Understanding the Explorer tree

Understanding the Explorer tree, however, is the key to managing your work pattern in PRIMER. In the above workspace, click on the successive entries. After the workspace name (Bristol Channel ws) two data matrices have clearly been opened into the workspace, BC salinity (a repeat of the salinity information for each site but in the form of a separate environmental matrix, rather than a factor of the zooplankton array – this will be useful later when displaying bubble plots of salinity on an MDS plot), and the community data BC zooplankton density. A fourth-root transform has been taken, indicated in the Overall Transform1 results window, giving Data1. The similarity calculation follows: Resemblance1 shows that this was Bray-Curtis, calculated for all samples using all species, to give the triangular resemblance sheet – by default this would be *Resem1* but has been renamed (e.g. by clicking twice on the name) to Bray-Curtis similarity on 4th root. Renaming important windows in this way is always a useful aid to navigating around a large workspace (and more of this should probably have been carried out in the current example!). The agglomerative (Group Average) cluster analysis generates the CLUSTER1 results window and the dendrogram plot, Graph3, the number indicating that two other graphs were produced before this (in an analysis from Section 6, under SIMPROF1 lower down the Explorer tree, on a branch stemming back to the transformed *Data1* sheet rather than from the Bray-Curtis similarity matrix). Note that all these steps, which create a derived sheet or plot file, possess an intervening results window. This is what distinguishes operations on the **Pre-treatment**, **Analyse**, **Plots** and **Tools** menus (and **PERMANOVA+**, if installed) from those under **File**, **Edit** or **Select**. The latter do not produce new, derived sheets or intervening results windows, but make changes (temporary or permanent) to the currently active sheet.

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