

Basic MVA for structured data (Fal nematodes)

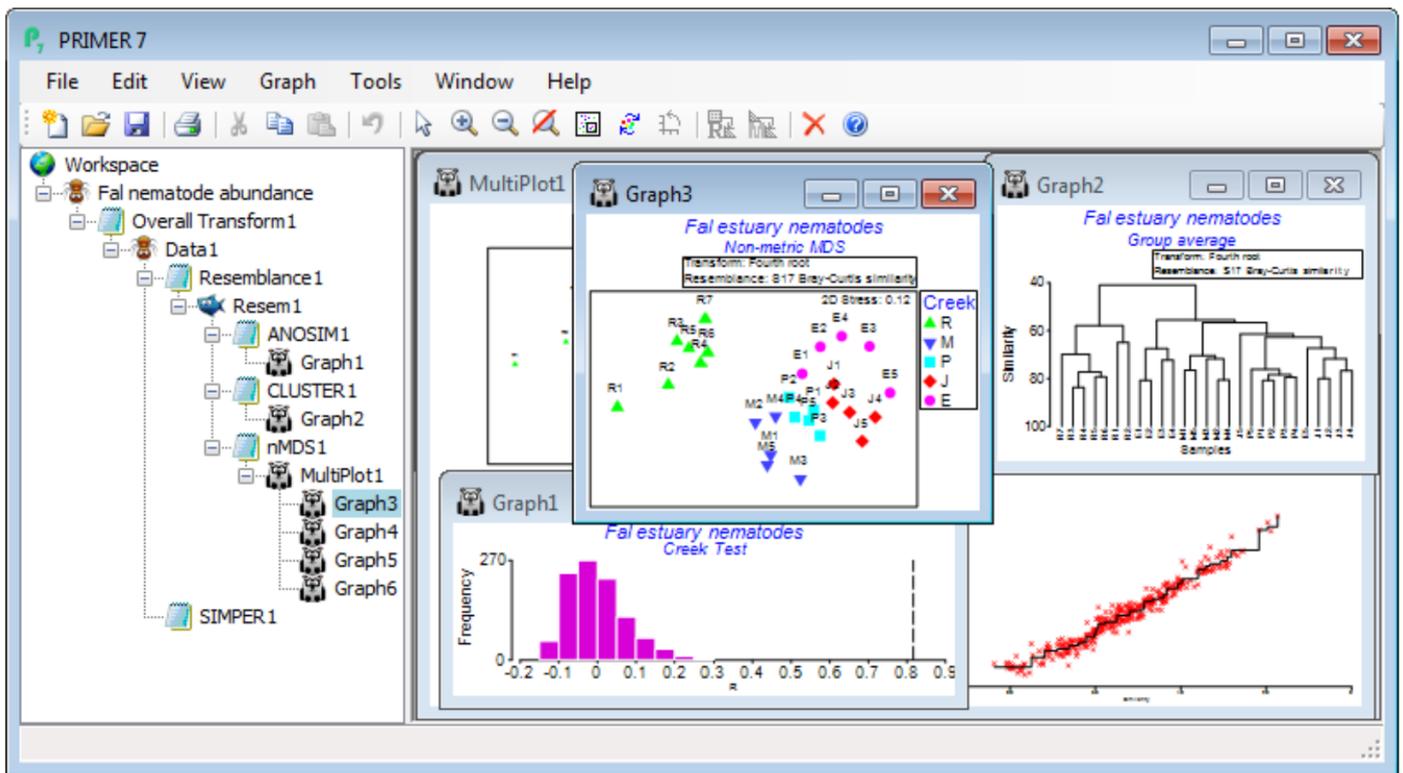
The benthic faunal study in the Fal estuary, Cornwall UK, was seen in Section 4. Sediment samples were taken at a total of 27 sites across 5 creeks running into the Fal estuary, with differing levels of heavy metal contamination from historic tin and copper mining – 7 sites in Restronguet (R) and 5 in each of Mylor (M), Pill (P), St Just (J) and Percuil (E) creeks. The existing workspace, *Fal ws*, concerns only the meiofaunal copepod community, and in Section 17 we shall see the macrofaunal component, but open here the nematode assemblages, *Fal nematode abundance* from C:\Examples v7\Fal benthic fauna, into a clear workspace (*Fal ws2*). **Wizards>Basic multivariate analysis** then offers the sequence of analyses shown below – in particular the routine picks up the existence of a *Creek* factor with repeated levels and checks the ANOSIM not SIMPROF boxes. In this case, a more severe transform is desirable to downweight the highly abundant *Metachromadora vivipara*, so change to (Transformation: *Fourth root*) – a shade plot (see later, and Section 4) helps here.

