Using hierarchical null models to study the assembly of fungal communities

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Abstract:
The study of assembly rules can inform us about the relative roles of dispersal, abiotic and biotic filters in structuring biological communities. The target of our work is arbuscular mycorrhizal fungi (AMF), a globally-distributed group of microorganisms that form an important symbiosis with most land plants. These organisms can be effectively identified from environmental samples using DNA-based methods, and their global taxonomic diversity appears to be low in comparison, for example, with that of their plant hosts. These characteristics allied to the fact that coarse global distribution data and a comprehensive phylogeny are available for AMF make analysis of the rules governing their assembly more tractable than for more mobile or abundant taxa.

We attempt to characterize the role of different processes influencing AMF community assembly using a series of hierarchical null models. The basis of the analysis is 'site by species' tables populated by counts of sequencing reads recorded for particular sample and fungal taxon combinations. The influence of different filters is assessed by generating randomized matrices corresponding to a null model (i.e. a null hypothesis). Here we discuss some assumptions of assembly rules (including phylogenetic assembly rules), decisions concerning the design and implementation of null models, and the ecological and biogeographical conclusions of the study.