Taxonomic distinctness

One of the distinctive features of PRIMER is its inclusion of a suite of biodiversity measures based on the relatedness of species within a sample, e.g. the average ‘distance apart’ of any two species or individuals chosen at random from the sample (termed *average taxonomic distinctness*). This is usually defined from a Linnaean tree (though could be phylogenetic, genetic or functionally-based) and requires availability either of an aggregation file (Section 11) covering all the species in the data matrix, which will be used to compute species distances, or a more direct species resemblance matrix, supplying genetic or functional distances among species. It provides an added dimension of information to that obtainable from the abundance distribution alone: as an average measure its construction makes it independent of the number of species, and it thus has much better statistical sampling properties than richness-related estimators when sampling effort is non-comparable over samples. This should be seen as the major sphere of application: uncontrolled studies over wide spatial or temporal scales, where classic diversity measures can be misleading. Several papers describe the methods, e.g. Clarke KR & Warwick RM 1998, *J Appl Ecol* 35: 523-531, Clarke KR & Warwick RM 2001, *Mar Ecol Prog Ser* 216: 265-278 and Warwick RM & Clarke KR 2001, *Oceanog Mar Biol Ann Rev* 39: 207-231. A detailed exposition is also given in Chapter 17, CiMC.

In just the same way as for the classic indices, PRIMER can calculate a range of such taxonomic-related measures (including the *PD* of Faith DP 1992, *Biol Conserv* 61: 1-10), through check boxes on the **Analyse>DIVERSE** menu. These can be separated into quantitative indices (e.g. Δ, $\Delta ^\ast$) and those which depend only on a species list (indicated by a superscript +). The latter are divided into average measures (e.g. $\Delta ^+$, $ \Lambda ^+$) which have the property of independence of sampling effort (in their mean values), and total measures (e.g. S$\Delta ^+$, S$ \Phi ^+$) which are alternative definitions of the taxonomic richness, combining the number of species with relatedness information. For two of the presence/ absence measures, a hypothesis testing structure can be erected to compare a location’s observed *average taxonomic distinctness* (AvTD, $\Delta ^+$) and *variation in taxonomic distinctness* (VarTD, $ \Lambda ^+$) with that ‘expected’ from a regional master list, assuming assembly rules for the species set which are independent of their taxonomic inter-relation. This is run by **Analyse>TAXDTEST**, when the active window is either an aggregation file or a variable (dis)similarity matrix.

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