

A landscape genomics approach to understanding and predicting species distribution

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In habitat modelling, an initial step is to define geoenvironmental variables to be included in a predictive model. According to Guisan and Zimmermann (2000), the selection of predictors can be made either arbitrarily, automatically by stepwise procedures, by following physiological principles (expert's decision), or by following shrinkage rules ("Ridge" or "Lasso" regression). I propose an alternative to select predictive variables based on the identification of loci likely to be under natural selection.

Indeed, it is possible to profit from the results provided by a recently developed Spatial Analysis Method SAM (Joost et al. 2007; Joost et al. in press) and to exploit the fact that identified environmental parameters possibly select particular regions of the genome analysed. As identified alleles possibly are selected, one can postulate that environmental parameters significantly associated with them play a role favouring the presence of a studied species in a given landscape, and that they participate in constituting an ideal habitat for the animal.

Once environmental variables involved in the most significant association models have been highlighted with SAM, it is necessary to confirm the outlier status of identified loci. This can be done with Fdist2 or Dfdist according to the type of marker used (Beaumont and Balding 2004; Joost et al. 2007). Then, only the association models for which loci were confirmed to be outliers are taken into account in the analysis. The different environmental variables involved in these models can be used as predictors and combined to calculate predictive models of habitat with the help of any standard habitat modelling method.

In the Scandinavian Brown Bear case study, data consist of 17 microsatellite loci extracted from 728 Brown Bears sampled across Scandinavia from 1985 to 2004 (Waits et al. 2000; Manel et al. 2004; Bellemain et al. 2005). The frequency of 181 alleles were compared to ten environmental variables, for a total of 1810 univariate models calculated to search for loci under selection. I applied an ordinary multiple regression in its generalized form (GLM) to the 4 selected predictors (percent of maximum sunshine, temperature, number of days with ground frost, coefficient of variation of precipitations) to produce maps showing the potential habitat of the Scandinavian Brown Bear (different combinations of selected predictors).

References

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3 Relevant publications

- Joost S, Bonin A, Bruford MW, Després L, Conord C, Erhardt G, Taberlet P (2007) A Spatial Analysis Method (SAM) to detect candidate loci for selection: towards a landscape genomics approach to adaptation. *Molecular Ecology*, 16, 3955–3969.
- Joost, S., Kalbermatten, M., Bonin, A. (In press) Spatial Analysis Method (SAM): a software tool combining molecular and environmental data to identify candidate loci for selection, *Molecular Ecology Resources*.
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