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Spatial pattern detection in genetic data

Landscape genetics studies using neutral markers have focused on the relationship between gene flow and landscape features. Spatial patterns in the genetic distances among individuals may reflect spatially uneven patterns of gene flow caused by landscape features that influence movement and dispersal. We present a method for identifying spatial patterns in genetic data that adopts a regression framework where the predictors are generated using Moran's eigenvectors maps (MEM), a multivariate technique developed for spatial ecological analyses and recommended for genetic applications. Using simulated and real genetic data, we show that our MEMGENE method can recover patterns reflecting the landscape features that influenced gene flow. We developed the MEMGENE package for R in order to detect and visualize relatively weak or cryptic spatial genetic patterns and aid researchers in generating hypotheses about the ecological processes that may underlie these patterns. MEMGENE provides a flexible set of R functions that can be used to modify the analysis.