The screenshot displays the 'Basic analysis wizard' software interface. The main window is titled 'Basic analysis wizard' and contains a 'Biotic Data' section. The 'Pre-treatment' section has a checkbox for 'Standardise samples' which is unchecked. The 'Transformation' dropdown menu is set to 'Fourth root'. The 'Analyse' section has a 'Resemblance' dropdown set to 'S17 Bray-Curtis similarity'. The 'ANOSIM (1-way)' checkbox is checked, with the 'Factor' dropdown set to 'Creek'. The 'CLUSTER' checkbox is checked, with the 'SIMPROF' sub-checkbox unchecked. The 'MDS' and 'SIMPER' checkboxes are also checked. At the bottom of the wizard are 'Next >', 'Finish', and 'Help' buttons.

Overlaid on the wizard is a 'Factors' dialog box with a table of factors:

Label	Creek	Creek name	Pos
R1	R	Restronguet	1
R2	R	Restronguet	2
R3	R	Restronguet	3
R4	R	Restronguet	4
R5	R	Restronguet	5
R6	R	Restronguet	6
R7	R	Restronguet	7
M1	M	Mylor	1
M2	M	Mylor	2

In the background, a 'Fal nematode abundance' spreadsheet is visible, showing columns for 'Samp' (R1, R2, R3) and rows for species: *Triploides gradis* (149, 181, 385), *Atrochromadora mi* (0, 0, 0), and *omadora macro* (0, 4, 29).



The main intention of the Wizards is to aid understanding of the steps involved, by examining the sequence of windows created in the Explorer tree. In this case, you can create precisely the same outcome by running the following. On **Fal nematode abundance**, take **Pre-treatment>Transform (overall)>**(Transformation: **Fourth root**) and, on the resulting transformed sheet **Data1**, **Analyse>Resemblance>**(Measure•Bray-Curtis similarity) & (Analyse between•Samples), giving **Resem1**. On **Resem1**, **Analyse>ANOSIM>**(Model:One-Way - A) & (Factors A: **Creek**)>(Type: Unordered) leads to ANOSIM test results, testing for significance of differences among creeks overall and pairwise, in **ANOSIM1**, and a histogram of the null distribution for the overall (global) test, **Graph1**. On **Resem1**, **Analyse>Cluster>CLUSTER>**(Cluster mode•Group Average)&(✓Plot dendrogram) but without the SIMPROF box ticked, displays a standard UPGMA clustering in **Graph2**. Again on **Resem1**, **Analyse>MDS>Non-metric MDS (nMDS)**, with the defaults of (Min. Dimension: 2) & (Max. Dimension: 3)&(Number of restarts: 50)&(Minimum stress: 0.01)&(Kruskal fit scheme•1)&(✓Configuration plot) & (✓Shepard diagrams), gives the results window for MDS, **nMDS1**, which contains important information on how many times the lowest stress solution was observed in the 50 random restarts (if only a handful of times, consider running again with more restarts), and then the **Multiplot1** window, which contains the (best) 2-d and 3-d ordination plots, along with Shepard diagrams. Clicking on any of these plots (or the + sign in front of the **Multiplot1** icon) unrolls the four individual plots in the Explorer tree, **Graph3** to **Graph6**. Finally, on the data sheet **Data1**, not the resemblance sheet **Resem1** note, taking **Analyse>SIMPER>**(Design•One way) & (Factor A: **Creek**) & (Measure•Bray-Curtis similarity), with the other two boxes ticked, will give the detailed results window **SIMPER1**, breaking down the average dissimilarity between pairs of the ANOSIM groups (the creeks) into contributions from each species - see later this section.

The main conclusions here are that there are clearly significant differences overall between creeks (global R very large at 0.816, $p < 0.1\%$) and, almost equally clearly, between all pairs of creeks - the only pairwise R value which drops as low as 0.5 is between St Just (J) and Percuil (E) ($p < 2.4\%$). Other pairwise R values are in the range 0.75-0.99, and all of them are the largest obtainable values - greatest separation possible - in all permutations of the labels between the pair of creeks

(i.e. 126 permutations for two creeks which both have 5 replicates, and 792 if Restronguet's 7 replicates are involved). In keeping with the pairwise ANOSIM R values for Restronguet (all $R > 0.9$ even though the variability in Restronguet sites is large), the *n*MDS plot displays the very different nematode assemblages for that creek - it has by far the highest sediment concentrations of heavy metals.

Revision #6

Created 2 August 2024 03:30:29 by Arden

Updated 29 January 2025 03:53:35 by Abby Miller