Transforms in Matrix display

The next dialog box on **Matrix display** is (Transformation:), with default of Square root. This in effect runs the routine **Pre-treatment>Transformation(overall)** and thus offers the choices of None, Square root, Fourth root, log(X+1) and Presence/absence. The chosen transform is naturally applied both to the full data matrix submitted to **Matrix display** and to the reduced matrix (if a reduction is specified) which will form the entries of the shade plot itself. After transforming the <u>full</u> matrix, Bray-Curtis similarities will be computed among samples and used to determine the ordering and/or clustering of the samples on the *x* axis of the shade plot. On the *y* axis, the ordering and/or clustering of the (reduced) species set does <u>not</u> use this transform (or any transformation). The definition of similarity among species uses the Index of Association (IA), as defined near the start of Section 5, and this incorporates a species standardisation, which is usually calculated on untrans¬formed data. The requirement for computation of IA on the original, untransformed data means that **Wizards>Matrix display** <u>should generally be run on the raw data</u>, and if a transformed matrix is submitted to it, this will elicit a warning box. You can happily ignore that if you wish to compute the similarities among species by standardising the transformed data – and there will be occasions when this is a reasonable thing to try. It would usually follow, of course, that when submitting transformed data you do not ask **Matrix display** for a further transformation step!

Note that there is no facility for changing the choice of sample similarity away from Bray-Curtis, or defining similarity among samples by anything other than the Index of Association, within the **Wizards>Matrix display** routine. That is not to say that other measures might not be sensible or desirable in some cases but you will then need to create the files to be input into a direct run of **Plots>Shade Plot**. You can see the steps created by the wizard in the Explorer tree below, along with the **Graph>Special>Reorder** dialog needed to change the *x* axis to the original sample order.
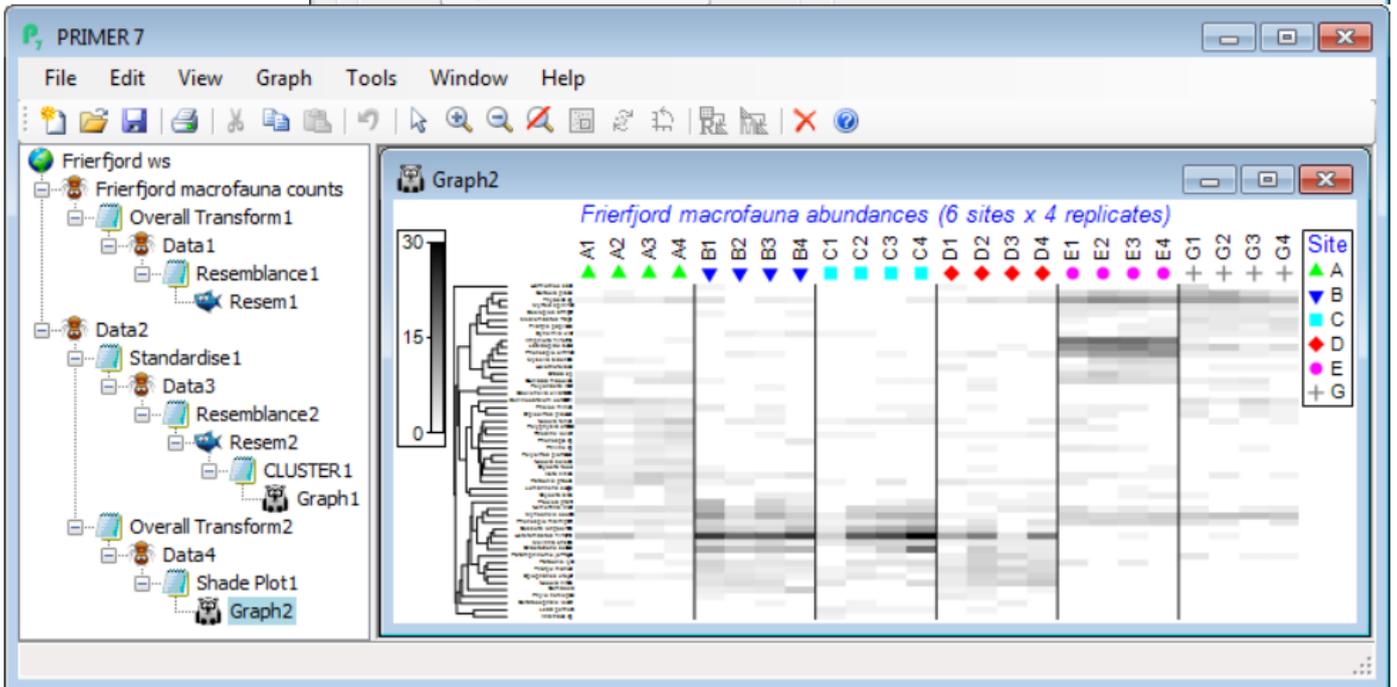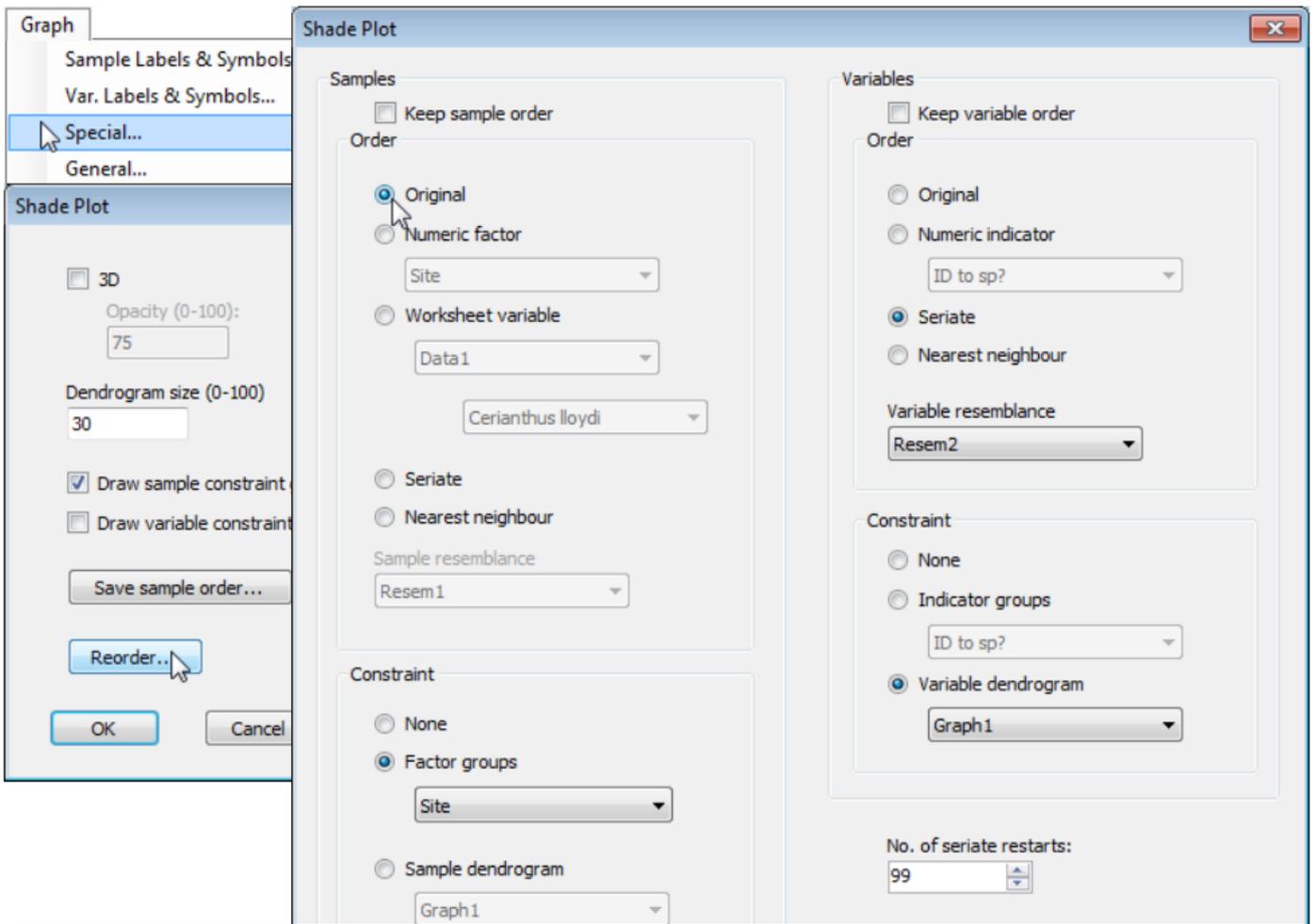
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