BP 14: Evolutionary Game Theory III (joint SOE, BP)

Time: Tuesday 14:00–16:00 Location: H44

Invited Talk BP 14.1 Tue 14:00 H44

Stochasticity and specificity in DNA repair — •Thomas Höfer[1], Martijn Luijsterburg[2], Gesa von Bornstaedt[1], and Roel van Driel[3] — [1]Deutsches Krebsforschungszentrum, Heidelberg, Germany — [2]Karolinska Institute, Stockholm, Sweden — [3]University of Amsterdam, The Netherlands

To understand how multi-protein complexes assemble and function on chromatin, we have combined quantitative analysis of a mammalian DNA repair machinery in living cells with mathematical modeling. We found that the individual components exchange rapidly at the repair sites whereas their net accumulation evolved on a much slower timescale. Based on the experimental data, we developed a predictive kinetic model of how multi-protein repair complexes assemble. Complex formation is orchestrated by progressive enzymatic modifications of the chromatin substrate, leaving considerable freedom for the binding mode of individual proteins. We demonstrate that the faithful recognition of DNA lesions is a time-consuming process, while subsequently repair complexes form rapidly through random and reversible assembly. Our analysis reveals a fundamental conflict between specificity and efficiency of chromatin-associated protein machineries and shows how a trade-off is negotiated through reversibility of protein binding.

BP 14.2 Tue 14:30 H44

Predicting correlated mutations of amino acids from protein structure — •Jonas Minning[1], Ugo Bastolla[2], and Markus Porto[1] — [1]Technische Universität, Darmstadt, Germany — [2]Centro di Biología Molecular, 'Severo Ochoa', CSIC-UAM, Madrid, Spain

Even though the average sequence similarity for homologous proteins sharing the same fold can reach the threshold of randomness, amino acid sequences maintain the fingerprint of selective pressures on structure and function. We have previously developed an analytical method for computing the probability to observe a given amino acid at a given site in a protein with known native structure, based on an independent site approximation of protein evolution subject to selective constraints on unfolding and misfolding stabilities [1]. However, substitutions at different sites are known to be correlated, and these correlated mutations may give important information for reconstructing native contacts, protein interaction interfaces, or clusters of functionally important residues. Here, we present a model which allows to quantitatively predict the correlated mutations that arise from selective constraints on unfolding and misfolding stabilities. Our model is verified against simulated data of protein sequence evolution and statistical data of proteins in the Protein Databank.

[1] U. Bastolla *et al.*, Proteins **73**, 872 (2008).

BP 14.3 Tue 14:45 H44

Stability of an underdominant polymorphism in the presence of migration — •Philipp M. Altrock, Arne Traulsen, R. Guy Reeves, and Floyd A. Reed — MPI f. Evolutionary Biology, Plön, Germany

In population genetics, underdominance refers to natural selection against individuals with a heterozygous genotype [1]. Here, we analyse a single–locus underdominant system of two large local populations that exchange individuals at a certain migration rate and can be characterized by fixed points in the joint allele frequency space. We specifically address the conditions under which underdominance can be applied to stably and reversibly transform a local population that is receiving untransformed migrants, where an exact relationship between the rate of migration and the degree of selection against heterozygotes, that allows stable local transformations, exists [2]. We also approximate the critical minimum frequency required to result in a stable population transformation. For doubly asymmetric configurations, i.e. different homozygote fitness and unequal migration rates, there is a regime where a stable transformation is only possible in one of the two populations. The stability of the system is robust to the migration of gravid females. We also address the relative influence of various forms of stochasticity (migration versus genetic drift).

[1] Hartl & Clark, *Principles of Population Genetics*, 2nd Edition. Sinauer Associates, Inc., Sunderland, MA. (1989).

[2] Karlin & McGregor, Theor. Pop. Biol. **3**, 186 (1972).

