Towards well-informed species distribution models to reconstruct species' past distribution

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Abstract

Climate change pushes species to redistribute or evolve to adapt to new conditions. To hindcast and forecast species redistribution under past and future climate, the state-of-the-art is to use all available information (e.g., presence-absence data, range maps) about the current species' distribution and relate it to climatic conditions, an approach known as species distribution models (SDMs). Traditional SDMs use all populations of a given species to encapsulate the species' climatic niche, an appropriate approach for interpolation purposes. However, when hindcasting a species distribution into the past based on current data for extrapolation purposes, the use of all extant populations of a given species to calibrate SDMs can be misleading as it may inflate the species' climatic niche width. Here, we hypothesize that SDMs calibrated either with (H1) basal lineages more likely to represent the common ancestor or (H2) populations from the migration front (i.e., leading edge) that are most likely to show higher levels of niche conservatism should lead to better reconstruction of the past distribution than SDMs calibrated with all populations. To test those hypotheses, we analysed distribution data from two species for which there is stablished phylogeographic structure: the brown snail *Cornu aspersum* and the European beech *Fagus sylvatica*. We calibrated and compared model performances between three types of SDMs: (i) a baseline SDM for all populations; (ii) a lineage-specific SDM based on basal lineages most likely to represent the common ancestor occurring during the last glacial maximum (LGM); and (iii) a leading-edge SDM based on populations from the postglacial re-colonisation front. All SDMs were calibrated with present data before hindcasting the past distributions during the LGM. Our preliminary results suggest that focusing on populations from the leading edge (H2) may contribute to more realistic reconstruction of species' past distribution.

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