BP 21: Population Dynamics and Evolution

Time: Thursday 12:15–13:15 Location: C 243

BP 21.1 Thu 12:15 C 243

Clonal interference in large populations — •Su-Chan Park and Joachim Krug — Institut für Theoretische Physik, Universität zu Köln, Köln, Germany

Clonal interference, the competition between lineages arising from different beneficial mutations in an asexually reproducing population, is an important factor determining the tempo and mode of microbial adaptation. The standard theory of this phenomenon neglects the occurrence of multiple mutations as well as the correlation between loss by genetic drift and clonal competition, which is questionable in large populations. Working within the Wright-Fisher model with multiplicative fitness (no epistasis), we determine the rate of adaptation asymptotically for very large population sizes and show that the standard theory fails in this regime. Our study also explains the success of the standard theory in predicting the rate of adaptation for moderately large populations. Furthermore we show that the nature of the substitution process changes qualitatively when multiple mutations are allowed for, since several mutations can be fixed in a single fixation event. As a consequence, the index of dispersion for counts of the fixation process displays a minimum as a function of population size, while the origination process of fixed mutations becomes completely regular for very large populations. We find that the number of mutations fixed in a single event is geometrically distributed as in the neutral case.

Reference: S.-C. Park and J. Krug, PNAS 104, 18135 (2007).

BP 21.2 Thu 12:30 C 243

Stability of food webs with structured populations — •Christian Guill and Barbara Drossel — TU Darmstadt, Institute of Condensed Matter Physics, Hochschulstraße 6, D-64289 Darmstadt

Most existing models of population dynamics in food webs treat species as homogeneous aggregations of identical individuals. They neglect the fact that not all individuals of a species are reproducing, but are juveniles that invest their energy intake into growth in body size. Here, we investigate model food webs with populations that are structured in terms of physiological state (juvenile/adult). Each stage of a species has its own feeding relationships and population dynamics, but the stages are coupled through maturation and reproduction. This leads to time-dependent traits of the species as a whole, such as its mean body size. Since body size is a key factor in determining predation behaviour and also influences metabolic rates, structuring of populations changes the population dynamics and stability of the entire network. Simulation results obtained from networks with structured populations are compared to networks with unstructured populations.

The population dynamics in ecosystems with structured populations are studied in more detail in the example of a real aquatic system consisting of a homogeneous resource (zooplankton), two consumers (salmon species), and a top predator (trout) with structured populations. Simulation results are tested against empirical data of the system.

BP 21.3 Thu 12:45 C 243

Cyclic dominance and biodiversity in well-mixed populations — •Jens Christian Claussen[1] and Arne Traulsen[2] — [1]Institut für Theoretische Physik u. Astrophysik, Christian-Albrecht Universität Kiel — [2]Max-Planck-Institut für Evolutionsbiologie, 24306 Plön

Coevolutionary dynamics is investigated in chemical catalysis, biological evolution, social and economic systems. The dynamics of these systems can be analyzed within the unifying framework of evolutionary game theory. Here, we show that even in well-mixed finite populations, where the dynamics is inherently stochastic, biodiversity is possible with three cyclic dominant strategies. We show how the interplay of evolutionary dynamics, discreteness of the population, and the nature of the interactions influences the coexistence of strategies. We calculate a critical population size above which coexistence is likely.

BP 21.4 Thu 13:00 C 243

Protein Thermodynamics and Population Dynamics — •Miriam Fritsche[1], Andreas Buhr[1], Ugo Bastolla[2], and Markus Porto[1] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Hochschulstr. 8, 64289 Darmstadt, Germany — [2]Centro de Biología Molecular 'Severo Ochoa', Campus UAM, Cantoblanco, 28049 Madrid, Spain

When investigating proteins one has to take into account both the physical constraints on folding stability and the biological constraints on their evolution, being the driving force of nature [1]. Based on previous work [2] we investigate thermodynamical properties of proteins during evolution applying a model which consists of mutations as well as purifying selection. In addition to the explicit consideration of thermodynamic stability, we account for the effect of mutational and translational load in the evolutionary process, therewith sheding light on the impact the spectrum of mutations has on natural selection. Investigating the interplay between protein thermodynamics, population dynamics as well as genomic features we are able to better understand several properties of proteins as well as their evolution, for instance, the existence of a strong mutation bias in the genome of intracellular bacteria.

[1] *Structural Approaches to Sequence Evolution*, U. Bastolla, M. Porto, H.E. Roman and M. Vendruscolo, ed., Springer, Berlin, 2007
[2] U. Bastolla, M. Porto, H.E. Roman and M. Vendruscolo, Phys. Rev. Lett. **89**, 208101 (2002); J. Mol. Evol. **56**, 243 (2003); Proteins **58**, 22 (2005); Mol. Biol. Evol. **22**, 630 (2005); BMC Evol. Biol. **6**, 43 (2006)