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Local adaptation under diversifying selection: A two-locus migration- selection model

A population-genetic model of local adaption in discrete space and time is studied. We model a population inhabiting two discrete demes with gene flow between them. Genetic drift is ignored as we assume that the population size is large. We consider two linked loci under selection and assume that the environment favors alternative alleles in the two demes. An important interpretation of the model is in terms of a quantitative trait that is under directional selection acting in opposite direction in the two demes. The trait is assumed to be determined additively, i.e., without epistasis, by two loci that may exhibit dominance. Thus, essentially, disruptive selection acts on the trait. This scenario allows us to answer interesting questions on local adaptation and the maintenance of genetic variation. We derive explicit results for the existence and amount of polymorphism in several limiting cases such as weak migration, weak selection, tight linkage, and free recombination. In particular, we present informative approximations of well-known measures of linkage disequilibrium and investigate the consequences of linkage and dominance on local adaption and genetic variation.

References

 Akerman, A., and R. Bürger. Local adaptation under diversifying selection: A two-locus migration- selection model. Manuscript (2011)