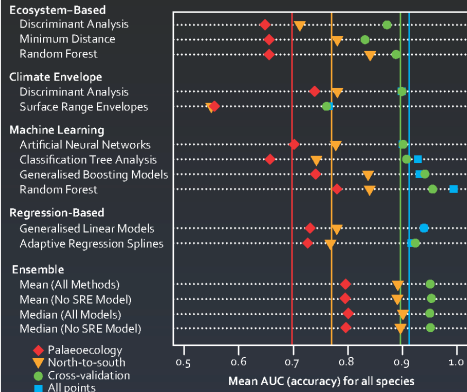


# The refugial history of western North American trees and the lasting effect on genetic diversity: a modelling approach

David R. Roberts<sup>1</sup> & Andreas Hamann<sup>1</sup>

<sup>1</sup> Department of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada



## 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 two species distribution models (1), including three novel ecosystem-based modelling techniques. Habitat hindcasts for 24 western North American tree reconstructions, were validated against 931 palaeoecological records from 6, 11, 14, 16 and 21 thousand years before the present (2,3). We also evaluate regional extrapolations based on geographic splits of 55 000 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 ( $r=0.70$ ,  $p=0.012$ ;  $r=0.89$ ,  $p<0.01$ ,  $n=24$ ). We also found little evidence of model over-parameterisation. Independent model validations are important to determine absolute model accuracy. However, for individual model method That said, ensemble methods are most effective (5) and benefit even from the inclusion of poor performing individual methods.

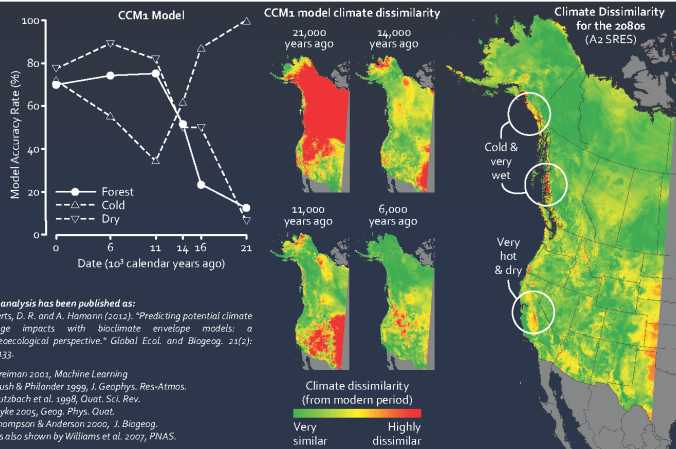
This analysis has been published as: Roberts, D. R. and A. Hamann (2012). "Method selection for species distribution modelling: are temporally or spatially independent evaluations necessary?" *Ecography*, In Press.

- (1) Thuiller 2009, *Glob. Change Biol.*
- (2) Dylke 2009, *Geog. Phys. Quat.*
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## Are no-analogue climates a barrier to accurate projections into the past? Into the future?

Using a boosted regression trees classifier (random forest, 1) with two general circulation models (NOAA-GFDL and CCM1) (2,3), we hindcast ecoregions for western North America for 6000, 9000, 11000, 16000, and 21000 years ago 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 1226 paleoecological records (4, 5).

**Summary:** Misclassification rates for forest ecosystems were strongly correlated with levels of climate dissimilarity ( $r=0.90$ ,  $p<0.001$ ,  $n=9$ ). Areas of mis-classification visually corresponded to areas of high climate 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-analogues predicted for the 2080s 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).



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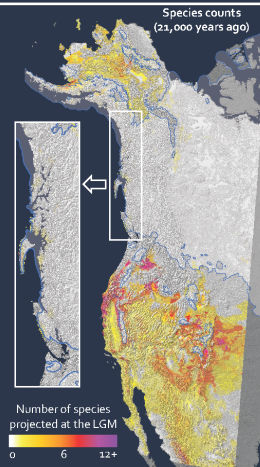
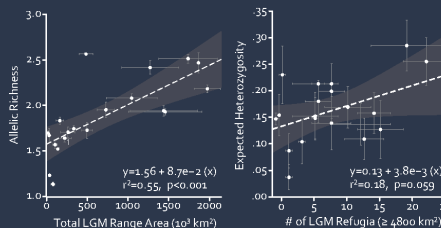
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## How did glacial range dynamics and species' refugial histories affect modern genetic diversity?

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 hindcast habitats (i.e. refugia) 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 representative evenness of more common alleles (4, 5).

Localised hotspots of glacial refugia emerge throughout North America in the projections for the LGM. This result offers support for phylogeographic hypotheses suggesting post-glacial dispersal of different species from inland and coastal areas in both the north and south of the continent (6). The models also offer strong support for refugia along the Pacific Coast, notably in the Haida Gwaii, as has been suggested by genetic investigations (7). A consistent shortcoming in the models is the lag of projected species ranges behind the fossil record in the Pacific Northwest USA, which could be attributable to the emergence of no-analogue climates in this region at the LGM.



- Submitted for publication: Roberts, D. R. and A. Hamann (2012). "Quaternary analyses of glacial ranges predict modern genetic diversity in western North American trees."
- (1) e.g. Hewitt (2000), *Nature*.
- (2) Thuiller et al. (2009), *Ecography*.
- (3) Roberts & Hamann (2012), *Glob. Ecol. Biog.*
- (4) As theorised by Nei et al. (1975), *Evolution*.
- (5) Corresponds with Camps et al. 2004, *Genetics*.
- (6) e.g. Hamrillo-Correa & Beaulieu 2009, *PLoS*.
- (7) e.g. Godbout et al. 2008, *Molecular Ecol.*

