

6. Some Wizards

- [Basic multivariate analysis](#)
- [Matrix display](#)

Basic multivariate analysis

A useful analysis pathway (including the Example Analysis Pathway done above, with its five steps), can be accomplished in one fell swoop using the **Basic multivariate analysis** wizard. This will perform a suite of multivariate analyses commonly performed for either biotic or environmental data types, with options available that match the typical choices made for handling these different types of data.

Run the 'Basic multivariate analysis' wizard

Let's suppose you wanted to repeat the step-by-step analyses we did before, but this time using a different pre-treatment option. For example, you may decide you'd like to analyse the same data using presence/absence information only, so as to emphasise only the turnover in species identities (and not differences in abundance values) across sample units. It would be great to run this whole set of analyses quickly, rather than going through them again one at a time.

Click on the original '**Fal nematode abundance**' datasheet in the Explorer tree and then click **Wizards > Basic multivariate analysis....**

The screenshot shows the PRIMER 7 software interface. The 'Wizards' menu is open, highlighting 'Basic multivariate analysis...'. The Explorer tree on the left shows the project structure, with 'Fal nematode abundance' selected. A preview window displays the data table for 'Fal estuary nematodes Abundance'.

	Samples						
	R1	R2	R3	R4	R5	R6	R7
Anoplostoma vivip	0	0	0	0	0	0	0
Halalaimus gradis	0	0	0	0	0	0	0
Halalaimus longica	0	0	0	0	0	0	0
Oxystomina elonga	0	0	0	0	0	0	0
Viscosia viscosa	0	0	0	0	0	0	0
Tripyloides gradis	149	181	385	289	170	614	
Atrochromadora mi	0	0	0	0	0	0	0
Chromadora macro	0	4	29	63	263	123	
Chromadora nudica	0	0	0	0	0	7	
Chromadorella ?du	0	0	0	0	0	0	0
Chromadorita nana	0	0	0	0	0	0	0
Chromadorita tenta	0	0	0	0	0	0	0
Dichromadora geop	5	0	0	0	0	7	
Hypodontolaimus b	40	44	25	18	5	14	
Ptycholaimellus po	174	424	178	99	107	123	
Neochromadora po	0	0	0	0	0	0	0

In the dialog box that follows, we can see that PRIMER is offering to perform a suite of basic multivariate analyses that are commonly performed for 'Biotic Data' (shown in bold blue font at the

