Distinguishing community assembly through functional redundancy models.

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Simplified habitat complexity leads to a decrease in biodiversity. For instance, when we opt for less diverse diets, we reduce the range of chemicals available to our gut microbes, resulting in lower diversity and potentially harming our digestive health. Similarly, monoculture farming, instead of polyculture, reduces the availability of nutrients to soil microbes, leading to soil fertility loss. Functional redundancy, which refers to the number of species performing a specific function in a community, is crucial for ecosystem stability. However, the impact of habitat simplicity on functional redundancy remains unclear. To address this question, we used a metacommunity framework to create models that explore how functional redundancy changes with ecosystem complexity under two community assembly scenarios: environmental filtering and niche partitioning. We derived analytical approximations for these models, when all taxa use the same number of resources and that all resources are used by the same number of species. In the environmental filtering model, species in the local community survive by finding the necessary resources. In contrast, the niche partitioning model involves species in the local community competing for resources while also meeting their persistence requirements. Our findings from the environmental filtering model suggest that functional redundancy remains constant concerning local habitat complexity. However, in the niche partitioning scenario, we observe that functional redundancy increases as local habitat complexity rises. This leads to a testable hypothesis that can be compared with empirical data in systems where redundancy can be assessed across communities with varying resource complexity.