Multivariate dispersion MVDISP

One of the few multivariate routines not so far met is **Analyse>MVDISP**, applied to a resemblance matrix from samples with a simple group structure (i.e. a 1-way layout, or a crossed design that can be turned into a 1-way layout by defining an appropriate combined factor). This gives a description of relative multivariate variability within each of the groups in a single ordination or, to be more precise, in the full-dimensional space of the rank similarity matrix underlying that ordination. (As such it is not a matching of multivariate patterns and doesn't really belong in this section – but it has to go somewhere!) The concept is again a simple non-parametric one – though rather limited in scope – and described in the Increased Variability section of Chapter 15 in CiMC, so only an example will be given here. Tables of the *dispersion sequence* of all groups (equation 15.4) and the *index of multivariate dispersion (IMD)*, comparing pairs of groups (equation 15.2), are output to the results window, and these measure differing relative dispersion across groups on the basis of dissimilarity (or any other resemblance measure) within groups – between-group dissimilarities are not used. [If a description retaining the actual similarity scale is required, an alternative – for the special cases of Bray-Curtis and Euclidean distance – might be to run **Analyse>SIMPER** on the transformed data sheet and look at the headings for the first set of tables, each of which gives the average similarity of all pairs of replicates within that group. More generally – for all other coefficients – the same information about average resemblance within groups is one of the tables output from the PERMANOVA+ add-on routine, PERMDISP, see the Anderson *et al* 2008 user manual].

The term *multivariate dispersion* rather than *variance* is used because the relationship between the univariate variance of the original variables and the dispersion in 'resemblance space' (and its low-dimensional ordinations) can be far from linear, depending on the choice of resemblance measure. For example, similarity measures in the quantitative Bray-Curtis family (see earlier this section on comparison of resemblance coefficients) are driven partly by the presence/absence structure of the data, as well as the magnitude of counts from species which are always present, and this inevitably involves a non-linear transformation of original variable scales. Similarly, something as simple as normalisation, used in a Euclidean distance analysis of environmental variables, will remove any direct link between variance on the original measurement scales and dispersion in the multivariate space. Any statement about relative dispersion, therefore, must be contingent on specifying the resemblance measure used. Clarke KR, Somerfield PJ, Chapman MG 2006 *J Exp Mar Biol Ecol* 330: 55-80, show the radically different conclusions that would be reached, for the Tikus Island reef coral study (met in Section 5), about the dispersion among transects before and after a coral bleaching event, under Chi-squared, Bray-Curtis (standard and zero-adjusted) and Euclidean-based analyses – with the intermediate (zero-adjusted) Bray-Curtis arguably giving the most informative description, in terms of identifying the inter-annual changes in coral community. (This interesting example is also extensively discussed in Chapter 16, CiMC, on resemblance coefficient choice.)

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