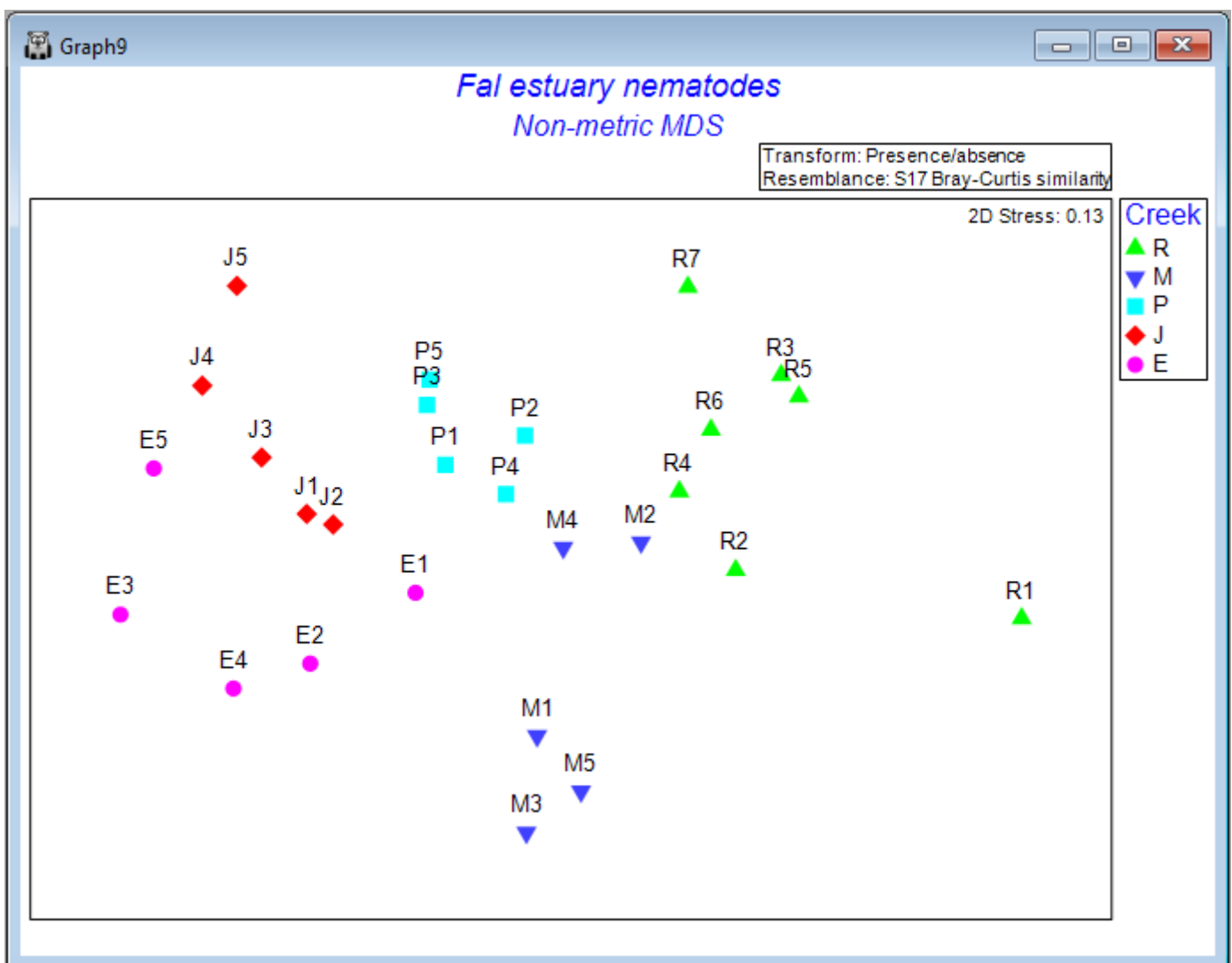
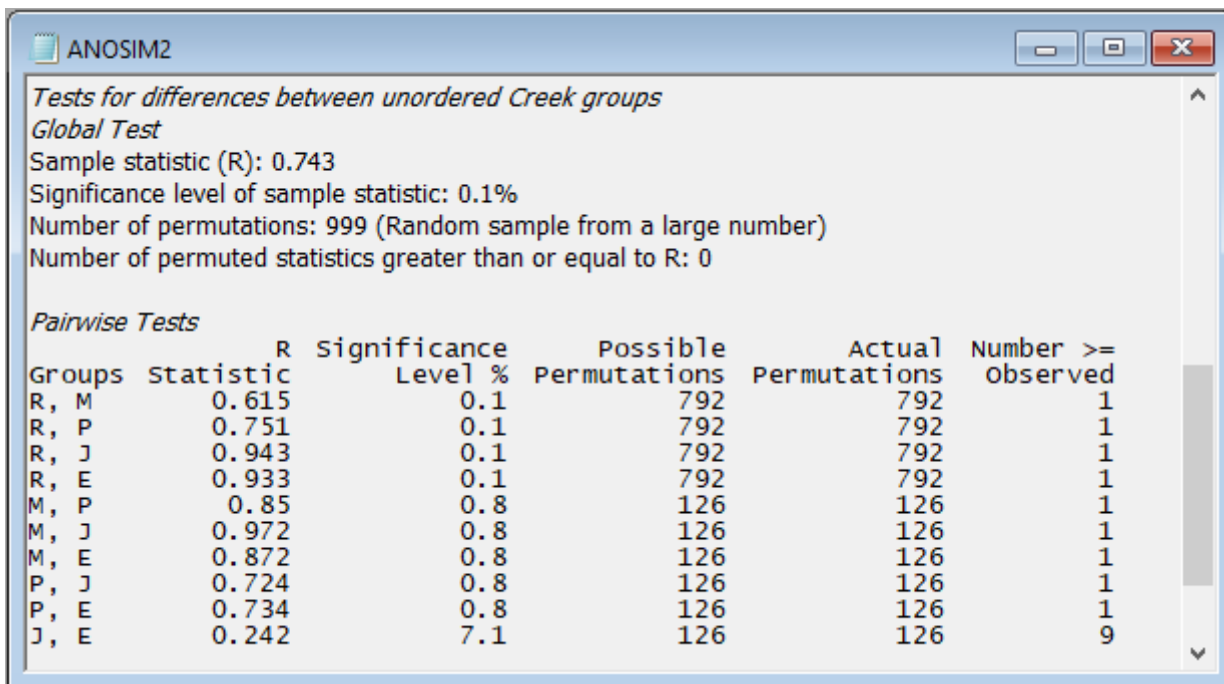
top). You can choose from a couple of (common) pre-treatment options, and then it will perform the analyses you choose (*via* the relevant checkboxes under 'Analyse'), using the default options for each routine. Note that different options would be shown for data of a different type (e.g., for environmental data). Recall that the 'type' of data is specified by you when you import the data into PRIMER. This can be changed for a given data sheet by clicking on **Edit > Properties** at any time.

