

# Selection in Space

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## ABSTRACT

Environmental heterogeneity has long been considered a likely explanation for the high levels of genetic variation found in most natural populations: selection in a spatially heterogeneous environment can maintain more variation. While this theoretical result has been extensively studied in models with limited parameters (e.g. two alleles, fixed gene flow and particular selection schemes), the effect of spatial heterogeneity is poorly understood for models with a wider range of parameters (e.g. multiple alleles, variable gene flow and more general selection schemes). We have compared the volume of fitness space that maintains variation in a single-deme model to the volume in a two-deme model for multiple alleles, randomly chosen selection schemes and varying levels of migration. Selection schemes were also analyzed in order to understand what quantitative properties are necessary to successfully maintain variation. Furthermore, equilibrium allele-frequency vectors were examined to see if particular patterns of variation are more prevalent than at first be expected.

The two-deme model successfully maintains variation for substantially larger volumes of fitness space than the single-deme model, especially for higher number of alleles and lower migration rates. The successful selection schemes have a higher average heterozygote advantage in the single-deme model than in the two-deme model and this result implies that selection schemes in the two-deme model can have a wider range of fitness patterns while still maintaining variation. The equilibrium frequency patterns emerging from the two-deme model are more variable than from the single-deme model and the patterns depend on both scale and migration rates. If the allele frequencies are averaged over both demes (i.e., over a larger scale), the allele frequencies tend to be similar to the single-deme model. However, if allele frequencies are observed in one of the demes (i.e., over a smaller scale), the allele frequencies tend to be much more skewed than the single-deme model, especially at lower migration rates.

In summary, the simulated spatial heterogeneity in our two-deme model improves the chances of the maintenance of genetic variation for a wide range of parameters, and the selection schemes maintaining variation further result in a wide range of different equilibrium allele frequencies.

**Keywords and phrases:** genetic variation, maintenance, selection, environmental heterogeneity, population structure