***Appendix S2. Evaluating potential issues with model extrapolation and clamping***

In our main niche models, we restricted the background points used for model calibration to the MCP representation of each species’ range. As a result, depending on how well a given MCP captures the true range limits of a species in the region where the transplant study was conducted, transplant sites (both in-range and over-the-edge) may fall outside of the boundaries from which background points were sampled (see Appendix S1). Thus, it is possible that the range of environmental values used to calibrate the models did not include those found at the transplant sites. Making predictions for sites that fall outside of the range of values used to calibrate a given model requires extrapolation and maxent attempts to mitigate this potential problem via “clamping” (Elith et al. 2010). Clamping may also be applied to derived features (i.e. the combination of environmental values and model coefficients) during the prediction phase. As clamping may affect the relative suitability assigned to sites during the prediction stage (via its effects on the constants and scaling parameter of the final model produced at the calibration stage), the potential effects of model extrapolation and clamping require specific examination.

To identify sites affected by model extrapolation and/or clamping, we did two things. First, using an approach similar to that proposed by Elith et al. (2010), we assessed whether environmental conditions at a given transplant site were more extreme than the range of values used during model calibration. Specifically, for each of the PC axes retained in the ENM for a given species, we determined whether the PCA scores for any of the transplant sites were outside of the range of values used for model calibration (values at presence and randomly chosen background points). Second, we examined the clamping grid files produced by maxent during the prediction step. These files specify the difference in the predictions for each site with and without clamping (sites affected by clamping will have non-zero values in these files).

Of the 223 transplant sites examined, only nine sites from four species were influenced by model extrapolation or were otherwise influenced by maxent’s clamping procedure. This list included both in-range and over-the-edge sites in roughly equal frequency (Table S2-1). In most cases, the effects of clamping were small relative to the predicted suitability of the site. However, for most of the affected sites, the difference between predictions with and without clamping was larger than the minimum difference between the prediction for the site and any other site (i.e. values >1 in the last column, Table S2-1). Thus clamping might affect the relative differences in suitability in comparisons involving these sites (although to affect the overall conclusions for a given species, only the comparisons between in-range and over-the-edge sites matter).

To fully explore the impact of these effects on our final results and conclusions we did two things. First, we repeated the downstream analyses with these sites excluded (Table S2-2), a conservative approach that presumes that no inferences about suitability can be drawn for sites with conditions falling outside of the range of values used during calibration. Second, we repeated the entire set of analyses from the modeling calibration step forward, this time turning off clamping for all species with the “dontdoclamp” argument. All results were robust to these changes (Tables S2-2, S2-3) and thus extrapolation and clamping do not appear to be of consequence in our analysis.

Table S2-1. Information about sites with predictions affected by model extrapolation and/or clamping.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Species | Site type | Number PC axes outside range of training data  (Total number PC axes in model) | Predicted suitability | Effect of clamping\* | Relative effects of clamping on differences in suitability† |
| *Abutilon theophrasti* | out | 1 (6) | 7.95E-05 | 3.53E-05 | 0.00028 |
| *Camissoniopsis cheiranthifolia* | in | 1 (3) | 0.90 | 2.20E-05 | 0.0093 |
| *Camissoniopsis cheiranthifolia* | in | 1 (3) | 0.90 | 0.094 | 39.79 |
| *Camissoniopsis cheiranthifolia* | out | 1 (3) | 0.87 | 0.11 | 7.73 |
| *Chamaecrista fasciculata* | in | 1 (6) | 0.35 | 0.025 | 0.312 |
| *Chamaecrista fasciculata* | out | 1 (6) | 0.27 | 0.069 | 2.059 |
| *Chamaecrista fasciculata* | out | 1(6) | 0.070 | 4.18E-05 | 0.00024 |
| *Protea aurea* | in | 1 (3) | 0.91 | 0.014 | 0.78 |
| *Protea aurea* | out | 1 (3) | 0.93 | 0.028 | 1.59 |

\* Values reflect the difference in predictions with and without clamping and were obtained from the “clamping.asc” files produced using maxent’s density.project function

† Calculated as the ratio of the effect of clamping to the minimum difference in the predicted suitability of the focal site and any other site (ignoring clamping effects on the latter set and not distinguishing between in-range and over-the-edge comparisons). Values greater >1 signal potential rank order of suitability of sites could be affected.

Table S2-2. Differences in the suitability of transplant sites across range limits when sites affected by clamping were removed from the analysis and when all sites were included but clamping was disabled during model calibration. Comparisons between the full and reduced model (i.e. without site type) were based on likelihood ratio tests (LRT). Significant values (p<0.05) are in bold.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Range Type | Sensitivity Test | Mean coefficient (SE) | LRT | p value |
| Combined | Sites affected by extrapolation/ clamping removed (n = 37) | -0.28 (0.060) | LRT4,3=20.76 | **<0.0001** |
| All sites included but clamping disabled (n = 40)\* | -0.28 (0.057) | LRT4,3=23.12 | **<0.0001** |
| Horizontal | Sites affected by extrapolation/ clamping removed\* (n=22) | -0.54 (0.098) | LRT5,4=26.23 | **<0.0001** |
| All sites included but clamping disabled | -0.34 (0.065) | LRT4,3=24.37 | **<0.0001** |
| Vertical | Sites affected by extrapolation/ clamping removed\* (n=18) | -0.47 (0.084) | LRT6,5=23.54 | **<0.0001** |
| All sites included but clamping disabled | -0.22 (0.052) | LRT4,3=15.86 | **<0.0001** |

\* To improve homoscedasticity, variances were allowed to vary by site type.

Table S2-3. Concordance between the direction of the change in the performance of individuals (best fitness proxy) and the suitability of sites across range limits when sites affected by clamping are excluded and when all sites were included but clamping was disabled during model calibration. The results are based on binomial tests with probability of success = 0.5. Significant values (p<0.05) are in bold.

|  |  |  |  |
| --- | --- | --- | --- |
| Range Type | Sensitivity Test | Number of species with fitness and suitability changing in the same direction | p value |
| Combined | Sites affected by extrapolation/ clamping removed (n = 37) | 28 | **0.0026** |
| All sites included but clamping disabled (n = 40) | 31 | **0.00068** |
| Horizontal | Sites affected by extrapolation/ clamping removed (n=22) | 14 | 0.29 |
| All sites included but clamping disabled (n=25) | 17 | 0.11 |
| Vertical | Sites affected by extrapolation/ clamping removed (n = 18) | 14 | **0.031** |
| All sites included but clamping disabled (n=19) | 15 | **0.019** |