Predicting diversity with Joint Species Distribution Models: a difficult case with species rich marine benthic communities

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Résumé

Predicting how communities respond to change in abiotic and biotic conditions is essential to understand their functioning. Species Distribution Models (SDM) can provide insights on how environmental filtering determine species occurrence. However, these methods assume statistical independence between species within a community. Joint Species Distribution Models (JSDM) recently emerged to address this limitation by modeling species community responses to environmental conditions simultaneously and by including latent variables accounting for residual correlations in species occurrences. Here, we asses the ability of a Bayesian JSDM implementation called Hierarchical Modelling of Species Communities (HMSC) to predict variability in (1) species occurrences, (2) species richness, (3) community structure in coastal marine benthic communities. We use a large marine benthic monitoring dataset that comprises 23 different sites sampled around Brittany over 8 years and tallies the abundance of 278 benchic species in two contrasted habitats. By including different combinations of environmental, taxonomic and trait data as explanatory variables, we assess predictive performances of 6 alternative HMSC models validated against independent data. We specifically analyse discrepancies in species and community-level predictions across space, habitat and time, and between alternative models. Thus, our results describe the trade-offs between model predictive performance and complexity, which varies with the use of presence-absence or abundance data and the inclusion of taxonomy and traits data.

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Mots-Clés: Species Distribution Models, Joint Species Distribution models, HMSC, Marine Benthic Communities