

Step 4: Ordination

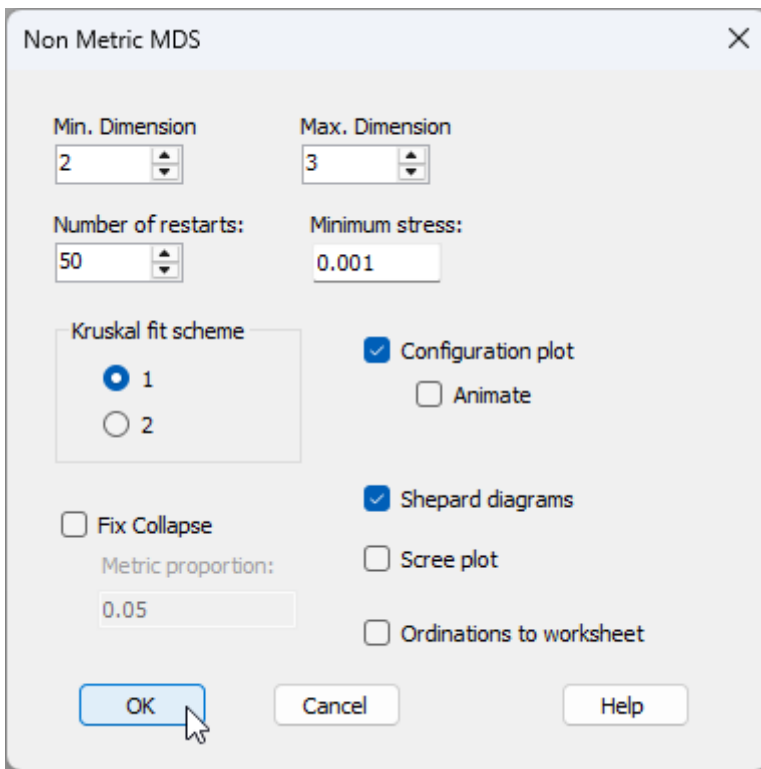
The cluster analysis goes some way towards helping us to understand potential patterns of similarity among the samples. It is particularly good at showing us clusters of samples that are highly similar. To better visualise patterns of relationships among all of the samples simultaneously, we can use methods of **ordination**. In particular, non-metric multi-dimensional scaling (nMDS) is a wonderfully robust tool for visualising high-dimensional systems on the basis of a chosen resemblance measure ([Kruskal & Wish \(1978\)](#) ; [Clarke \(1993\)](#)). Non-metric MDS essentially places points into an arbitrary Euclidean space of set dimension (typically producing a 2D or 3D plot) so as to preserve, as well as possible, the rank-order of the dissimilarities between pairs of samples. For more details on multi-dimensional scaling, see [Chapter 5](#) of '*Change in Marine Communities*'.

Create a non-metric MDS plot

From the Bray-Curtis resemblance matrix ('BC_4th-root' in this example), click **Analyse > MDS > Non-metric MDS...**, then click **OK** to run the MDS algorithm with all of the default options.

