Using IBMs to Investigate Spatially-dependent Processes in Landscape Genetics Theory

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Much of landscape and conservation genetics theory has been derived using non-spatial mathematical models. Here, we use a mechanistic, spatially-explicit, eco-evolutionary IBM to examine the utility of this theoretical framework in landscapes with spatial structure. Our analysis explores the following fundamental questions:

1. In well-connected landscapes exhibiting little genetic drift, how does isolation by distance (IBD) affect inferences of genetic structure?

2. In disconnected landscapes, how does drift interact with IBD, and thus affect inferences of genetic structure?

3. In poorly-connected landscapes, how effective is dispersal at homogenizing population structures resulting from both IBD and drift?

4. In poorly-connected landscapes, how does dispersal ability influence genetic structure when populations are subjected to IBD, drift, and selective pressure?

We use our study to examine the potential that eco-evolutionary IBMs have for contributing to landscape and conservation genetics theory.