Contribution Evenness: A functional redundancy metric for microbially-mediated biogeochemical rates and processes

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The concept of functional redundancy has received considerable attention in both the macroecology and microbial ecology literature. As a result, multiple metrics of functional redundancy have been proposed. These vary in how they weight trait levels, species abundance, functional richness, and species richness. Trait-based models are also increasingly popular ways to represent the function of microbial ecosystems. Here we present a new functional redundancy measurement tailored to be useful for community-aggregated parameters, which are summed ecosystem processes contributed by species, such as rates of chemical transformations. We focus in particular on community-aggregated parameters mediated by microbial communities. We call this approach contribution evenness (CE). CE measures how evenly species contribute to a community-aggregated parameter based on species contribution levels and abundances. As CE is an evenness measurement, quantitative representation of functional redundancy spans between 0 and 1, where 0 corresponds to a single species contributing and 1 corresponds to all species contributing equally to a community-aggregated parameter. CE is sensitive to the resilience of an ecosystem function to species extinction—an ecological consequence of functional redundancy. To illustrate how CE can be used, we analyzed the functional redundancy of eight nitrogen-transforming pathways using 2,631 metagenome-assembled genomes from 47 marine sites. We found that, on average, NH_4^+ assimilation pathway was the most functionally redundant (0.44 ± 0.08) while dissimilatory nitrate reduction had the lowest functional redundancy (0.005 ± 0.005). As demonstrated here, CE is a metric that is sensitive to trait resilience and allows for comparative analysis of functional redundancy for different traits.