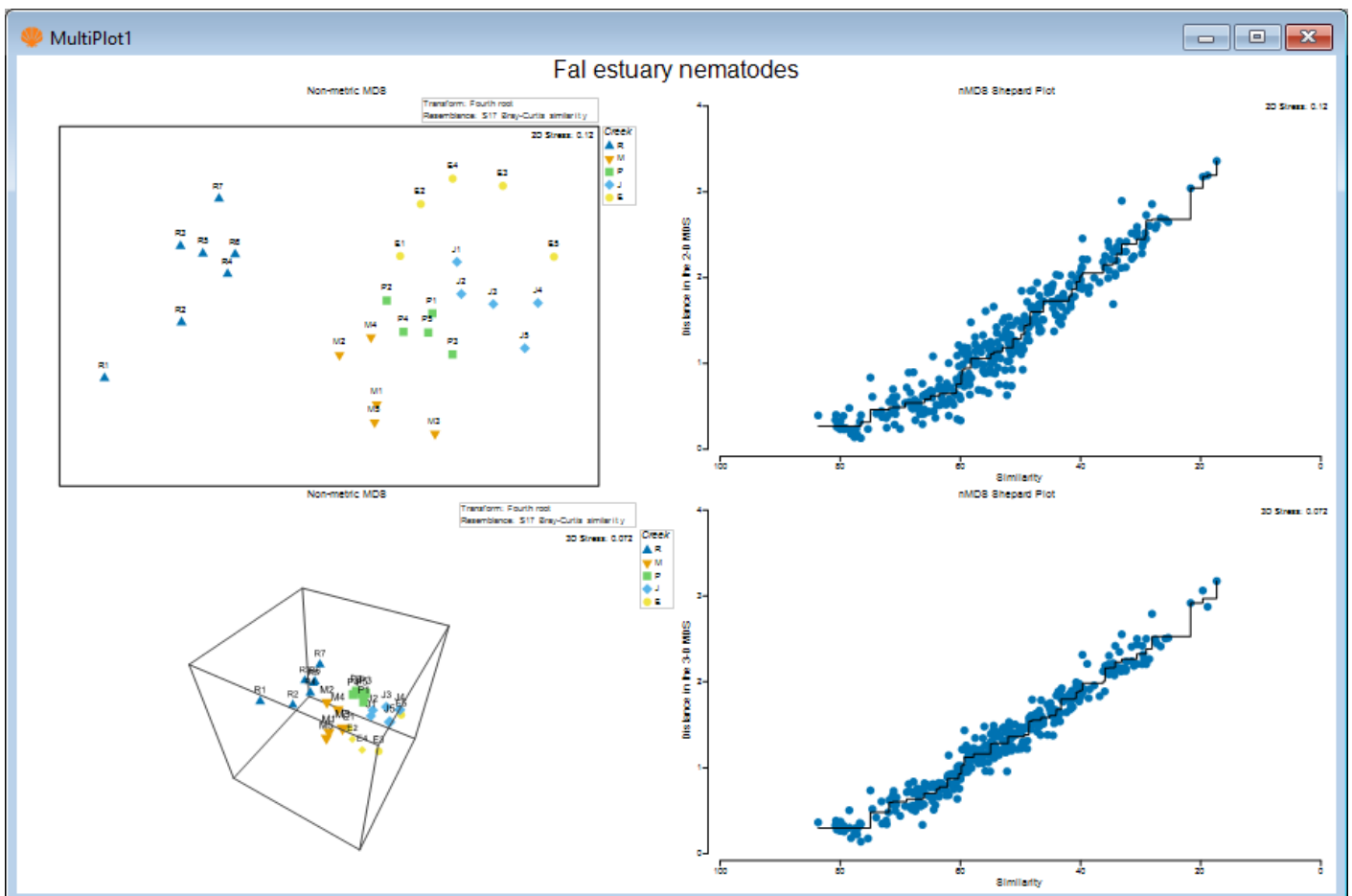
The screenshot shows the PRIMER software interface. The 'Analyse' menu is open, and the 'MDS' option is selected, which has opened a sub-menu where 'Non-metric MDS (nMDS)...' is highlighted. In the background, a table of sample dissimilarities is visible. The table has columns labeled R2, R3, R4, R5, R6, R7, and M1. The rows are labeled R4, R5, R6, R7, M1, M2, M3, M4, M5, P1, P2, P3, and P4. The values represent dissimilarities between the samples.

	R2	R3	R4	R5	R6	R7	M1
R4	53.602	78.516	83.701				
R5	54.444	61.138	77.211	78.462			
R6	51.61	60.184	76.57	77.119	79.357		
R7	43.462	55.112	66.678	67.859	70.821	74.032	
M1	40.004	52.708	38.665	46.935	41.623	43.638	39.71
M2	43.811	49.494	52.47	56.677	57.561	58.843	54.027
M3	32.397	37.747	29.797	39.536	32.493	40.112	32.463
M4	36.844	46.684	47.671	56.551	53.946	59.747	53.01
M5	40.491	44.13	38.527	48.595	41.647	44.155	40.729
P1	29.593	42.889	45.549	49.238	44.34	49.873	43.439
P2	33.267	47.414	51.927	55.219	52.441	57.512	49.872
P3	31.531	40.719	39.818	44.122	40.254	46.193	43.476
P4	36.263	47.423	44.059	51.68	49.344	52.629	44.588

