

BP 21: Population Dynamics and Evolution

Time: Thursday 17:30–18:45

Location: HÜL 186

BP 21.1 Thu 17:30 HÜL 186

Determinants of food-web stability — ●LARS RUDOLF and THILO GROSS — Max Planck Institute for the Physics of Complex System, Nöthnitzer Str.28, 01187 Dresden, Germany

Since the publication of Robert May's seminal work the stability of ecological food webs is a topic of intense research and hot debate. Contrary to many field observations, May showed that large, densely connected food webs are in general unstable. The only way to reconcile May's proof with observation is to find the special properties that lend natural food webs their unusual stability. It has been pointed out that the identification of such stabilizing network properties could have broad implications beyond the field of ecology. Most recent theoretical work focuses on numerical models based on explicit rate equations. These and empirical studies have revealed that weak trophic links may play an important role for stability. However, in contrast to May's abstract random matrix model, numerical constraints limit most simulative studies to the investigation of relatively few instances (approx. 10000) of relatively small food webs (approx. 10 species). Recently, generalized modeling, a novel numerical approach for the analysis of stability in families of nonlinear rate equations, has been proposed. Here we utilize this approach to study several billion instances of food webs of up to 50 species with nonlinear interactions. While we find a stabilizing effect of weak links in small food webs, this stabilization is absent in larger webs. Instead, we identify a universal feature in the distribution of links that is important for stability.

BP 21.2 Thu 17:45 HÜL 186

Life on the Edge: Gene Surfing in Microorganisms — ●OSKAR HALLATSCHKE^{1,2} and DAVID R. NELSON² — ¹Max Planck Institut für Dynamik und Selbstorganisation, Bunsenstr. 10, 37073 Göttingen — ²Lyman Laboratory of Physics, Harvard University, Cambridge, MA 02138

It is widely appreciated that population waves have played a crucial role in the evolutionary history of many species. Genetic footprints of many pioneer species are still recognizable today, and neutral genetic markers can be used to infer information about growth, ancestral population size, colonization pathways, etc. Bacterial growth on a Petri dish can be used to model this phenomenon, using the change of a single amino acid residue in a fluorescent protein encoded on a plasmid as a marker. The frontier of acts as a moving genetic bottleneck, and neutral mutations optimally positioned on the edge of a growing population wave can increase their abundance via a "surfing" phenomenon. Striking patterns of gene segregation and lineage histories are observed for both radial and linear inoculations of populations of bacteria and yeast. Recent experimental and theoretical studies of this effect will be presented, using bacteria and yeast as model systems, including results for surfing of deleterious and favorable mutations during range expansions.[1] O. Hallatschek and D. R. Nelson, <http://arxiv.org/abs/0810.0053>, and references therein.

BP 21.3 Thu 18:00 HÜL 186

Quasispecies theory with frequency-dependent selection — ●BENEDIKT OBERMAYER and ERWIN FREY — Arnold Sommerfeld Center and Center of NanoScience, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München

The Eigen model describes the evolution of macromolecules such as

RNA under strong selection and large mutation rates in the limit of infinite population size. For mutation rates below a critical value (the error threshold), its stationary state is characterized by a broad mutant distribution about a fitness peak (the quasispecies). While so far mainly static fitness landscapes have been considered, the fitness of macromolecules depends also on the presence and nature of interaction partners, leading to dynamic and frequency-dependent selection. We analyze quasispecies theory for generic frequency-dependent fitness and obtain qualitatively new analytical and numerical results for the population distribution and the error threshold phenomenon.

BP 21.4 Thu 18:15 HÜL 186

The pace of evolution across fitness valleys — ●CHAITANYA GOKHALE and ARNE TRAUlsen — Max-Planck-Institute for Evolutionary Biology, 24306 Plön, Germany

How fast does a population evolve from one fitness peak to another? We study the dynamics of evolving, asexually reproducing populations in which a certain number of mutations jointly confer a fitness advantage. We consider the time until a population has evolved from one fitness peak to another one with a higher fitness. The order of mutations can either be fixed or random. If the order of mutations is fixed, then the population follows a metaphorical ridge, a single path. If the order of mutations is arbitrary, then there are many ways to evolve to the higher fitness state. In this case, evolution proceeds on a hypercube in d dimensions, where d is the number of required mutations. We address the time required for fixation in such scenarios via analytical expressions for small mutation rates and approximations based on differential equations for higher mutation rates. We also study how the time is affected by the order of mutations, the population size and the fitness values. We also compare a single path, in which the intermediate states have the same fitness values as the initial state, to a hypercube with a fitness valley and ask whether it is faster to cross the fitness landscape via a ridge or a broad fitness valley.

BP 21.5 Thu 18:30 HÜL 186

Estimating the Role of Fluctuations in Evolutionary Games — ●JONAS CREMER¹, TOBIAS REICHENBACH², and ERWIN FREY¹ — ¹Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians Universität München, Germany — ²Howard Hughes Medical Institute and Laboratory of Sensory Neuroscience, The Rockefeller University New York, NY USA

Evolutionary game theory describes the temporal development of different interacting strategies in a population. Within the standard formulation by replicator equations the dynamical behavior of simple evolutionary games is well known. This description, however, does not take stochasticity into account and thus fails if fluctuations are important. In such a case a stochastic description is required. Having investigated the effects of finite-size fluctuations within the asymmetric two-player game *Battle of the Sexes* [1] we now study the role of stochastic fluctuations within symmetric two-player games. We analyze mean extinction times, i.e. the time until coexistence of an originally mixed population is lost and only one strategy remains, and show that its dependence on the system size is a strong and general applicable concept to reveal the role of fluctuations on the evolutionary dynamics.

[1] Jonas Cremer, Tobias Reichenbach, and Erwin Frey, Eur. Phys. J. B 63 373-380 (2008)