Under 'Pre-treatment', choose 'Transformation: **Presence/absence**' and under 'Analyse', leave all of the default options, except you can *untick* the checkbox next to the 'SIMPER' routine (for now), then click **Finish**.

The image shows a 'Basic analysis wizard' window for 'Biotic Data'. It is divided into two main sections: 'Pre-treatment' and 'Analyse'. In the 'Pre-treatment' section, the 'Standardise samples' checkbox is unchecked, and the 'Transformation' dropdown is set to 'Presence/absence'. In the 'Analyse' section, the 'Resemblance' dropdown is set to 'S17 Bray-Curtis similarity'. Under 'ANOSIM (1-way)', the 'Factor' dropdown is set to 'Creek'. The 'CLUSTER' checkbox is checked, and the 'SIMPROF' sub-option is also checked. The 'MDS' checkbox is checked, and the 'SIMPER' checkbox is unchecked. At the bottom of the window, there are five buttons: 'Cancel', '< Previous', 'Next >', 'Finish' (which is highlighted with a blue border and a mouse cursor), and 'Help'.

All of the requested analyses are done, and the resulting output files and graphics are shown in the Explorer tree window. Click on any of the items in the Explorer tree to see the steps that were taken, including specific data sheets, resemblance matrices, graphical outputs and results files. Although you will generally use PRIMER to perform individual analyses, one routine at a time, this wizard provides a quick way to achieve multiple analyses (provided you know *a priori* that you want to do them) with a single stroke.

The ANOSIM results ('**ANOSIM2**') and the 2D nMDS output (**Graph9**) obtained by this run of the wizard are shown below:



In this example, we can see that there are statistically significant differences in the identities of nematode species among the five creeks (ANOSIM $R = 0.743$, $P = 0.001$ with 999 permutations), although the pattern in the nMDS plot suggests that the difference between Restronguet Creek and

the other creeks is not as great as what was observed when abundance information was included in the Bray-Curtis calculation. (Compare 'Graph9', as shown above, with 'Graph2' that we obtained earlier.)

