

Borrowing information: Hierarchical multispecies distribution models

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Abstract: There are not enough readily available data to accurately predict the distribution of rare or difficult to detect species using conventional species distribution modelling techniques. To fill this gap, I constructed a hierarchical, Bayesian, multispecies detection-occupancy model with functional trait-based hyper-distributions in order to ‘borrow information’ from common species to help predict distributions of rare species. Regression coefficients and intercepts vary for each species and are informed by trait-based hyper-distributions. The model accounts for imperfect detection as well as including random effects to account for residual variation. I compare performance of this multispecies distribution model to progressively simpler models, and those models to each other, along a species prevalence gradient for woodland-dependent birds of the highly-fragmented box-ironbark forests of southeastern Australia. I evaluate if, and by how much, model performance is improved with respect to accuracy, precision and bias by the addition of random effects, hierarchical structures, functional traits and detection-occupancy modelling. I ask: can species distributions be accurately and precisely predicted without bias in the absence of occurrence data? Overall, the addition of a hierarchical structure, without traits, improved accuracy and precision of the model. The subsequent addition of random effects decreased precision to lower than a basic logistic regression with all species modelled independently, a comparatively more honest representation of the confidence in the predictions. Before accounting for imperfect detection, low prevalence species occurrence probability tends to be well predicted by simpler models because of a potentially false high certainty of low probability of occurrence.