

Ecography

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Supplementary material

Appendix 1

Model assessment

We sampled model parameters while ignoring data, which effectively sampled from model priors. However, sampling without the constraints of data led the Markov chain to wander into parameter space where computation was numerically unstable, particularly for parameters associated with migration ($\beta_{M,k}$, α_k , and the parameters of their gamma hyperdistributions) and precision of normal distributions. To prevent this problem, we truncated distributions of $\beta_{M,k}$, α_k , and the parameters of their gamma hyperdistributions to lie between 10^{-10} and 10^{10} and truncated the lower bound for precision of normal distributions at 10^{-10} . We found that estimated $\beta_{M,k}$ parameters, determining species-specific importance of putative migration, tended to be much closer to zero than parameters inferred from actual data, with sample medians of $\beta_{M,k}$ for all species equal to zero. We also found that these parameters decreased as we further lowered the truncation point, thus without truncation and data the model would likely estimate even lower values for migration parameters.

We also ran our model using permuted occurrence data, that kept island differences in richness and species difference in occurrence constant (Gotelli and Entsminger 2001). We similarly found very low estimates for the importance of migration. The mean of the gamma hyperdistribtuion was 0.040 (compared to 0.264 on real data) and the variance was 0.007 (compared to 0.069 on real data), and only three species had $\beta_{M,k} > 0.1$, compared to 196 species for the real data.

To assess the influence of quantile choice in regressing HWI versus $\beta_{M,k}$, we also test 75th and 95th percentiles of $\beta_{M,k}$ for quantile regression. Both values gave similar

results (75th percentile: posterior median of quantile regression coefficients, β_{med} , between HWI and $\log \beta_{M,k}$, $\beta_{\text{med}} = -0.025$, 95% CI = -0.033, -0.017 log units $\beta_{M,k}$ / unit HWI; 95th percentile: $\beta_{\text{med}} = -0.040$, 95% CI = -0.052, -0.021).

Figure A1. Alternative version of Figure 4 in the main text, treating subspecies as full species. Top panel: importance of putative dispersal ($\beta_{M,k}$), and bottom panel: scale of distance decay for subspecies, versus HWI. Circle size is proportional to the variance in occurrence across islands, which affects power. The lines represent 0.9 quantile regressions of $\log(\beta_{M,k})$ on HWI, and linear regression of α_k on HWI, respectively.

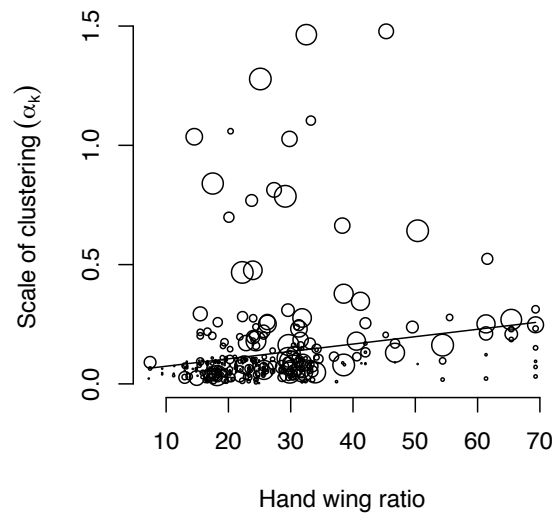
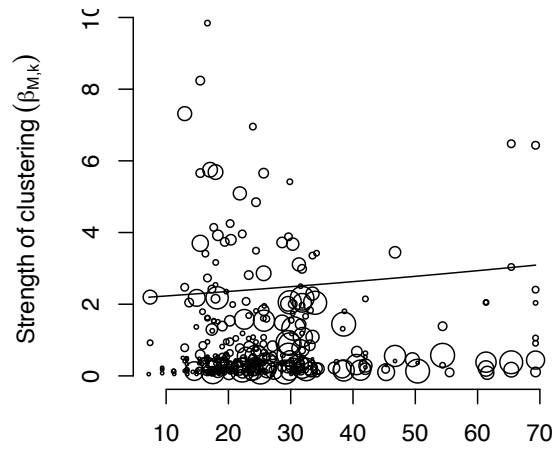


Figure A2. Strength of clustering versus estimated abundance categories from Mayr & Diamond (2001) with 5 indicated the greatest local abundance and 1 indicated the locally rarest species.