Expanding and collapsing the Explorer tree

Note that this new set of analyses, performed using the wizard on the original imported data, will initiate its own new branch of the Explorer tree. You can always initiate a new analysis starting from a given item in the tree (e.g., from a data sheet or a resemblance matrix, etc.), and the tree will expand, generating a new branch, to accommodate these new analyses. You can use the '+' and '-' symbols in the Explorer tree to 'roll up' or 'unpack' the items in the tree belonging to a particular branch at any time.

For example, clicking on the '-' symbol next to the item named '4th-root' will 'roll up' all of the items associated with our original analysis (based on a fourth-root transformation), so the analyses that were done by the Wizard (based on presence/absence) are now closer to the top of the Explorer tree window. For clarity, we might choose to rename the sheet called 'Data1' (the data sheet produced by the wizard after performing the presence/absence transformation) to 'Pres abs'.

The screenshot displays the PRIMER 7 software interface. The title bar reads "PRIMER 7 - [Pres_abs]". The menu bar includes File, Edit, Select, View, Wizards, Pre-treatment, Analyse, Plots, PERMANOVA+, Tools, Window, and Help. A toolbar with various icons is located below the menu bar.

Left Panel: Fal_Workspace

- Fal nematode abundance
 - Overall Transform1
 - 4th-root
 - Overall Transform2
 - Pres_abs** (selected)
 - Resemblance2
 - Resem1
 - ANOSIM2
 - Graph7
 - CLUSTER2
 - Graph8
 - nMDS2
 - MultiPlot2
 - Graph9
 - Graph10

Right Panel: Species Abundance Matrix

Fal estuary nematodes
Abundance

| | Samples | | | | | | | | |
|---------------------------------|---------|----|----|----|----|----|----|----|--|
| | R1 | R2 | R3 | R4 | R5 | R6 | R7 | M1 | |
| Anoplostoma vivipa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Halalaimus gradlis | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Halalaimus longicaudatus | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Oxystomina elongata | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | |
| Viscosia viscosa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Triploides gradlis | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| Atrochromadora munda | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Chromadora macrocephala | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| Chromadora nudicauda | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | |
| Chromadorella ?dubius | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Chromadorita nana | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Chromadorita tentaculata | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Dichromadora geophila | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | |
| Hypodontolaimus bicanaliculatus | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| Ptycholaimellus pectinatus | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| Neochromadora poorei | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Xinema sp. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Paracomerosoma dubium | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Sabatieria breviseta | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Sabatieria celtica | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Sabatieria praedatrix | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Sabatieria pulchra | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| Comesa ?cuanensis | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | |
| Paracanthonus hebes | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | |
| Preacanthonus putrescentiae | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |

