A forty-year-old divided highway does not prevent gene flow in the alpine newt *Ichthyosaura alpestris*. 

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Appendix A: Monmonier's Maximum Difference Algorithm

In individual-based genetic studies, Safner et al. (2011) recommended favouring Bayesian clustering methods to the expense of local edge detection methods (Appendices A), since the performance of the latter may be weakened by high within-individual genetic variability. Considering our own results, we argue that, taking into account this potential bias, their use may contribute to the evidence needed to correctly interpret observed genetic patterns.

Method: Monmonier's Maximum Difference Algorithm (Monmonier 1973) implemented in AIS (Miller 2005) identifies genetic boundaries between pairs of individuals (Dupanloup et al. 2002; Manni et al. 2004; Kuehn et al. 2007), along a connectivity network based on a Delaunay triangulation. We performed these analyses using residual genetic distances derived from the linear regression of all pairwise genetic distances on Euclidean distances (Manni et al. 2004; Miller 2005). For each sex, the number of barriers to detect was set to 4 (the number of distinct LTI sections; Fig. 1).

Results: Barriers inferred using the Monmonier's algorithm were mainly located close to one individual or only a few neighbours (all barriers in males and the fourth one in females, Fig. A). These barriers actually indicated individuals distinct from their direct neighbours and were not interpretable as boundaries. However, the three first barriers detected in females (Fig. A-b) were connected and thus consistent with the presence of a landscape barrier to gene flow. They segregated south-eastern females from the rest of the study area, as did the combination of boundaries II and IV detected with second and third sPCA scores in females (Fig. 4c-d).
**Figure 1.** Four genetic barriers detected by Monmonier’s algorithm implemented in AIS (Miller 2005), numbered from 1 (bold black lines) to 4 (thin black line) and projected over Figure 1b; (a) in males (dataset M); (b) in females (dataset F).
Appendix B: Age structure in CDpop simulations

Figure 2. In CDpop simulations (Landguth and Cushman 2010), the age structure was defined according to a normal distribution with a mean $\mu = 0$ and a standard deviation $\sigma = 5$. As a result, the maximal longevity of individuals was 18 years. X-axis: Age of individuals. Y-axis: Probability distribution.

$$Y = \frac{1}{\sigma\sqrt{2\pi}} \times e^{-\frac{(X-\mu)^2}{2\sigma^2}}$$

$\mu = 0$

$\sigma = 5$
Literature cited


