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# Sharing detection heterogeneity information among species in community models of occupancy and abundance can strengthen inference

The estimation of abundance and distribution and factors governing patterns in these parameters is central to the field of ecology. The continued development of hierarchical models that best utilize available information to inform these processes is a key goal of quantitative ecologists. However, much remains to be learned about simultaneously modeling true abundance, presence, and trajectories of ecological communities. Simultaneous modeling of the population dynamics of multiple species provides an interesting mechanism to examine patterns in community processes and, as we emphasize herein, to improve species-specific estimates by leveraging detection information among species. Here we demonstrate a simple but effective approach to share information about observation parameters among species in hierarchical community abundance and occupancy models, where we use shared random effects among species to account for spatiotemporal heterogeneity in detection probability. We demonstrate the efficacy of our modeling approach using simulated abundance data, where we recover well our simulated parameters using N-mixture models. Our approach substantially increases precision in estimates of abundance compared to models that do not share detection information among species. We then expand this model, and apply it to repeated detection/non-detection data collected on six species of tits (Paridae) breeding at 1191 km sq. sampling sites across a P. montanus hybrid zone in northern Switzerland (2004-2020). We find strong impacts of forest cover and elevation on population persistence and colonisation in all species. We also demonstrate evidence for interspecific competition on population persistence and colonization probabilities, where the presence of marsh tits reduces population persistence and colonisation probability of sympatric willow tits, potentially decreasing gene flow among willow tit subspecies. While conceptually simple, our results have important implications for the future modeling of population abundance, colonization, persistence, and trajectories in community frameworks. We suggest potential extensions of our modeling in this paper, and discuss how leveraging data from multiple species can improve model performance and sharpen ecological inference.