NUS National University of Singapore | Department of Biological Sciences
Faculty of Science

BIOLOGY COLLOQUIUM

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Hosted by Dr Ryan Chisholm

Rarefaction and extrapolation:

Standardizing samples to make fair comparisons of biodiversity among multiple assemblages

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The goal in many biodiversity analyses is to make a fair comparison and assessment of diversity measures (e.g., species richness, species diversity, phylogenetic diversity and functional diversity) among multiple assemblages. For most measures, it is well known that the empirical diversities in a sample are dependent on sample size or sampling efforts. When samples are incomplete, standardization via rarefaction and extrapolation is needed; rarefaction and extrapolation methods allow for fair and meaningful comparison of diversity estimates for standardized samples on the basis of sample size or sample completeness. In this talk, two types of standardization methods are reviewed: (1) Sample-size-based rarefaction and extrapolation methods aim to compare diversity estimates for equally-large samples determined by samplers. (2) Coverage-based rarefaction and extrapolation methods aim to compare diversity estimates for equally-complete samples; the sample completeness in this method is measured by sample coverage (the proportion of the total number of individuals that belong to the species detected in the sample), a concept originally developed by Alan Turing and I. J. Good in their cryptographic analysis during World War II. Contrary to intuition, sample coverage for the observed sample, rarefied samples, and extrapolated samples can be accurately estimated by the observed data themselves. These two types of standardization methods allow researchers to efficiently use all available data to make robust and detailed inferences about the sampled assemblages, and also to make objective comparisons among multiple assemblages. Hypothetical and real examples are presented for illustrating the use of the online software iNEXT (iNterpolation/EXTrapolation) to compute and plot seamless rarefaction/extrapolation sampling curves based on several diversity measures.

Artwork by Ann Nee, DBS, NUS