Species dis-criminating two groups (Bristol Ch. zooplankton)

Re-open the Bristol Channel ws workspace from C:\Examples v7\BC zooplankton, for which the shade plot was seen a few pages ago. The BC zooplankton density sheet was 4th-root transformed (4rt density) prior to Bray-Curtis calculation (BC resem) and binary divisive clustering (**Analyse>Cluster>UNCTREE**), giving four SIMPROF groups of samples (a to d), factor Unctree. On the transformed 4rt density sheet, run **Analyse>SIMPER**>(Design•One way>Factor A: Unctree) & (Measure•Bray-Curtis similarity) & (✓List only higher-contributing variables>Cut-off percentage: 80) & (✓List pair-wise groups). [This last check box has been added in PRIMER 7 to allow runs on very large numbers of groups where the interest is solely in the species which mainly contribute to the within-group similarities defining each group, rather than cross-group comparisons – there can be sufficiently large numbers of pairs of groups to make SIMPER non-viable unless the cross comparisons are excluded, by unchecking this box]. The restriction to a cut-off (of 80% here) is probably unnecessary when there are only 24 species, but can be useful to avoid long tables, listing all species however small their %contribution to the average dissimilarity between two groups.

From the results window, _SIMPER1_, find the table comparing _Groups a & c_ (above) – these are the groups of sites _a: 1-10, 12, 24_ and _c: 11,13-22, 25-27, 29_ (the left-hand groups in the shade plot in this section). The average of the Bray-Curtis dissimilarities between all pairs of sites (one in _a_, the other in _c_) is 57.9, and this is made up of 7.92 from _C. hamatus_, 6.78 from _E. affinis_ etc, given in the third data column of the table. The _C. hamatus_ contribution is 13.7% of the total of 57.9 and _E._

affinis gives 11.7% of the total, etc (column 5), and these percentages are cumulated in column 6, until the cut-off of >80% is reached. Column 4 is the ratio of the average contribution (column 3) divided by the standard deviation (SD) of those contributions across all pairs of samples making up this average. A good discriminating species is one which contributes relatively consist¬ently to that distinction for all pairs of sites, i.e. with a low SD and thus a higher ratio (e.g. *P. parvus*, with ratio only 0.85 does contribute something to the difference between *a* and *c* but does so inconsistently). Whether the emphasis is on column 3 – which is used to order the species – or column 4 depends on the context. If you are trying to identify species which contribute the most to the differentiation of those groups in the multivariate analyses then it should be the *Av. Diss.* column – they will tend also to be the species with the larger abundances – but if you are looking for the best indicator of the differences between those conditions the *Diss/SD* ratio should also be considered. It can some-times pick out species which are completely absent in one group and with very consistent presence in the other, but with low abundance. Columns 1 and 2 aid the interpretation by giving the average abundance (or biomass, cover etc) for each species in each of the two groups – something the shade plot also gives a good feel for (note that both these columns and the shade plot present transformed abundances). *C. hamatus* appears in good numbers in *c*, having been absent in *a*, with the opposite pattern for *E. affinis*. Back-transforming for *C. hamatus* gives a change from 0 to 159 (3.55^4) on the original abundance scale (time-averaged numbers per m^3), with the reverse pattern for *E. affinis*.

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