Matrix display wizard

On active sheet Fal nematode abundance, run **Wizards>Matrix display**, not taking all the defaults in this case but unticking/unchecking the (Reduce species set) box so that all species are retained, and taking (Transformation: Square root) & (✓Retain sample groups>By Factor: Creek). A quite complex set of steps are then carried out, culminating in a run of **Shade Plot** from the **Plots** menu (fully described in Section 10) but, for our current purposes, all that needs to be understood is that the resulting shade plot is simply an image of the data matrix, in which the abundance for each species is represented by the shade of grey, from white (absent) to black (the largest count in the worksheet). Replicates from the 5 creeks are kept together along the *x* axis and the species on the *y* axis have been clustered and ordered in such a way that species with similar distribution across these samples are placed together in the re-ordering. (Multivariate analysis does not use the order of species in the matrix but it helps the human eye to visualise data structures by performing such re-arrangements). Apart from it being clear that some creeks contain a rather different set of species – or at least different abundances of the same species – an observation which is formally tested by the **ANOSIM** routine, e.g. as part of the **Basic multivariate analysis** wizard, the other message is that no one species will dominate an assessment of similarity of samples (columns) to each other. Equally clearly, quite a number of the less frequently occurring species have (transformed) values which are still sufficiently small in relation to the main players that they are almost invisible to the ensuing similarity calculation. This is probably desirable, and suggests we may have a reasonable transformation here. Contrast this with **Wizards>Matrix display** run again on the Fal nematode abundance sheet, but this time with (Transformation: None) – you can ignore the warning that PRIMER gives you (it is trying to tell you this is a bad idea!) – and it is clear from the resulting shade plot that only a few species will now contribute to the similarity computations. So an assessment of biotic differences among creeks, and how this relates to differences in heavy metal levels will really only be about a few numerically dominant species and not broadly community-based. At the other extreme, if you try the severest pres/abs transform, the rare species are now having far too much of an effect and will dilute genuine patterns from species sampled in reasonable numbers.

Section 4 also discusses an alternative approach to balancing contributions from different species, that of **Pre-treatment>Dispersion Weighting**, which downweights species with highly variable counts in replicates, which the sampling device captures in clumps rather than single individuals –relatively more weight is therefore given to species with consistent numbers over replicates of the same condition and these will be more reliable for assessment. If you try that pre-treatment and put the resulting rebalanced matrix into the **Matrix display** wizard, the shade plot gives a matrix image not unlike that for the square root transform, and this is certainly a possible pre-treatment here.

Revision #9
Created 12 March 2024 22:34:16 by Arden
Updated 7 January 2025 22:58:42 by Abby Miller