SIMPER (Similarity Percentages)

Shade plots are an excellently succinct way of displaying the abundance (or other quantity) of all the influential species (or other taxon category), in the pre-treated state in which they are input to the multivariate analysis of the community samples. However, they stop short of identifying the precise contribution that each species makes because they take no account of the resemblances calculated on these (transformed) abundances. In the case where there are (a few) established major groupings of the samples, either *a posteriori* by (Type 1) SIMPROF tests or *a priori* by ANOSIM, the average (Bray-Curtis) dissimilarity between each pair of groups can be broken down into the contributions from each species using the similarity percentages routine **Analyse>SIMPER**. This is preceded by a breakdown of the average (Bray-Curtis) similarity within each group into species contributions. Both sets of tables – one table for each group defining the *typical* species and one table for each pair of groups defining the *discriminating* species – have their species ordered into decreasing contributions to the overall average (dis)similarity. SIMPER can be used with shade plots to identify species it may be useful to show on a samples MDS in the form of segmented or simple bubble plots (Section 8). However, as with the SIMPROF and ANOSIM tests, the SIMPER routine operates on the (dis)similarities themselves and not the approximate 2- or 3-d ordination space, so is capable of aiding interpretation for established group structures when these are not adequately represented in low-d (i.e. for high MDS stress). It extends also to cases of (squared) Euclidean distance, e.g. from abiotic analyses, broken down into components from each variable, and to two-way crossed layouts, comparing two groups from factor A, within the strata of factor B.

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