TAXDTEST (European groundfish)

Further theoretical details and discussion can be found in Chapter 17 of CiMC, which also presents analyses for the Europe groundfish data, whose workspace Groundfish ws2 should still be open. These taxonomic distinctness tests (on presence/absence data only) are accessed by **Analyse>TAXDTEST** when the active window is either a variable information sheet (an aggregation file) or a variable resemblance matrix. These determine the *master list* (**Master taxonomy** on the TAXDTEST dialog box) from which random subsets of species will be drawn, in order to construct the probability histogram, funnel or ellipse plots. It is also the default aggregation sheet used in calculating the observed $\Delta^{\scriptscriptstyle +}$ and $\Lambda^{\scriptscriptstyle +}$ for any specific set of samples, to superimpose as points on the simulated funnels or ellipses (Sample data✓Use Sample data>Taxonomy•Use master). However, with (Taxonomy•Specify different>**Taxonomy**), a different aggregation sheet could be supplied, for the sample data calculation only. This would normally be quite unnecessary because the species relatedness needed for any particular sample can be drawn from the master taxonomy: as noted earlier, there is no necessity for the sample data matrix to contain all the same species in the same order as the aggregation (or variable resemblance) sheet – it is just necessary that all the species are found in the master list. However, it could be valid to place data from a region (or geological time), with its own aggregation information, on an expected funnel from an entirely different region (or time), with a different master list, so this option is catered for. If based on a variable information sheet (aggregation file), **Taxonomy** buttons will give the dialog seen earlier, allowing compression of the taxonomic tree and path step lengths which can be altered from equal weighting.

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