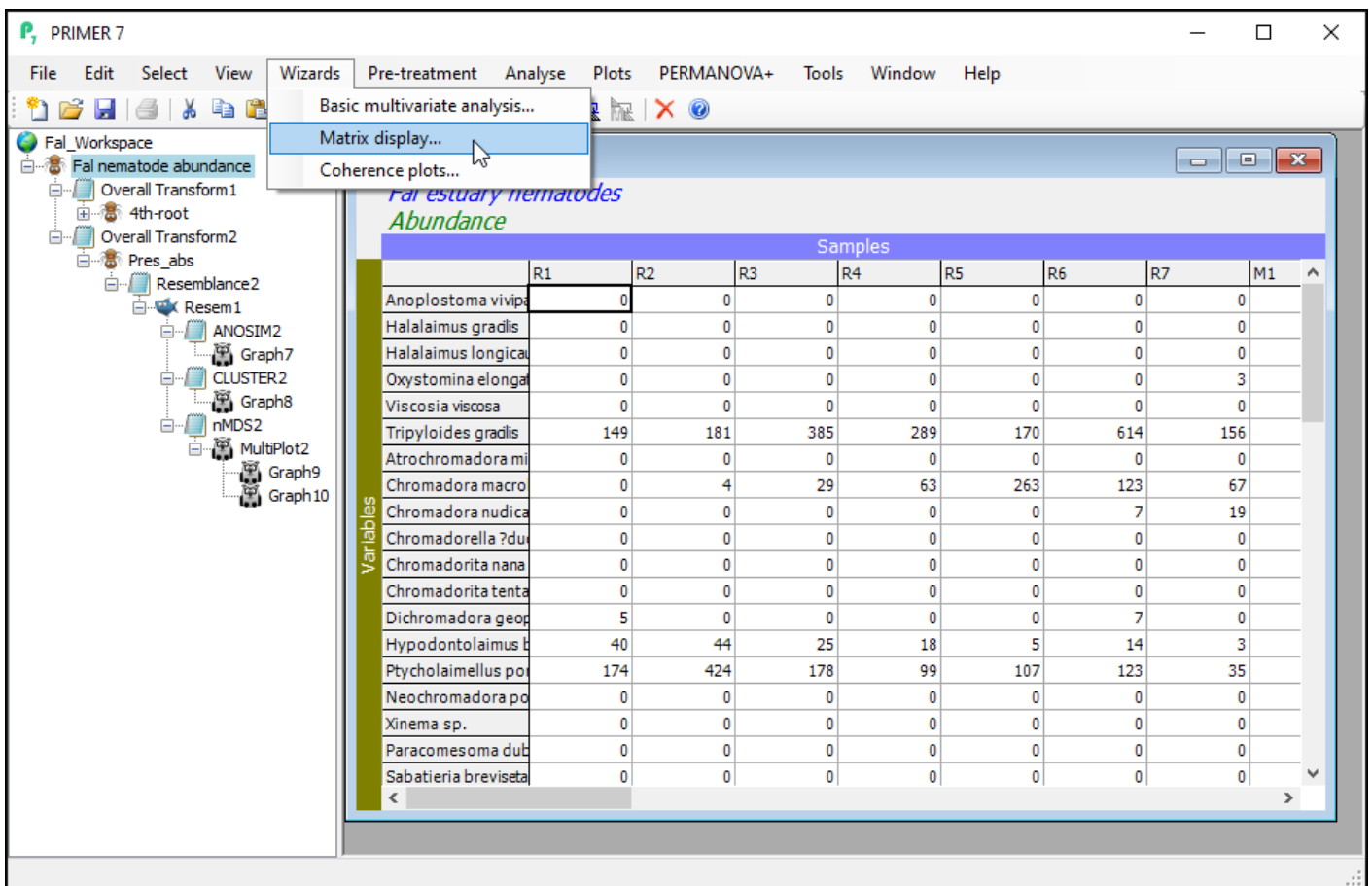
Row 1 Col 1 ...

Matrix display

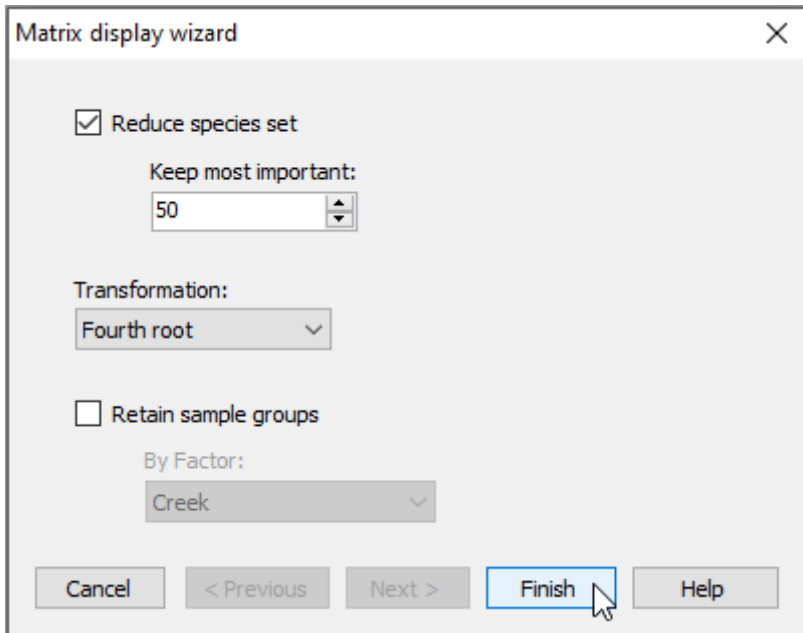
The **Matrix display** wizard produces a shade plot of a multivariate data matrix, with a useful ordering of its rows and columns that can help to clarify inter-sample and inter-species relationships, as well as gradients in turnover based on a resemblance matrix of choice.

