# Weighting of tree step lengths

The other box in this Taxonomy (data) dialog can be used to alter the weights given to the various branch lengths in the tree (and includes the previous compression at the top or bottom of the tree as a special case, with those step lengths set to zero). By taking (Weights•User specified)> **Weights**, the default lengths are displayed: equal steps are assumed, and any values placed here will always be standardised, subsequently (and automatically), so that the longest path in the tree is set to 100. Thus a change to step lengths of 2 for all categories would not alter the values of any of indices, but a change to decreasing step lengths of 6 (species to genus), 5 (genus to family), 4 (family to order) etc. could be worth exploring because it would put relatively more weight on the shorter branch lengths between species (of which there are fewer) rather than leaving much of the emphasis on the longer branch lengths (because there are many). One logical basis for altering the step lengths from their default would be to make them depend on the decrease in the number of taxa in the master list when making that step – the smaller the decrease in the number of taxa, the shorter the step length. This has the merit of consistency if, for example, an arbitrary taxonomic level (e.g. subfamily) is interpolated but not used (i.e. there are as many subfamilies as families in the master list). The set of distinctness indices would then remain unchanged. The detail is given in Clarke KR & Warwick RM 1999, *Mar Ecol Prog Ser* 184: 21-29, and their weighting scheme can be implemented here by taking (Weights•Taxon richness) in the Taxonomy (Data) dialog box.

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