

A genetics-style document using RMarkdown

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Abstract

Most new mutations that affect fitness are deleterious and tend to be eliminated from a population. The amount of time that a deleterious mutation segregates depends on the strength of selection against genomes that carry it, with very damaging mutations kept at low frequencies and purged relatively rapidly. In the time between mutation and fixation or loss, selected variants, both beneficial and damaging, can dramatically impact patterns of variation in nearby linked regions. This distortion away from neutral expectations is now empirically documented using sequencing data from an ever-growing set of study systems, but questions remain about the primary mode of interactions between multiple linked variants and their joint effects on genome-wide patterns of diversity.

Introduction

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Results

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Some results:

Discussion

Previous theoretical and simulation studies have shown that interference and interactions between selected mutations reduce the efficacy of selection at linked loci, impacting substitution rates, the deleterious muta-

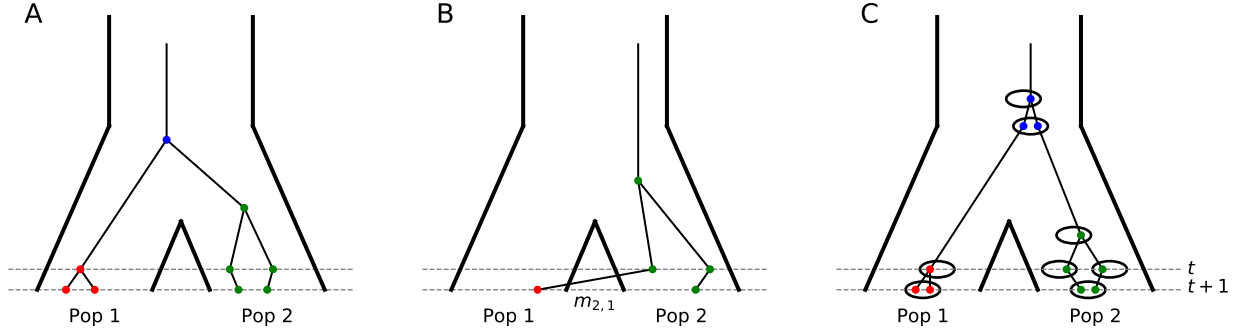


Figure 1: **Figure 1 caption.** This is the caption for figure 1.

tion load, and dynamics of segregating mutations (HILL and ROBERTSON, 1968; BIRKY and WALSH, 1988; BARTON, 1995; McVEAN and CHARLESWORTH, 2000).

Methods

Existing theory and numerical methods

Many well-known properties of two-locus dynamics and equilibrium LD come from early work on the multi-locus diffusion approximation (KIMURA, 1955; HILL and ROBERTSON, 1968; OHTA and KIMURA, 1969, 1971).

Moment equation for Ψ_n

The system of linear ordinary differential equations for the entries of Ψ_n takes the form

$$\Psi_n^{t+1}(i, j, k; t) = \mathcal{D}_{N(t)} \Psi_n^t + \mathcal{R}_r \Psi_{n+1}^t + \mathcal{U}_u \Psi_n^t + \mathcal{S}_{s_A, s_B, \dots, h_A, h_B, \dots} \Psi_{n+2}^t. \quad (1)$$

Here, $\mathcal{D}_{N(t)}$ is a sparse linear operator accounting for drift with population size $N(t)$, \mathcal{R} accounts for recombination with per-generation recombination probability r between the two loci, \mathcal{U} accounts for mutation, either under an infinite sites or biallelic reversible mutation model, and \mathcal{S} accounts for selection.

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