Create a Matrix display

Click on the original data sheet ('Fal nematode abundance', at the top of the Explorer tree window), then click on **Wizards > Matrix display...**



In the 'Matrix display wizard' dialog, leave the defaults, but choose (Transformation: **Fourth root**), then click **Finish**.

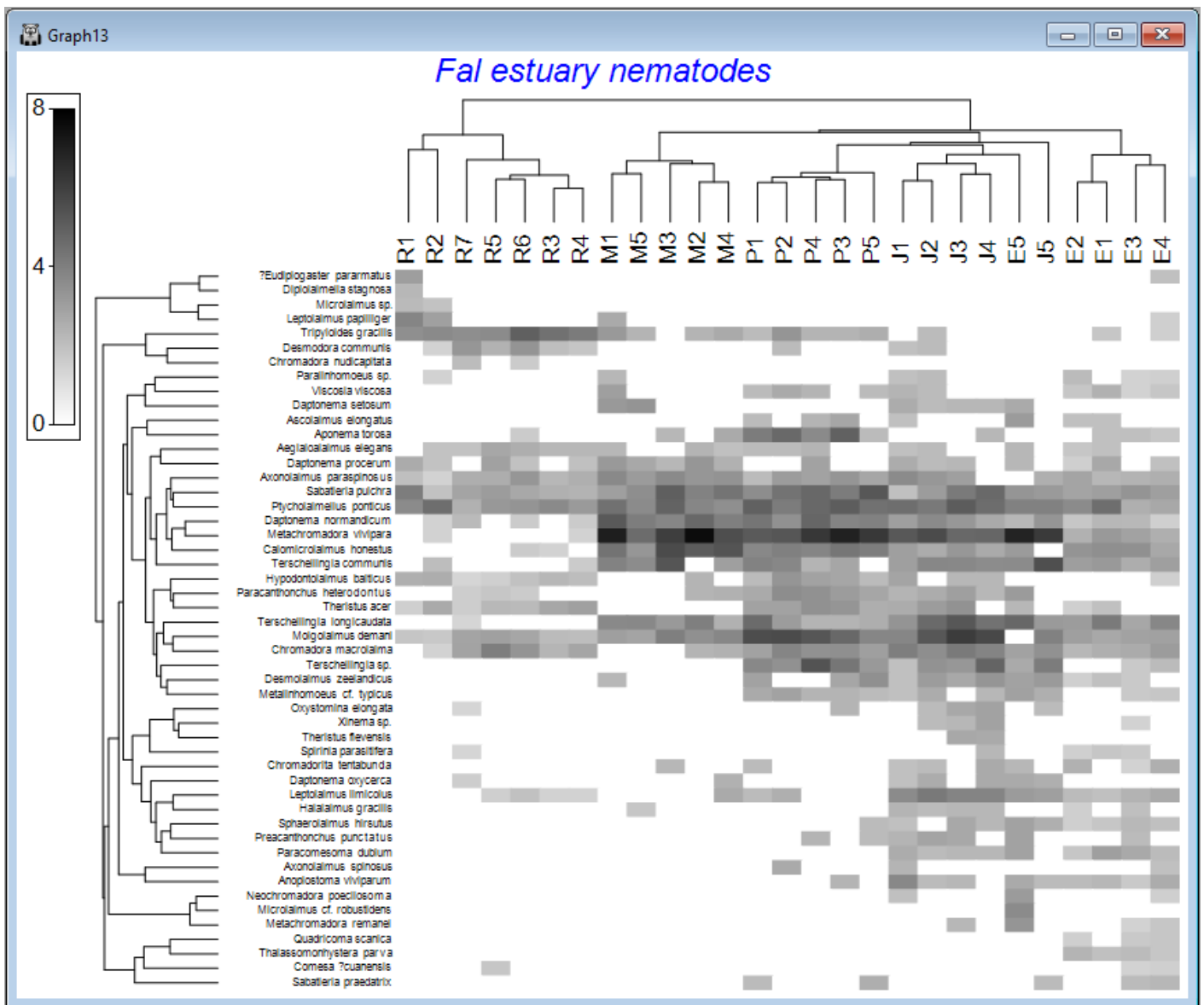


The image shows a 'Matrix display wizard' dialog box with a close button (X) in the top right corner. It contains the following settings:

- ☒ Reduce species set
 - Keep most important: 50 (spin button)
- Transformation: Fourth root (dropdown menu)
- ☐ Retain sample groups
 - By Factor: Creek (dropdown menu)

