

Appendix 6: Comparisons of threshold selection rules

Converting SDM output to presence-absence predictions via thresholds is problematic with presence-only data. Various studies recently pointed out that the best-performing rules of threshold selection require knowledge of model sensitivity and specificity (i.e., presence and absence data; Bean et al. 2012). Suboptimal threshold selection has been related to the trend for overprediction in biodiversity estimation from SDM-derived range maps (Calabrese et al. 2014). Our data, as with any SDM data for poorly known taxa, does not contain reliable absence information for most species, and hence has to rely on other thresholding rules. However, we investigated effects of thresholding with two approaches.

First, for species with balanced amounts of presences and absences, we found very similar threshold rules, whereas recommended thresholds led to high omission error for species with highly unbalanced data. Second, we estimated richness by stacking non-thresholded SDM output (as suggested by Calabrese et al. 2014). These data correlated not much better with observed species richness than thresholded data did, but it underpredicted data to a similar degree as thresholded data overpredicted. We tentatively conclude that threshold-based data are not worse, and possibly better, than species richness data based on non-thresholded SDM output.

Presences and absences of species was measured at 'well-sampled' 5 km grid cells (see Methods), which were then used to calculate 'true' AUC_{TS} and set thresholds (Thr) according to the *sensitivity equals specificity* (S=S), *maximum sensitivity+specificity* (maxS+S) and *ROC curve closest to point (0,1)* (ROCplot) -rules. Minimum predicted area (MPA) thresholds (in ***bold italics***) were used for all species in this study, as they do not require absence information.

The last column (%Rng) gives the differences in range sizes according to MPA and S=S thresholds, as percentage of MPA-derived ranges (positive number: MPA gives larger range). For species of moderate prevalence at test sites, AUC, thresholds and therefore range assessments did not vary much between different selection rule.

However, for species with very high prevalence (>0.7) we found substantial differences, notably much higher thresholds and therefore smaller range estimates for S=S and maxS+S, in comparison to MPA. A comparison of range maps to recorded presences (S2.9) for these species reveals huge omission error, i.e. prediction of absence in regions where the species has been recorded at hundreds of sites (e.g. Western Europe, South Korea). We conclude that these high thresholds certainly do not lead to better range prediction, presumably because high prevalence at test sites biased the calculation of recommended threshold.

Species	Test sites (TS)	Prevalence at TS	AUC _{Mx}	AUC _{TS}	<i>Thr</i> _{MPA}	<i>Thr</i> _{S=S}	<i>Thr</i> _{maxS+S}	<i>Thr</i> _{ROCplot}	%Rng _{MPA-S=S}
<i>Cephonodes hylas</i>	31	0.581	0.853	0.821	0.272	0.25	0.3-0.33	0.25	-4.8
<i>Delephila elpenor</i>	38	0.605	0.672	0.762	0.082	0.13	0.06-0.08	0.06-0.08	11.5
<i>Hyles livornica</i>	34	0.412	0.819	0.760	0.056	0.04	0.04	0.04	-6.8
<i>Laothoe populi</i>	21	0.857	0.747	0.259	0.121	0.48	0-1	0.28-0.31	66.9
<i>Smerinthus ocellata</i>	19	0.895	0.808	0.190	0.150	0.56	0.83	0.56	77.9
<i>Sphinx ligustri</i>	28	0.714	0.667	0.269	0.097	0.38	0.53-0.62	0.04-0.09	55.1

References

- Bean WT, Stafford R, Brashares JS (2012) The effects of small sample size and sample bias on threshold selection and accuracy assessment of species distribution models. *Ecography* 35:250–258
- Calabrese JM, Certain G, Kraan K, Dormann CF (2014) Stacking species distribution models and adjusting bias by linking them to macroecological models. *Glob. Ecol. Biogeogr.* 23:99–112

Comparison of *minimum predicted area* thresholds (as used throughout this study; left column, black) with *sensitivity = specificity* thresholds (right column, purple; based on presence/absence at 'well-sampled' sites, Fig. 2 of main text) for 6 widespread species. The central column shows presence records for each species (black = precisely georeferenced, used for modelling; grey = georeference precision 1°, not used for model fitting).



