**METHODS**

*Simulations to compare the performance of genetic distance metrics*

Although we were able to compare the results of resistance surface optimization using different metrics, and identify the ones with the highest fit, we cannot be certain that highest fit represents the most accurate metrics. Specifically, we cannot know whether the highest fit indicates models that most appropriately assign values and ranks to different resistance surfaces. In order to evaluate the performance of different metrics rigorously, we conducted spatially-explicit demo-genetic simulations using CDPOP (Landguth & Cushman, 2010) based on the lizard dataset (Beninde et al., 2016). In those simulations, we input resistance values for each level of the categorical variable and create a cost distance matrix based on this input landscape before running simulations where individual’s dispersal was constrained base of this cost distance matrix (Landguth & Cushman, 2010).

We respected the biology of *Podarcis* *muralis* in several aspects in the simulations. For example, we ranked the resistance values of different land cover categories meaningfully according to the general patterns found in the analysis of the empirical dataset. We constrained available habitat to land cover categories where they were originally sampled in large numbers (>20 individuals). Thus, we excluded river and very urbanized areas from carrying lizards in the lizards in the simulations, but lizards can potentially move through them. We also input reasonable parameters for reproductive ability (Ji & Braña, 2000) and density (Avery & Perkins, 1989; Barbault & Mou, 1988). We simulated 16 loci with 12 alleles each to mimic the original dataset (16 loci and an average of 11.81 alleles per locus).

To evaluate how the ecological and demographic contexts affect inference we considered two factors in the simulations: isolation-by-distance (IBD) strength (Wright, 1943), and the maximum absolute resistances values. We calculated IBD by relating Loiselle’s kinship (Loiselle et al., 1995) to the logarithm of the geographic distances between simulated individuals (Rousset, 2000). The slope in the original dataset was -0.013. We considered strong IBD scenarios to be more than 30% lower (larger absolute value) and weak IBD scenarios to be more than 30% higher (smaller absolute value) than the observed value. We achieved varying IBD by changing dispersal ability through several CDPOP parameters (Landguth & Cushman, 2010) in our simulated lizards. We set the resistance values for five levels of a categorical land cover variable in a biologically meaningful way (e.g., river is a barrier), following previous literature (Beninde et al., 2016) and our previous results on the empirical dataset. We designed low resistance scenarios to present two weakly resisting land cover categories, and high resistance scenarios to present two strongly and two weakly resisting land cover categories (Table X). as 20, 10, 70, 80, 1 and 1, 1, 8, 10, 1, for

For the high resistance scenarios IBD values ranged from -0.018 to

We increased the spatial grain of the landscape by a factor of three prior to simulations to achieve workable computation times for simulations and for subsequent optimizations. This should not affect our results much because spatial grain (i.e., cell size in our case) has been shown to have only limited effects on landscape genetics inference (Cushman & Landguth, 2010; McRae et al., 2008; McRae & Beier, 2007). This is especially true as we made sure to preserve the continuity of linear features in the landscape during the coarsening of the landscape grain (see Sup. Mat. 1).

**SUPPLEMENTARY MATERIAL**

***Function used to simulate and explore simulation results***