DY 36: Statistical Physics in Biological Systems IV (organised by BP)

Time: Thursday 14:00–16:45　　　　　　　　　　　　　　　　　　　　　　　　　Location: ZEU 260

DY 36.1　Thu 14:00　ZEU 260

Evolution of complex chemical mixtures: a problem linked to the origin of life — •Eva Wollrab[1], Sabrina Scherer[1], Christian Lay[1], Manuel Worst[1], Philipp Zimmer[2], Karsten Kruse[2], and Albrecht Ott[1] — [1]Universität des Saarlandes, Biologische Experimentalphysik, 66123 Saarbrücken — [2]Universität des Saarlandes, Theoretische Biologische Physik, 66123 Saarbrücken

How self-reproducing structures can form in a chemical mixture and how a steady increase in biochemical complexity of these cycles may occur is still unknown. We approach this question experimentally from two different directions.

In the first class of experiments highly reactive, primitive compounds are mixed. We track the temporal development of the mixture using mass spectroscopy for analysis. Tools from bioinformatics help us to develop ideas about the underlying chemical network.

The second class of experiments employs DNA. The DNA is designed to form autocatalytic reaction pathways. These experiments are designed to inductively find new conditions for self-reproducing chemical cycles. We suggest that this situation can be simulated in silico by autocatalytic reactions that exhibit fluctuations of the reaction pathways.

DY 36.2　Thu 14:15　ZEU 260

Complexity-stability relations in generalized food-web models with realistic parameters — •Sebastian Plitzko, Christian Guill, and Barbara Drossel — Institut für Festkörperphysik, TU Darmstadt, Hochschulstraße 6, 64289 Darmstadt, Germany

We investigate conditions for positive complexity-stability relations in the niche model for food webs by evaluating the local stability of the fixed points of the system. We use a generalized method, where the fixed points are normalized to 1, which allows for an efficient numerical evaluation. We find that positive relations between local stability and complexity can be obtained if prey is not scarce, biomass loss due to predation is low and density-dependent mortality effects dominate over other contributions to mortality. Since these conditions are expressed in terms of the generalized parameters, we then determine the range of values of these parameters within locally stable niche model food webs with explicit dynamical equations. These equations include allometric scaling and parameter values that are realistic. We find that the values of the generalized parameters obtained from this explicit dynamical model depend on the trophic level. The range of these parameters is such that positive complexity-stability relations can be obtained.

DY 36.3　Thu 14:30　ZEU 260

Statistical topography of fitness landscapes — •Jasper Franke[1], Alexander Klözer[1], J. Arjan G. M. de Visser[2], and Joachim Krug[1] — [1]Cologne University, Cologne, Germany — [2]Wageningen University, Wageningen, Netherlands

The adaptive evolution of a population under the influence of mutations and selection is governed by the structure of the underlying fitness landscape. Previous theoretical studies of topographical quantities on fitness landscapes have mostly focused on local properties such as local maxima.

Here we investigate the global property of accessible paths traversing the complete genome configuration space towards the global optimum. Numerical and analytical studies and comparison to empirical data suggest a surprising unversality across almost all established theoretical models, indicating high accessibility of the globally optimal configuration in the biologically relevant limit of very long genome sequences.

DY 36.4　Thu 14:45　ZEU 260

Speed of Evolution in Spatially Extended Populations — •Erik A. Martens and Oskar Hallatschek — Group for Biophysics and Evolutionary Dynamics, Max Planck Institute for Dynamics and Self-Organization, 37073 Göttingen, Germany

How fast do species adapt to a given environment? This is one of the most fundamental questions in evolutionary biology. Many theoretical models are restricted to the case of well-mixed populations. To characterize the speed of evolution in spatially extended populations, it is necessary to consider the wave-like spread of evolutionary novelties.

The presence of such wave-like sweeps reduces the speed of evolution for two reasons. First, the waves are slower than the exponential spread of beneficial mutations known from well-mixed populations. Second, because these sweeps are slower, spatially extended populations are more prone to be in a state where multiple beneficial mutations sweep simultaneously. This problem of clonal interference has been demonstrated in microbial experiments and has recently gained strong interest. We simulate the spread of mutations in spatial dimensions using computer simulations, where we include effects of recombination and long-range migration. We find that 1) the adaptation rate obeys robust power laws, which 2) are independent of the particular choice of selective fitness distributions ("universality"), 3) that spatial populations experience clonal interference over a broader range of parameters, and 4) that the effects of clonal interference can be mitigated by recombination and long-range migration. We therefore speculate that both processes are selectively favorable.

DY 36.5　Thu 15:00　ZEU 260

Predators, parasites and food web stability — •Lars Rudolf[1], Neo Martinez[2], and Thilo Gross[1] — [1]Max-Planck-Institut für Physik komplexer Systeme, Dresden — [2]Pacific Ecoinformatics and Computational Ecology Lab, Berkley, USA

Predator-prey interactions and their influence on food web stability are a major topic of ecological research. The investigation of parasitic interactions, which are another fundamental part of the most ecological communities, has been less intensive. To close that gap, we used generalized modeling and studied several million replicates of food webs with different proportions of parasitic species. In this way we determine the impact of parasitism on different food web properties and how these properties affect food web stability. Specifically, we show that a moderate proportion of parasitic species enhances food web stability.