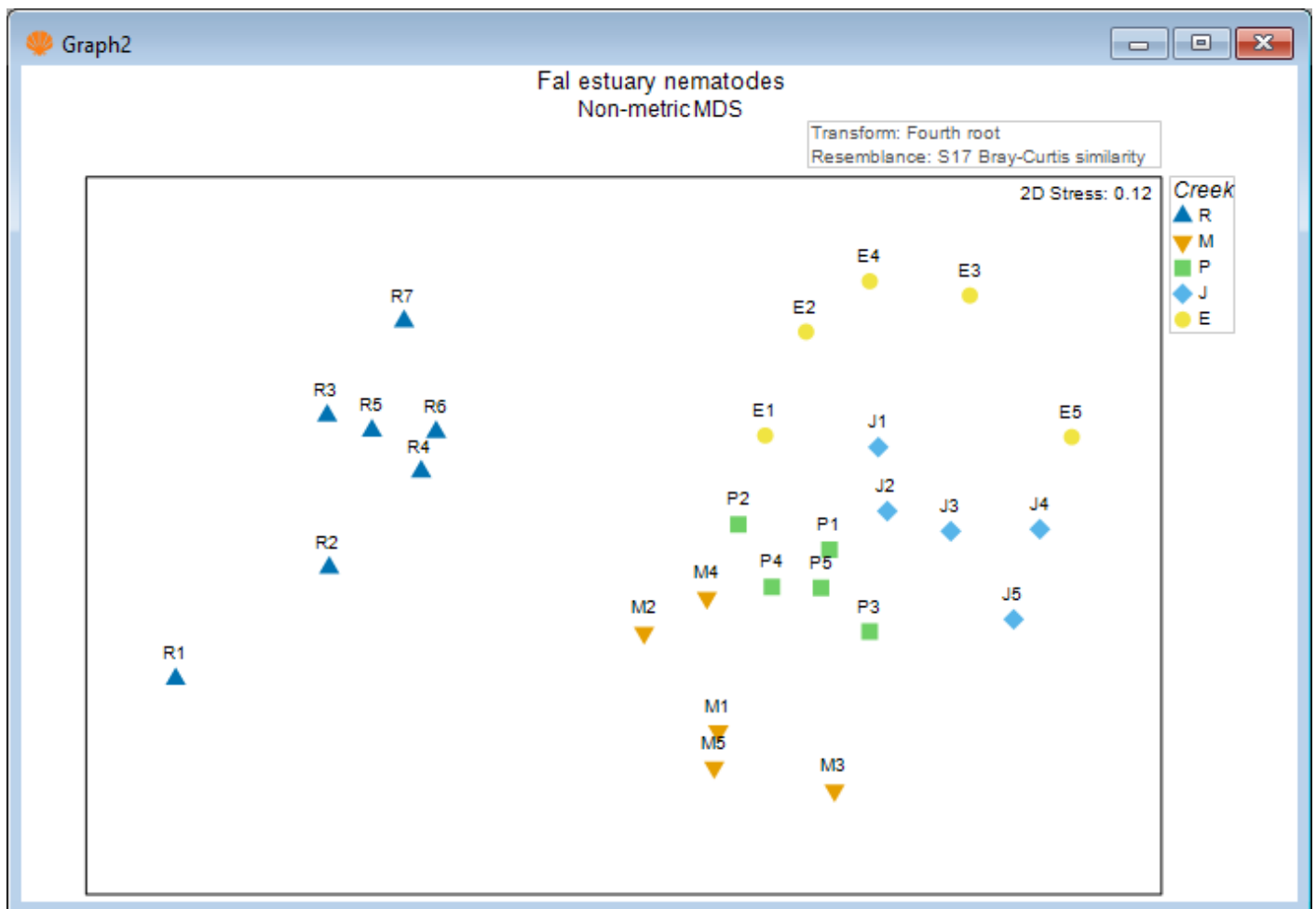


The resulting 'Multi-plot1' output graphic gives you 4 individual plots (in a 2-by-2 array), as follows:

- the best 2D solution (from 50 random starts)
- the Shepard diagram for the best 2D solution
- the best 3D solution (from 50 random starts); and
- the Shepard diagram for the best 3D solution



Clicking on the '+' symbol next to the word 'MultiPlot1' in the Explorer tree reveals the four graphics that comprise this multi-plot object ('Graph2', 'Graph3', 'Graph4', 'Graph5'). If you then click on 'Graph2' in the Explorer tree, or if you click in the Multi-plot itself anywhere on the plot in the upper left-hand corner, you will see a single graphic now; namely the best (lowest-stress) 2-dimensional non-metric MDS plot for the Fal estuary nematodes.



Interpretation

The plot does not have x and y axes, as the scale here is arbitrary. The non-metric MDS algorithm attempts only to preserve rank-order dissimilarities, so interpretations are restricted to relative distances among points in the plot. For example, we can make statements like: "*The dissimilarity between sample R7 and M3 appears to be larger than the dissimilarity between sample M3 and M2*", but we cannot tell (directly from the plot) what the specific sizes of those particular dissimilarities are.

It is clear from this output that Restronguet Creek ('R') has assemblages of nematodes that are quite dissimilar from those found in the other four creeks. That's consistent with what we saw in the cluster analysis of these data. We can, however, get quite a few more insights from the nMDS plot than were apparent in the cluster dendrogram. For example, relationships among the assemblages from the other four creeks seem to be ordered (from the bottom-left towards the top of the plot) as follows: Percuil → St. Just → Pill → Mylor. It is also apparent that the samples from Pill Creek ('P') form a tighter cluster hence are not as variable as the samples from (say) Restronguet Creek ('R'), which are more spread out. Being able to see potential gradients of change in

assemblages, the degree of between-group differences, as well as the relative sizes of within-group dispersions, is all very useful.

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