ABSTRACT

INTEGRATING LANDSCAPE ECOLOGY AND POPULATION GENETICS:
CONVENTIONAL TOOLS AND A NEW MODEL

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The manuscripts in this dissertation apply different approaches to investigate the effect of landscape connectivity on genetic structuring in natural populations. In the first manuscript I used traditional molecular genetic analyses to examine the effects of habitat discontinuities on genetic structuring of pumas (Puma concolor) in the southwestern USA, where a high degree of habitat heterogeneity provides for a wide range of connective habitat configurations. Strong genetic differentiation between northern and southern populations indicates a historical split between pumas in the two regions, with little migration across habitat barriers separating them. Within each region, gene flow appears to be strongly limited by distance, with greater structuring apparent when habitat discontinuities exist between samples. Significantly greater genetic diversity in the south is consistent with a previous hypothesis of a Pleistocene extinction of North American pumas, followed by recolonization from more southern populations. The results of this study begin to complete a picture of how different habitat types facilitate or impede gene flow among puma populations.

The second manuscript describes a new model of gene flow in heterogeneous landscapes based on circuit theory. Although the model can be used to estimate effective migration and pairwise $F_{ST}$ values directly, its most promising use may be as an index of landscape connectivity, without the need to model demographic parameters explicitly. The latter approach may be particularly useful in correcting for limited habitat extent in studies of isolation by distance in natural populations. Because of its basis in population genetic theory and its ability to integrate all possible routes of interpatch movement simultaneously, the conductance model may also be an improvement over current methods used in conservation planning and in predicting genetic effects of landscape change.

The third manuscript tests the model with genetic data from North American wolverines (Gulo gulo) and Mesoamerican mahogany (Swietenia macrophylla). By correcting for limited and irregular habitat extent, the model produces a better fit to genetic data than do traditional models in both cases. I conclude with a chapter discussing the conductance model’s potential for use with finer-scaled datasets, such as the puma dataset described in the first manuscript.