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A comparison of predictive performance of joint species distribution models for presence-absence data

While there has been substantial literature on the evaluation of predictions from single species distribution models, the topic of prediction has only recently begun to be addressed for joint species distribution models (JSDMs). These studies have been limited in what aspects of prediction they cover: limited selection of models being compared, limited number of evaluation metrics, and/or not comparing the different prediction types available to JSDMs. In this study we perform a large scale comparison of the predictive performance of eight models: two stacked species distribution models (SSDMs) and six JSDMs. We fit these models to 22 real and simulated datasets, undertake four JSDM prediction types, and evaluate up to 32 metrics from five different classes that analyse different aspects of species distributions and the community assemblage process. We found that likelihood-based metrics indicated the JSDMs were better fit to the data than the SSDM, but that most other metric classes showed the SSDM outperforming the JSDMs by generally small amounts. The spatial and non-spatial implementations of the hierarchical multivariate probit regression model with latent factors typically performed better than the other JSDMs, but overall still performed worse than the SSDM. The SSDM predictions constrained with the spatially-explicit species assemblage modelling framework (SESAM) consistently outperformed both the SSDM and all JSDMs for both species- and community-level metrics. Our results indicate that despite the additional inference they provide about the community assemblage process by accounting for the residual association between species, JSDMs generally perform worse predictions than stacked single species models when evaluated at either the species or community level. The strong performance of the SESAM framework suggests that applying it to JSDM predictions is an interesting future avenue of research.