At the bottom, there are five buttons: 'Cancel', '< Previous', 'Next >', 'Finish' (highlighted with a blue border and a mouse cursor), and 'Help'.

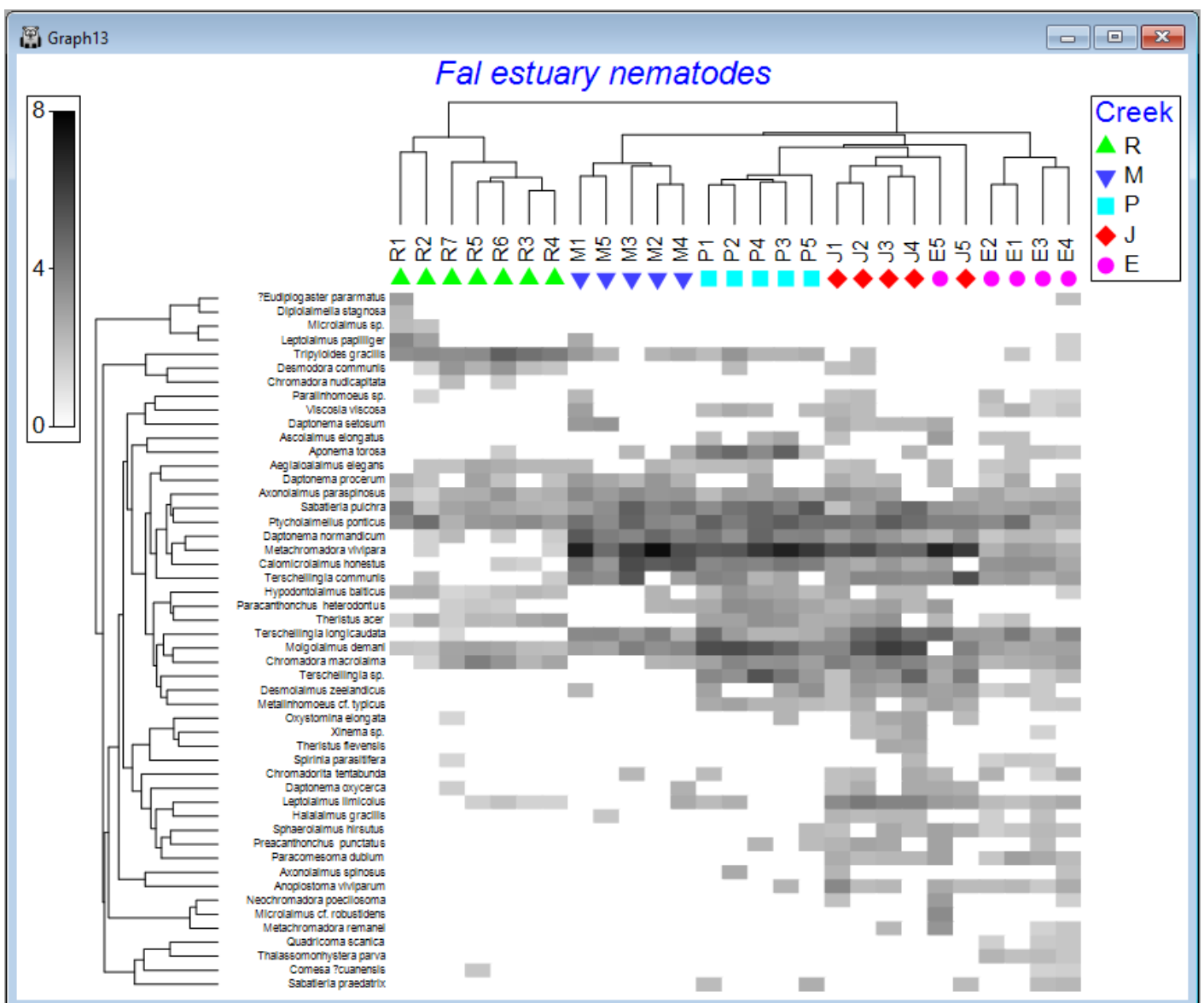
The default graphic ('**Graph13**') shows a shade plot of the 50 most important species (here, 'most important' is defined based on the percent(%) of the total abundance obtained by a species in *any* sample). Each value in the data matrix is represented by a shaded rectangle (from white to black, by default), where the degree of shading corresponds to the abundance values (after fourth-root transformation), as shown in the key (in this example, the transformed data values range from 0 to 8).



