

A Bayesian network approach to trophic metacommunities shows habitat loss accelerates top species extinctions

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Abstract

We develop a novel approach to trophic metacommunities and use it to study the effect of habitat loss on food webs. Our method assigns a spatially realistic Levins-type metapopulation model to each species, then couples them by making species extinction rates depend on the likelihood of the presence of species' prey items via a Bayesian network representation of the food web. The method yields general insights into metacommunity ecology, revealing that metacommunity processes alone can restrict the maximum number of trophic levels to a handful at most over fragmented landscapes, independent of energetic or other constraints. It also allows one to repurpose known results of classical metapopulation theory for metacommunities, such as ranking the habitat patches of the landscape with respect to their importance to the persistence of the metacommunity as a whole. Using these tools, we explore how progressive habitat loss affects species extinction rates. The outcome depends on the order of habitat removal: focusing on removing patches which are least crucial to persistence first (best-case scenario) means the metacommunities can often tolerate the removal of more than 90% of their patches. Whereas removing the most crucial patches first (worst-case scenario) leads to the collapse of metacommunities very quickly. Surprisingly, removing patches at random is nearly indistinguishable in its effects from the worst-case scenario. In all cases, species' vulnerability to habitat loss is greater at higher trophic levels, stressing the risk of network downsizing for food webs under progressive habitat loss.

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