

Parallel Session

Evolutionary Dynamics V

DISENTANGLING ECOLOGICAL NOISE AND EVOLUTIONARY DYNAMICS DURING TRAIT FIXATION

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Keywords: Eco-evolutionary theory, Fixation probability.

We study the fixation probability of a mutant type when introduced into a resident population which fluctuates in size. We focus on the interplay between ecological and evolutionary processes and their effects on the fixation probability of the newly introduced mutant. Using techniques from population genetics, evolutionary game theory and theoretical ecology we are able to disentangle the eco-evolutionary effects on the fixation probability. We approximate this quantity under weak selection in both, the evolutionary and the ecological, components. Our main result shows that the location of potential internal fixed points plays a crucial role in the formula and their stability determines the evolutionary success of the mutant trait. Hence, the qualitative behavior of the fixation probability can be reduced to the corresponding replicator equation while this is not true in case of fixed population sizes.

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EXACT SIMULATION OF COUPLED WRIGHT FISHER DIFFUSIONS

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Keywords: Population genetics, Interaction, Wright-Fisher diffusion, Exact simulation.

Increased availability of molecular phylogenetic information has triggered the development of new models and computational methods in evolutionary biology. Detection of co-evolution mechanisms at the molecular level is of great interest in this context, as it is key for the study of genetic variants associated with numerous diseases. The coupled Wright-Fisher diffusion, a multilocus and multiallele diffusion model recently proposed by Timo Koski and Erik Aurell, aims to characterize the evolution of pairwise interactions between allele types at different loci. Expressed as a system of stochastic differential equations, the coupled Wright-Fisher diffusion includes coupling terms, one added to each drift, that reflect the nature of such interactions. While simulation methods for other diffusion processes have been widely studied, exact simulation methods for the coupled Wright Fisher diffusion are currently unavailable. We propose an exact rejection algorithm for coupled Wright-Fisher diffusions, extending the simulation techniques presented in [1]. Our algorithm uses as candidates independent Wright-Fisher processes for which exact simulation is possible, and imposes only mild conditions on the coupling terms, covering a wide range of coupled Wright-Fisher diffusion models that include mutation and selection.

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FATE OF POPULATIONS IN A STOCHASTIC SYSTEM WITH MUTATIONS

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Keywords: Eco-evolutionary dynamics, Stochastic process, Extinction phenomenon.

Trait variation emerging from mutations is common in nature. Once a mutant emerges in the population, new interactions are drawn between types, which may lead to changes in the population size. Using the game theory, we implement this population dynamics in a stochastic system [1, 2]. Since interactions between types are described by a game payoff matrix, the emergence of a mutant is interpreted as extending the payoff matrix [3]. New equilibria can emerge by the change of the payoff matrix. If the population settles to a new equilibrium state, the population size changes. We examine the change of population size in time and quantify the extinction risk by the mean time to extinction.

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STABLE POLYMORPHISMS DUE TO SEASONALLY FLUCTUATING SELECTION AND THEIR GENETIC FOOTPRINT

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Keywords: Population genetics, Coalescent theory, Maintenance of genetic variation, Stochastic modeling.

Natural selection not only affects the exact loci under selection but also leaves “footprints” in patterns of genetic variation in linked genetic regions. Thus genome-wide data offer exciting opportunities for inferring selection. Past studies on genetic footprints have mostly focused on simple scenarios of selection: fixation of a single new mutation under constant positive selection (selective sweep) or balancing selection maintaining an allele at constant frequency. Yet, other modes of selection such as polygenic adaptation, adaptation from the standing genetic variation, or fluctuating selection may be more prevalent in nature and may produce distinct footprints that can be missed by standard scans for selection. To increase ecological and genetic realism in models for the footprints of balancing selection, we here consider balancing selection at one or more loci with seasonal fluctuations in the allele frequencies. Using coalescent theory and stochastic simulations, we show that seasonal allele frequency fluctuations can have important (and partly unexpected) consequences on the genetic footprint of balancing selection. Fluctuating balancing selection generally leads to an increase in genetic diversity close to the selected site, but reduces diversity further away from the selected site, often even leading to a net decrease in diversity on the scale of the chromosome. For two or more linked loci under seasonally fluctuating selection, qualitatively different behaviors emerge depending on whether the genetic distances between loci are below or above a certain threshold distance. Above the threshold distance, recombination breaks up linkage disequilibria faster than selection generates them. Below the threshold distance, recombination is not strong enough and linkage disequilibrium builds up. Depending on the initial conditions, the population reaches one of two or more alternatively states with qualitatively different linkage patterns, seasonal dynamics, and genetic footprints. These results might contribute to explaining empirical observations of long-range linkage disequilibria in natural populations.

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**NEAR-NEUTRALITY IN EVOLUTIONARY MODELS:
THE FIRST ARRIVAL TIME PROBLEM**

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Keywords: Crow-Kimura model, Wright-Fisher model, Nearly-neutral fitness landscape, Hamilton-Jacobi equation.

In this study, we discuss the microscopic theory for the evolution on nearly neutral fitness landscapes. This concept originates from the M. Kimura's [1] and T. Ohta's [2, 3] researches that show the impact of random fluctuations and slightly deleterious mutations on the evolutionary process. While a neutral network like fitness landscape gives a negligible increase in the mean fitness, it can drastically affect the arrival time for the new mutants. We suppose the difference between one-point mutation neighbors to be small and construct a modification of the Crow-Kimura model for infinite populations. For the case of finite populations, the version of the Wright-Fisher model is analyzed. We also proposed a continuous model using Hamilton–Jacobi method. For these models, the estimation for the first arrival time is derived. We claim that the proposed approach gives an advantage (in comparison to the classical Wright-Fisher model with few sequences) in describing the evolutionary dynamics of RNA viruses.

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