

Abstract Submitted
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Learning about evolution from sequence data ADEL DAYARIAN, BORIS SHRAIMAN, KITP — Recent advances in sequencing and in laboratory evolution experiments have made possible to obtain quantitative data on genetic diversity of populations and on the dynamics of evolution. This dynamics is shaped by the interplay between selection acting on beneficial and deleterious mutations and recombination which reshuffles genotypes. Mounting evidence suggests that natural populations harbor extensive fitness diversity, yet most of the currently available tools for analyzing polymorphism data are based on the neutral theory. Our aim is to develop methods to analyze genomic data for populations in the presence of the above-mentioned factors. We consider different evolutionary regimes - Muller's ratchet, mutation-recombination-selection balance and positive adaption rate - and revisit a number of observables considered in the nearly-neutral theory of evolution. In particular, we examine the coalescent structure in the presence of recombination and calculate quantities such as the distribution of the coalescent times along the genome, the distribution of haplotype block sizes and the correlation between ancestors of different loci along the genome. In addition, we characterize the probability and time of fixation of mutations as a function of their fitness effect.

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