

Testing for k -dominance curves

Testing for differences in ABC curves for group structures of sites, times or treatments etc., where there are replicate samples within each group, is probably best accomplished by using the W index. This is computed for every replicate and the W values are treated like any other diversity measure, by univariate statistics. A different approach is needed for k -dominance curves, because of the lack of an internal comparison of curves to generate a univariate statistic. Single cumulative curves now need to be compared across replicates, both within a group and between groups. Clarke KR 1990, *J Exp Mar Biol Ecol* 138: 143-157 suggests a solution here, which is implemented in the **Analyse>DOMDIS** routine. This starts from an active sheet of a single species \times samples array (abundances, for example, though it could equally be biomass or area cover as in the example that follows), then calculates separately for each sample the cumulative relative abundances of species ranked in their decreasing order, as for the k -dominance plots. The distances apart of all pairs of cumulative curves (samples) is now computed, using Manhattan distance D_7 (see Section 5), and the routine therefore generates a resemblance matrix (dissimilarity of curves) among all samples. This can be entered into the multivariate PRIMER routines in just the same way as for any other dissimilarity matrix. (The possibility of inputting pairwise distances between curves – growth curves, PSA curves etc. – to multivariate analysis was seen in Sections 4 and 5). In particular, a run of **Analyse>ANOSIM** on this distance matrix will produce a significance test for the differences among groups. Replicate curves across groups that tend to be further apart from each other than replicates within groups will give ANOSIM $R > 0$, and this is tested by permutation as usual. In fact, there is a choice of two *curve separation* statistics offered by the dialog box in **DOMDIS**, namely Manhattan distance and a modification of it, which is the default: (Log weighting of species ranks). This multiplies the absolute difference between the curves at the i th point on the x axis (the i th ranked species) by $\log(1 + i^{-1})$, which successively downweights the contributions from the lower ranked species. It reflects the fact that k -dominance curves are usually plotted with a log scale on the x axis (of ranks), and it approximates to the visually-observed area between the two curves. The unweighted form would be relevant if plots are used without a logged x scale (as seen in an earlier example).

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