Here, samples are ordered so as to maximise their concordance with a model of 'seriation' (or turnover), defined on the basis of Bray-Curtis similarities calculated on fourth-root transformed data. They are (furthermore) constrained according to a dendrogram constructed from a hierarchical group-average cluster analysis of those similarities ('Graph12' in the Explorer tree). The species, in turn, are ordered according to a model of seriation based on an Index of Association calculated among species after first standardising the species variables by their total abundance. They are (similarly) further constrained by their own cluster dendrogram ('Graph11' in the Explorer tree).

It would perhaps be helpful to see the different creeks as different symbols on this plot. With Graph13 (the shade plot itself) as the active item in the Explorer tree, click **Graph > Sample Labels & Symbols**, then choose (Labels ☒ Plot) & (Symbols ☒ Plot > ☒ By factor Creek) and click **OK**.

The screenshot shows the 'Graph Options' dialog box with the 'Samp. labels & symbols' tab selected. The 'Labels' section on the left has 'Plot' checked and 'By factor' unchecked. The 'Creek' factor is selected in the dropdown, and the 'Data font...' button is visible. The 'Symbols' section on the right has 'Plot' checked, 'By factor' checked, and 'Creek' selected in the dropdown. The 'Size' is set to 100. In the 'Default' section, the 'Symbol' is a black square and the 'Colour' is blue. The 'Key...' button is also present. At the bottom are 'OK', 'Cancel', and 'Help' buttons.



We can see from the above image that some creeks contain a rather different set of species and/or different abundances of the same species. The ordering of whole creeks shown in the shade plot (obtained using the 'seriation' model) reflects the ordering we saw in the nMDS plot for these creeks as well (see the page ['Step 4. Ordination'](#)).

From a matrix display (or shade plot), clicking on **Graph > Special** reveals a very large number of colours and other graphical options and parameters allowing the user to alter and enhance this graphic for their purposes. These are too numerous to describe in detail here, but they include a host of methods for sorting the rows and/or columns (i.e., by clicking on the **Reorder...** button in the **Graph > Special** dialog).