
Using metacommunity graphs to address multiscale biodiversity dynamics – application to French meadows.

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Abstract

A challenging issue of community ecology is to acknowledge and relate both local assembly rules and large-scale environmental gradients and biogeographical influences. Analyzing occurrence and co-occurrence patterns in metacommunity graphs (or networks) sheds light on these entangled processes. Specifically, characterizing the modularity of these bipartite networks allows addressing the nature of species pools and ecological filters operating from regional to local scale. We show that the partition of sampling sites and species into modules can be used to address the extent of biogeographical, abiotic and biotic constraints on species distributions. We propose a novel way to characterize ecological specialization on the basis of this partition. We apply the approach to an extensive dataset of meadows plant communities from the DIVGRASS project, including around 70 000 sampling sites and more than 4000 species. We identified basic functional and biogeographic modules of the network representing distinct species pools. We then addressed the influence of dispersal limitation and habitat filtering on the spatial extent of these pools. Spatial mismatch between the extent of the pools and potential species distributions reveals historical limitation in recolonization from refugia. We further addressed the relationship between species specialization in the metacommunity, species functional traits and local environmental constraints. We also address non-random patterns of co-occurrence within and between modules to address the nature and the spatial scaling of biotic interactions. We underline the promise of using metacommunity graphs as a basic framework to disentangle the ecological and biogeographical drivers of biodiversity dynamics.

Keywords: Metacommunity, network, plant

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