU 260

The role of population size in the evolution of microbial populations — •Joachim Krug[1], Kavita Jain[2], and Su-Chan Park[3] — [1]Institut für Theoretische Physik, Universität zu Köln, Cologne, Germany — [2]Theoretical Sciences Unit and Evolutionary and Organismal Biology Unit, Jawaharlal Nehru Centre, Bangalore, India — [3]Department of Physics, The Catholic University of Korea, Bucheon, Korea

The speed of adaptation of a population placed into a new environment is generally expected to increase with increasing population size, for at least two reasons: The supply of beneficial mutations is proportional to population size, and the probability of fixation of deleterious mutations is negligible in large populations. Contrary to this expectation, recent experiments on microbial populations have shown that small populations evolving in a complex nutrient medium may achieve a higher fitness than large ones due to the increased heterogeneity of adaptive trajectories. We introduce a class of haploid three-locus fitness landscapes that allows to investigate this scenario in a precise and quantitative way. Our main result derived analytically shows how the probability of choosing the path of largest initial fitness increase grows with the population size. This makes large populations more likely to get trapped at local fitness peaks and implies an advantage of small populations at intermediate time scales. Additional studies using ensembles of random fitness landscapes show that the results achieved for a particular choice of three-locus landscape parameters are robust and also persist as the number of loci increases.