國 立 東 華 大 學 應 用 數 學 系
專 題 演 講

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講　　題：Phylogenetic Diversity, Similarity and Differentiation Measures based on Hill Numbers

時　　間：100年3月11日(星期五)15:10-16:40

摘　要

The compositional diversity of community, and the related concept of compositional similarity or differentiation of multiple communities are concepts widely used in conservation plans decision-making. We proposed a parametric class of phylogenetic diversity (PD) measures that are sensitive to both species abundance and species taxonomic or phylogenetic distances. This work extends the conventional parametric species-neutral approach (based on "effective number of species" by Hill numbers) to take into account species relatedness, and also generalizes the traditional phylogenetic approach (based on "total phylogenetic length") to incorporate species abundances. The new measures generalize and unify many existing measures and lead to a natural definition of taxonomic diversity as a special case. The replication principle (or doubling property), an important requirement for species-neutral diversity, is generalized to phylogenetic diversity. The widely used Rao's quadratic entropy and the phylogenetic entropy do not satisfy this essential property, but a simple transformation converts each to our measures, which do satisfy the property.

Hill numbers or "effective number of species" resolve many of the interpretational problems caused by classical diversity indices (e.g. Shannon entropy and the Gini-Simpson index), but they treat all species as equally distinct. Here we show how to partition these new phylogenetic diversity measures into phylogenetic alpha and beta diversities. The resulting beta diversity is independent of alpha diversity for both ultrametric and non-ultrametric trees. This beta diversity measures pure phylogenetic differentiation, and can be transformed into normalized measures of relative similarity and differentiation. We derive phylogenetic generalizations of the Sørensen, Jaccard, Horn, Morisita-Horn similarity measures, and a phylogenetic generalization of Jost's measure of genetic differentiation D. We show by example that the similarity and differentiation measures derived from this multiplicative framework are superior to previous measures that are based on the additive partitioning of phylogenetic generalization of classical diversity indices.

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