15 min. break

DY 36.6　Thu 15:30　ZEU 260

Dynamics of mutants in a stochastic compartment approach of hematopoiesis — •Benjamin Werner and Arne Traulsen — Research Group for Evolutionary Theory, Max Planck Institute for Evolutionary Biology, 24306 Plön

Cancer is typically caused by at most a handful of mutations that increase the reproductive fitness of a single cell. The probability of such a mutation, the dynamics of the resulting clone of cancer cells, and thus the effect to an organism is under intense investigation. First we present an established stochastic multicompartment model of hematopoiesis [1,2] (CML) as well as other blood disorders [3,4] can be embedded and analyzed in this framework. We show that there is a closed deterministic solution to the dynamics of mutants in this model that fits the averages of the stochastic process. This solution enables us to connect different model parameters directly to observed cell dynamics and thus gives in principle yet unknown information about disease progression and the impact of drug treatment.

Ref.:

[1] D. Dingli, A. Traulsen and J. M. Pacheco,
PLoS ONE 2, e345 (2007).

[2] D. Dingli, A. Traulsen, T. Lenaerts and J. M. Pacheco,
Genes & Cancer 1(4) 309-315 (2010).

[3] D. Dingli, J. M. Pacheco and A. Traulsen,
Phys. Rev. E 77, 021915 (2008).

[4] A. Traulsen, J. M. Pacheco, L. Luzzatto and D. Dingli,
BioEssays Vol.32 Issue 11 (2010).

DY 36.7　Thu 15:45　ZEU 260

Stochastic slowdown in evolutionary processes — •Philipp M. Altrock, Chaitanya S. Gokhale, and Arne Traulsen — Max-Planck-Institute for Evolutionary Biology, Plön

We examine birth–death processes with state dependent transition probabilities and at least one absorbing boundary. In evolution, this describes selection acting on two different types in a finite population where reproductive events occur successively. If the two types have equal fitness the system performs a random walk. If one type has a fitness advantage it is favored by selection, which introduces a bias (asymmetry) in the transition probabilities. How long does it take un-

til advantageous mutants have invaded and taken over? Surprisingly, we find that the average time of such a process can increase, even if the mutant type always has a fitness advantage. We discuss this finding for the Moran process and develop a simplified model which allows a more intuitive understanding. We show that this effect can occur for weak but non–vanishing bias (selection) in the state dependent transition rates and infer the scaling with system size. We also address the Wright–Fisher model commonly used in population genetics, which shows that this stochastic slowdown is not restricted to birth–death processes.

[1] Altrock, Gokhale, and Traulsen, Physical Review E 82, 011925 (2010)

DY 36.8 Thu 16:00 ZEU 260

Food Quality in Producer-Grazer Models — •DIRK STIEFS[1], GEORGE VAN VOORN[2], BOB KOOI[3], ULRIKE FEUDEL[4], and THILO GROSS[1] — [1]Max-Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Wageningen University and Research Centre, Wageningen, The Netherlands — [3]Vrije Universiteit, Amsterdam, The Netherlands — [4]ICBM, Carl von Ossietzky Universität, Oldenburg, Germany

Stoichiometric constraints play a role in the dynamics of natural populations, but it is not yet resolved how stoichiometry should be integrated in population dynamical models, as different modeling approaches are found to yield qualitatively different results. We use the approach of generalized modeling to investigate the effects of stoichiometric constraints on producer-grazer systems. The stability of steady states can be analyzed by using a normalization technique to plot 3-dimensional bifurcation diagrams. Because we do not specify the functional form of the processes in the generalized model our results hold for a whole class of stoichiometric producer-grazer systems.

To understand the differences and commonalities between specific stoichiometric models we map the specific bifurcation diagrams into the generalized parameter space. On the one hand, these combined bifurcation diagrams show how the generic results of the generalized analysis are represented in the specific model. On the other hand, it becomes clear that some model features like the sequence of bifurcations observed during enrichment scenarios can be tied to specific modeling assumptions and are hence not structurally stable.

DY 36.9 Thu 16:15 ZEU 260

Evolutionary Game Theory in Growing Populations — •ANNA MELBINGER, JONAS CREMER, and ERWIN FREY — Ludwig-Maximilians Universität, Munich, Germany

Existing theoretical models of evolution focus on the relative fitness advantages of different mutants in a population while the dynamic behavior of the population size is mostly left unconsidered. We here present a generic stochastic model which combines the growth dynamics of the population and its internal evolution. Our model thereby accounts for the fact that both evolutionary and growth dynamics are based on individual reproduction events and hence are highly coupled and stochastic in nature. We exemplify our approach by studying the dilemma of cooperation in growing populations and show that genuinely stochastic events can ease the dilemma by leading to a transient but robust increase in cooperation.

[1] Phys. Rev. Lett. 105, 178101 (2010)

DY 36.10 Thu 16:30 ZEU 260

A Non-Equillibrium Phase Transition in Expanding Populations — •JAN-TIMM KUHR and ERWIN FREY — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München

Recently, expanding bacterial populations found much attention in both experimental and theoretical work [1]. These "range expansions" have interesting statistical properties, as constant genetic re-sampling from a small population at the expanding front induces strong fluctuations. The influence of non-neutral mutations on the dynamics is less well studied. Here, we introduce an extension of the Eden model [2], including mutations. Using Monte Carlo simulations, we analyze the interplay of kinetic surface roughening, mutations and selection at the front. While beneficial mutations always take over the front eventually, for detrimental mutations one finds two generic cases: if rare, mutant sectors are independent and wild types prevail. If mutants spawn more frequently, sectors coalesce and wild types are soon lost in the bulk. Between these regimes one finds self-affine patterns, and we identify a non-equilibrium phase transition. We measure critical exponents near this transition, and find universal scaling behavior for this model of evolution in expanding populations.

[1] O. Hallatschek and D. Nelson, Life at the front of an expanding population. Evolution, **64**, 193-206, (2010) – [2] M. Eden, A two-dimensional growth process, Proc. of the Fourth Berkeley Symposium on Mathematical Statistics and Probability, **4**, 223-239, (1960)