

Abstract Submitted
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Quantifying genetic diversity under a broad spectrum of deleterious mutations BENJAMIN GOOD, MICHAEL DESAI, Harvard University — Recent studies have shown that selection against deleterious mutations may play a major role in shaping observed patterns of sequence variation in natural populations. However, our understanding of these patterns remains limited, since selection creates correlations along the genome that are difficult to disentangle from each other. Previous theoretical work has focused on the qualitative effects of selection on sequence diversity, using simplified models in which all selected mutations have the same fitness cost. Yet it is known that deleterious mutations follow a wide distribution in most organisms, so it is necessary to extend our theoretical predictions to this more general case before we can make quantitative connections with existing data. The evolutionary dynamics of this regime are complicated: extant mutant lineages represent large, correlated fluctuations away from the background expectation, which hinders efforts to apply existing methods based on deterministic or “mean-field” approximations. Here, we will describe recent progress towards this goal, which is based on a “coarse-graining” of the underlying distribution of fitnesses in the population.

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