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Modeling Functional Redundancy in Microbial Community

Sandra Annie Tsiorintsoa
Clemson University, andrassandy@gmail.com

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MODELING FUNCTIONAL REDUNDANCY IN MICROBIAL COMMUNITY

In recent years, many microbiome habitats, such as human guts, soils and oceans, have been simplified as a result of human activity. By choosing less complex and varied diets, for example, we decrease the number of different chemicals available to our gut microbes, decreasing gut microbiome diversity and causing a poor digestive health. Likewise, practicing monoculture farming instead of polyculture diminishes soil nutrients availability to microbes resulting in loss of soil fertility. Many studies show that simplified habitat complexity leads to less diversity in microbial communities. What is less clear is if this simplicity also affects functional redundancy, which is the number of species that perform a given function, of these communities. High levels of functional redundancy are important, because they contribute to ecosystem stability. To answer this question, we use metacommunity models to explore the connection between functional redundancy and habitat complexity. Specifically, we consider various paradigms for local community assembly within a larger metacommunity, including environmental filtering and niche partitioning. Our model for environmental filtering indicates that functional redundancy is constant with respect to the local habitat complexity. As for niche partitioning, we observe that functional redundancy rises with the local habitat complexity. These models suggest that different modes of community assembly yield different relationships between habitat complexity and functional redundancy. We explore these findings as they pertain consequences for maintaining stable microbial ecosystem services in anthropogenically simplified landscapes.