Systematic method for capturing microbial community dissimilarity using Hill numbers

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Abstract

Microbial communities are an important part of our everyday lives. They cycle nutrients across the planet, keep our metabolism balanced, impact our infrastructure, and lend their services for the production of clean water and fuel. One important property researchers use to understand microbes is the dissimilarity between microbial communities. The problem is that there are many dissimilarity indices to choose from and choosing one over another could influence the conclusions drawn from an experiment. To provide a measure of standardization, a new study proposes a framework for capturing dissimilarity based on Hill numbers. Hill numbers measure diversity within a macroscopic community or dissimilarity between communities and now, it appears, Hill numbers can do the same for microbial communities. When coupled with a null model, Hill numbers allow for the analysis of the mechanisms driving microbial community assembly. To calculate Hill-based dissimilarity and null models, researchers developed the open-source software `qdiv`. `qdiv` is provided as a package for the widely used programming language Python and can be used by researchers to evaluate factors shaping microbial communities.