Are no-analogue climates a barrier to accurate projections into the past? Into the future?

Using a boosted regression trees classifier (random forest), we with two general circulation models (GCMs) for 24 western North American tree species at the last glacial maximum (LGM). The degree of novel arrangement of climate variables was quantified with a multivariate Mahalanobis distance to the nearest modern equivalent. Model projections were validated against 226 palaeoecological records (6). Summary: Misclassification rates for forest ecosystems were strongly correlated with levels of climate dissimilarity (n=0.99, p<0.001, n=9). Areas of mis-classification visually corresponded to areas of high climatic dissimilarity. While no-analogue climates are prevalent at the last glacial maximum, in future projections they emerge only in isolated areas. The degree of no-analogue predicted for the zonos is similar to mid-to-late Holocene climate conditions, in which model accuracy remains high. We therefore conclude that, with localised exceptions which may be identified, no-analogue climates should not compromise the accuracy of model predictions for the coming century in this region (6).

How did glacial range dynamics and species’ refugial histories affect modern genetic diversity?

Cold temperatures and extensive continental ice sheets dominated North America through the Pleistocene, restricting species ranges (1). We used an ensemble ecological niche model (2,3) based on climate variables to predict habitats for 23 western North American tree species at the last glacial maximum. We quantitatively assess the relationship between species’ refugial patterns and their modern genetic diversity, testing the hypothesis that species with less observed diversity were more geographically restricted during the last glaciation. Summary: While tree species ranges at the last glacial maximum account for much of the observed difference in modern allelic richness whereas the relationship with heterozygosity is limited. This suggests that population bottlenecks have a greater effect on rare alleles rather than on the representativeness of more common alleles (4).

Are independent validations of ecological niche model projections necessary?

To assess the realism of habitat projections in the context of climate change, we conduct independent evaluations of twelve species distribution models (3), including three novel ecosystem-based modelling techniques. Habitat hindcasts for 24 western North American tree reconstructions, were validated against 33 palaeoecological records from 6, 14, 16 and 21 thousand years before the present (2,3). We also evaluate regional extrapolations based on geographic splits of 500 sample plots, projecting from Canada to the USA (north-to-south) to simulate a warming climate.

Summary: Model accuracy declines across all techniques and all species when subject to independent validations, confirming previous research (4). However, we found high correlations between AUC (accuracy) values for non-independent and independent validations (r=0.70, p<0.02; r=0.89, p<0.01, n=24). We also found little evidence of model over-parameterisation. Independent model validations are important to determine absolute model accuracy. However, for individual model methods, that said, ensemble methods are most effective (5) and benefit even from the inclusion of poor-performing individual methods.