Branches created in the Explorer tree

The first branch takes the square root of the full matrix Frierfjord macrofauna counts, giving Data1, on which sample Bray-Curtis is calculated, Resem1. This was only used to seriate the *x* axis on the original shade plot but, as seen above, **Special>Reorder**>Samples>(Order•Original) in place of the default (Order•Seriate) has restored the axis to the label order of the data matrix. If the **Wizards>Matrix display** default of not retaining sample groups had been followed (no factor supplied), then Resem1 would be input to **Analyse>Cluster>CLUSTER**, creating a dendrogram (without running SIMPROF), displayed on the *x* axis and with Resem1 used to seriate samples within the constraints of dendrogram rotation. Resem1 is the right resemblance matrix to use for multivariate routines such as *n*MDS and ANOSIM. The second branch starts with a **Tools>Duplicate** copy (Data2) of Frierfjord macrofauna counts on which **Select>Variables** >(•Use n-most important where n is 50) has been run. It is species-standardised by **Pre-treatment>Standardise**>(Standardise•Variables) & (By•Total) to give Data3, on which **Analyse>Resemblance**>(Measure•Index of association) & (Analyse between•Variables) then gives the species similarities Resem2 on which CLUSTER is run in just the same way as it would be for samples. [The Standardise step is not really needed here because IA will restandardise species again as part of its equation. It is included partly to remind you that there is a species standardisation step but also because there are other cases, such as the Type 3 SIMPROF tests for *coherent species curves* (statistically distinguishable species clusters) later in this section, in which an initial species standardisation is required even though an index of association will be calculated afterwards, so this is a good habit to adopt. (The issue arises there because the permutation direction in Type 3 SIMPROF is across species, and this only makes sense if species are scaled to add to the same total).] The final sub-branch in the Explorer tree, off the data matrix Data2, with its reduced number of species, is the one that generates the Shade Plot. Data2 is transformed with the specified square root, to give Data4, which is input to **Plots>Shade Plot** to give Graph2. If you repeat that last step manually, you will see that the resulting graph is a simple snapshot of the data matrix with samples and species in exactly the same order as the input matrix and no clustering or other ordering of the axes.

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