BP 14.4 Tue 15:00 H44

Recombination suppresses peak escape in rugged fitness landscapes — •Joachim Krug and Su-Chan Park — Institut für Theoretische Physik, Universität zu Köln, Germany

The adaptive value of recombination is at the heart of the long-standing debate about the evolutionary role of sex. Intuitively one might expect recombination to aid the escape of a population from sub-optimal fitness peaks and hence to accelerate the adaptive process. Here we show that the converse is true. For a deterministic, haploid two-locus model with two fitness peaks of unequal height, a stationary low-fitness solution concentrated at the lower peak emerges beyond a critical value of the recombination rate. The bifurcation giving rise to this solution is formally equivalent to an Ising-like phase transition. Numerical simulations show that the phenomenon persists in more complex multilocus landscapes derived from experimental fitness measurements for the asexual fungus *Aspergillus niger*.

BP 14.5 Tue 15:15 H44

Chemical Evolution in Simulating Experiments — •Eva Wollrab and Albrecht Ott — Biologische Experimentalphysik, Saarbrücken, Deutschland

In 1953 Stanley Miller and Harold Urey made a pioneering experiment, simulating possible primitive earth conditions. In a sealed apparatus they boiled water in an atmosphere of methane, ammonia and hydrogen circulating these compounds past an electric discharge during periods of the order of a week. The resulting samples contained several organic molecules among them also amino acids. In the following decades several experiments were made to test the spontaneous formation of the most important biomolecules under possible primitive earth conditions.

We have performed Miller's experiment. The resulting samples were analyzed by HPLC and mass spectroscopy. Our analysis performed following different run-times gives us information about the composition of the reaction products. It reveals an evolution of the emerging substances and their compositions towards increased complexity as well as a (universal?) distribution of molecular masses.

This is a first step in order to determine conditions, which ultimately allow for the birth of autocatalytic chemical cycles.

BP 14.6 Tue 15:30 H44

Evolutionarily stable demographics — •Oskar Hallatschek — Biological Physics and Evolutionary Dynamics, MPI DS, Goettingen

It has long been noticed that demographic stochasticity can seriously interfere with Darwin's evolutionary principles of heritable variation and selection. Avantageous genes are sometimes lost accidentally. These chance effects are considered as major retardation of Darwinian evolution. Here, we show that, in spatial systems, they can sometimes accelerate adaptive evolution. We describe a whole class of demographic parameters for which demographic stochasticity actually drives adaptive evolution. Among these traits are dispersal rates and carrying capacities, for which evolutionary optimal values (ESS's) can be given. These new class of noise driven adaptations suggests that demographic stochasticity must be considered also as an important creative Darwinian force, not only as a disrupting one.

BP 14.7 Tue 15:45 H44

Sexual and asexual reproduction in iteroparous species — •Yixian Song[1], Barbara Drossel[1], and Stefan Scheu[2] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Deutschland — [2]J.F. Blumenbach Institute of Zoology and Anthropology, University of Goettingen, Germany

The evolution of sex has been discussed intensively since Charles Darwin. By considering explicitely the important fact of limited and structured resources, we explore the conditions for the maintenance of sex in spite of the cost of producing males. In this model, asexual species win over sexual species only when mortality rates are large, resources regrow quickly, many different genotypes are allowed to coexist at the same place, or when resource diversity is small. Here, we modify the limited structured resource model of Scheu and Drossel (Proc. Roy. Soc. B. 2007) such that it applies to iteroparous species, which reproduce more than once during their life. We therefore include age and size of individuals into the model, with the corresponding metabolic

rate, mortality and fecundity. Metabolic rate per biomass and mortality decrease with increasing body weight, while the fecundity increases. Therefore, phenotypes with smaller size at maturity have a higher mass dependent metabolic rate, a higher mortality, and a lower fecundity. However, they reach maturity earlier with the same growth rate and increase thereby the chance of survival until reproduction. We determine the optimum size at reproduction and the optimum offspring size under different environmental conditions, and we evaluate the parameter range for which sexual reproduction wins over asexual reproduction.