

Rarefaction and extrapolation with phylogenetic diversity

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Abstract

The measurement and evaluation of biodiversity plays a vital role in the field of ecological research. However accurate estimation of diversity indices from sampling data have been elusive. Hill number (the so-called effective number of species) has recently been widely used to characterize phylogenetic diversity of an assemblage or functional diversity of an ecosystem. Nevertheless, Hill numbers, including species richness, tend to be an increasing function for sample effort. For comparing diversity of different assemblages, standardization of samples is necessary. In this paper, we suggest standardizing sample to the same sample size or sample completeness, and integrate phylogenetic diversity indices to rarefaction/extrapolation curves. Since incomplete sample contains undetected species, using traditional bootstrap method to calculate the variance of diversity estimators usually underestimated. This paper also presents a modified bootstrap resampling method to assess the variance of diversity estimators. Estimation of rarefaction/extrapolation curves is proposed and test through simulation. The rarefaction and extrapolation estimators proposed in this paper will be featured in the online freeware phylo-iNEXT using R language and its package Shiny

Keywords: abundance data, extrapolation, Hill numbers, interpolation, rarefaction, sample coverage, sample completeness, species diversity, phylogenetic diversity