

Balance trees reveal microbial niche differentiation

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Advances in sequencing technologies have enabled novel insights into microbial niche differentiation, from analyzing environmental samples, to understanding human diseases and informing dietary studies. However, identifying the microbial taxa that differentiate these samples can be challenging. These issues stem from the compositional nature of 16S rRNA gene data (or, more generally, taxon or functional gene data), which changes in the relative abundance of one taxon influence the apparent abundance of the others. Here we acknowledge that inferring properties of individual bacteria is a difficult problem, and instead introduce the concept of *balances* to infer meaningful properties of sub-communities, rather than properties of individual species. We show that balances can yield insights about niche differentiation across multiple microbial environments including soil environments and lung sputum. These techniques have the potential to reshape how we carry out future ecological analyses aimed at revealing differences in relative taxonomic abundance across different samples.