

# 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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