Wizard for Matrix display

Another significant addition to the descriptive tools now available in PRIMER 7 is that of **Plots>Shade Plot**. This is particularly helpful in two ways. Firstly, we have already seen it used in simple form in Section 4 in relation to choice of transformation. A useful way of determining the effects of differing transformations – and thus which one might be adopted routinely for future analyses of particular community types in specific contexts – is to view differently pre-treated versions of the data matrix through shade plots (see Clarke KR, Tweedley JR, Valesini FJ 2014. 'Simple shade plots aid better long-term choices of data pre-treatment in multivariate assemblage studies'. *J Mar Biol Assoc UK* 94: 1-16). Shade plots are visual representations of the data matrix itself, in which the larger the entry in a specific cell, the darker the shade (or colour) plotted, white representing the absence of that species, and full black the largest entry (rounded up) in the whole matrix.

Secondly, a shade plot can be an extremely useful tool at the later stages of an analysis, when the statistical tests have demonstrated the existence of structure, whether that is *a priori* sample groups or gradients tested with ANOSIM or RELATE, or whether a result of clustering and SIMPROF on unstructured samples, i.e. whenever we have licence from statistical testing to interpret the sample analyses in terms of individual taxa. If the rows and columns of the shade plot are re-ordered carefully enough, such a plot sometimes has a surprising amount of interpretative capacity, even if that is just to narrow down the set of species used in bubble plots on a sample *n* MDS. This is also the function of the **Analyse>SIMPER** routine (examples of which are given later in this section) but that has a focus on identifying species which contribute to differences among well-defined groups (as established by ANOSIM or SIMPROF), and is restricted to comparing pairs of groups at a time. It will therefore function poorly, if at all, for gradient structures where patterns of species change are more continuous – and where clear clusters of samples may not even exist. Shade plots can shed light on the reasons for both gradient and group structures and, for example, neatly distinguish between cases where a clear gradient on an *n*MDS plot is the result of a small number of species with strongly increasing or decreasing abundances across the full gradient, or a larger number of taxa which occupy quite different parts of the gradient, or whether in fact the multivariate summary comes from putting together information from a great number of species, each carrying limited or highly variable information – it is one of the triumphs of multivariate analysis that it is sometimes able to fashion a clear community structure from what would be most unpromising population data.

The **Special>Reorder** button after **Plots>Shade Plot** offers a myriad of combinations of clustering and re-ordering, both of rows and columns of the shade plot. The steps that are needed to exploit these to best advantage are quite complex, and **Wizards>Matrix Display** gets you started.

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