Diagnostics for MDS: join pairs

There are a number of new diagnostic tools available in PRIMER 7 for assessing how well a low-d ordination represents the structure in the resemblance matrix. One of the simplest is to join pairs of points on the ordination which have similarity greater than some supplied threshold value. Choice of which value(s) to use requires a certain degree of experimentation, perhaps guided by a cluster dendrogram – too large a threshold and there are not enough joined pairs for an informative plot, too small and the plot is over-cluttered. For the Exe ws data, and the 2-d MDS plot Graph3, take the Overlays tab on the Special menu, i.e. **Graph>Special>Overlays**>(Join points✓Join pairs)> (Resemblance matrix: Resem1) & (Threshold: 30), which joins all pairs with similarity >30%. Whilst there is little conflict with the representation of such dissimilarities (<70%) by distances in the MDS plot, a small amount of inaccuracy (i.e. stress – low, at 0.05, but not entirely negligible) is evident in the way site 15 is connected with 16 but not sites 17 or 18, to which it appears closer in the 2-d plot. Note that if the same Join pairs operation is taken on the subset MDS of the last page, for sites 12-19 alone, this inaccuracy is resolved, as is the slight conflict noted previously for sites 12-14 – the reason site 19 is joined to 14 but not 12 in the full plot is evident from the subset MDS.

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