The use and misuse of regression models in landscape genetic analyses

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Abstract

The field of landscape genetics has been rapidly evolving, adopting and adapting analytical frameworks to address research questions. As landscape genetic analyses have shifted away from Mantel-based analytical frameworks, studies are increasingly using regression-based frameworks to understand the individual contributions of landscape and habitat variables on genetic differentiation. This paper outlines appropriate and inappropriate uses of multiple regression for these purposes. Of concern is the prevalence of studies seeking to explain genetic differences by fitting regression models with effective distance variables calculated independently on separate landscape resistance surfaces. When moving across the landscape, organisms cannot respond independently and uniquely to habitat and landscape features. Therefore, independent resistance surfaces and their effective distance measures have no mechanistic meaning or relevant statistical interpretation. There are also tremendous challenges to fitting and interpreting regression models that include 'independent' effective distance measures as predictors, including statistical suppression. As such, regression analyses seeking to understand how landscape resistance affects gene flow should be univariate models, with the creation of a single resistance surface being a necessary precursor to the regression analysis. There are, however, important statistical advances underway that explicitly model the covariance of allele frequencies or genetic distances as functions of spatial landscape variables. The growth and evolution of landscape genetics as a field has been rapid and exciting. It is the goal of this opinion paper to highlight past missteps and to ensure that future use of regression models will appropriately consider the process being modeled, which will provide clarity to model interpretation.

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