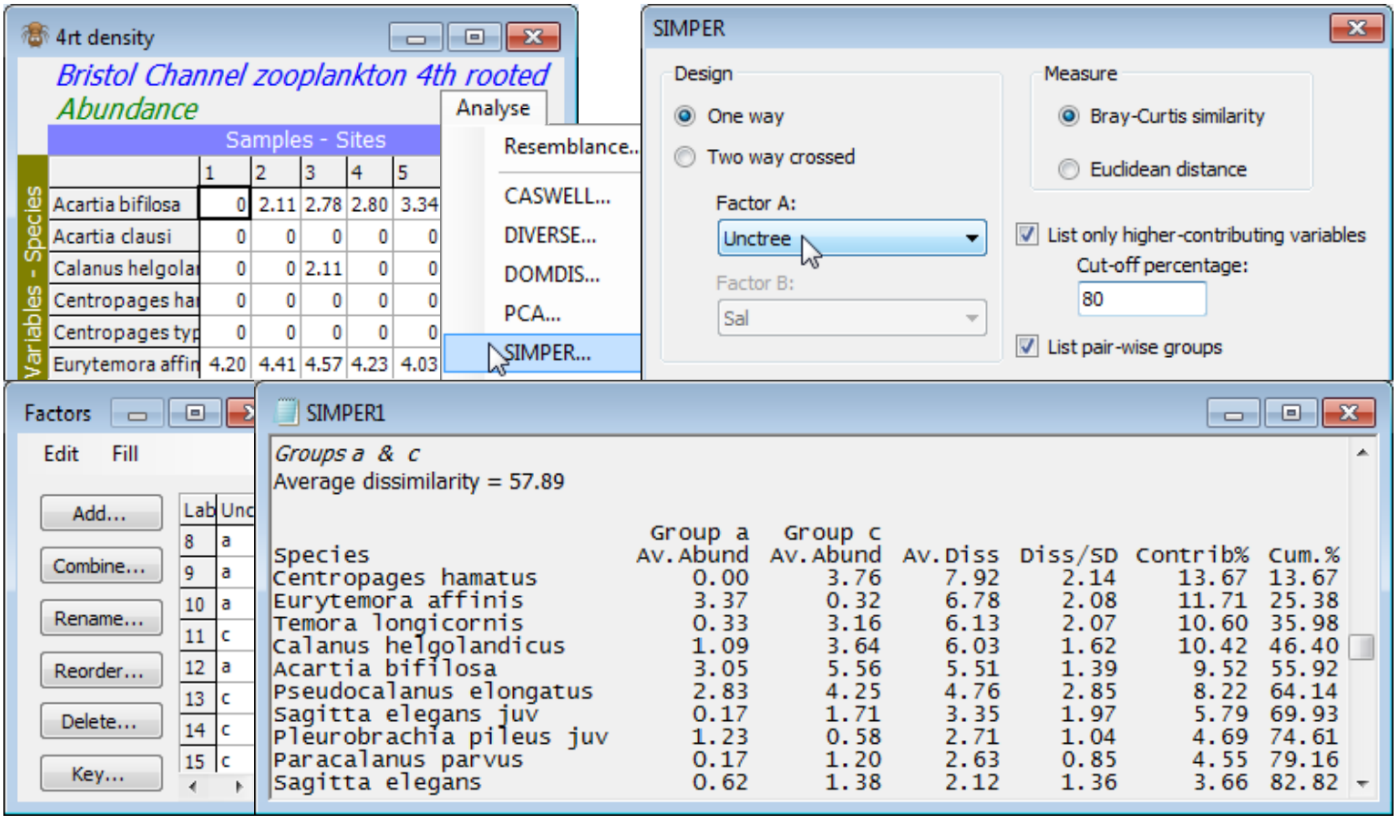
Species dis-criminating two groups (Bristol Ch. zooplankton)

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 consistently 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 sometimes 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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