
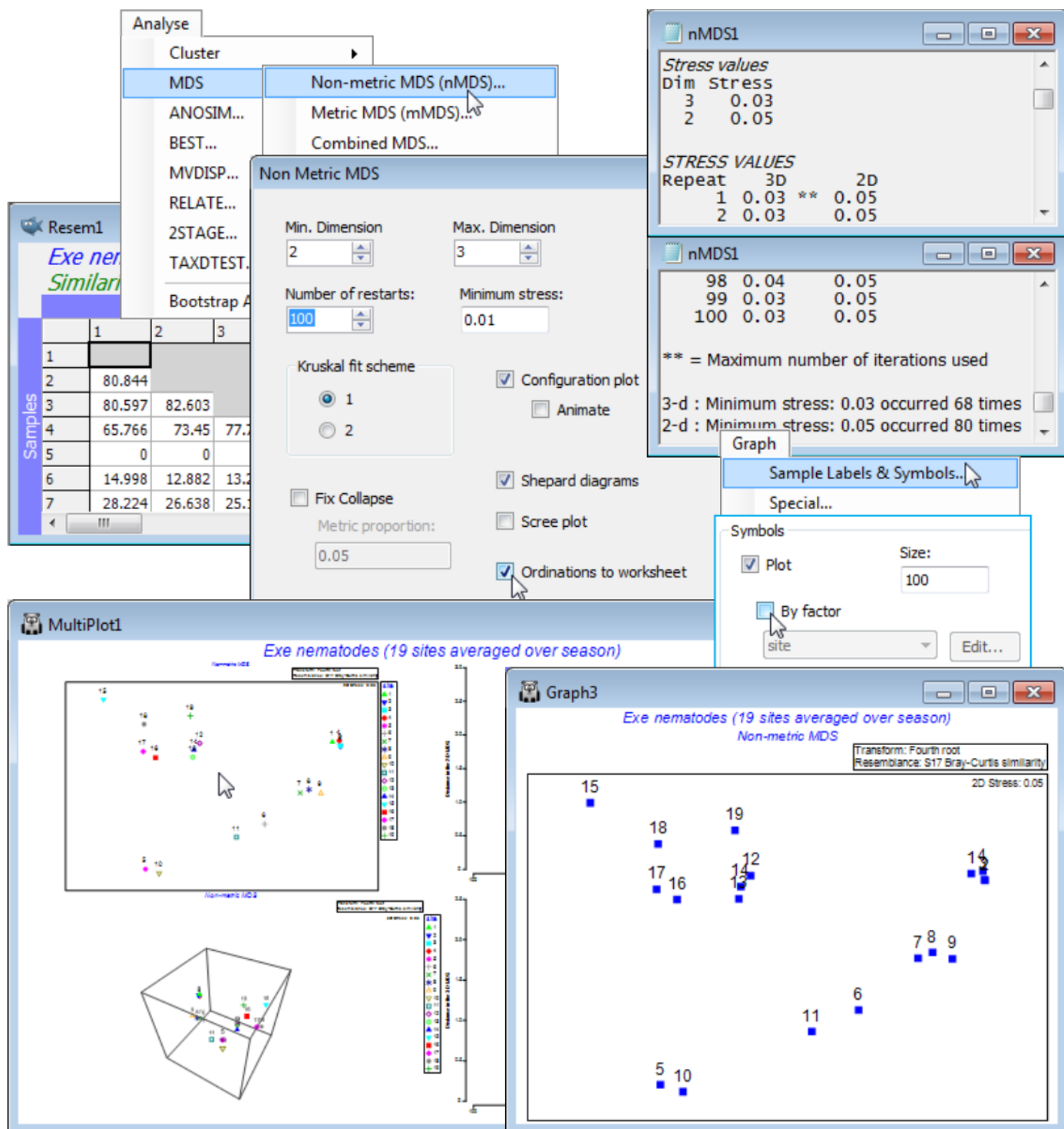


Running an nMDS (Exe nematodes)

From the directory C:\Examples v7\Exe nematodes, **File>Open** the workspace **Exe ws**, last seen in Section 6, of the sediment nematode communities at 19 inter-tidal sites in the Exe estuary. If this does not exist, open the data file **Exe nematode abundance**(.pri) in a clear workspace, and re-run the UPGMA clustering, with **Pre-treatment>Transform (overall)>Transformation: Fourth root** and **Analyse>Resemblance>(Measure•Bray-Curtis similarity)&(Analyse between•Samples)**, then **Analyse>Cluster>CLUSTER>(Cluster mode•Group average)**, and on the resulting dendrogram, **Graph>Special>(Slicing✓ Show slice)>(Resemblance: 30)>Create factor>(Add factor named: 30% slice)**. The Bray-Curtis similarity matrix is in **Resem1** and the dendrogram **Graph1**.

With **Resem1** as the active window, take **Analyse>MDS>Non-metric MDS (nMDS)** and options of (Min. Dimension: **2**)&(Max. Dimension: **3**)&(Number of restarts: **100**)&(Minimum stress: **0.01**) &(Kruskal fit scheme•1)&(✓ Configuration plot)&(✓ Shepard diagrams)&(✓ Ordinations to work sheet) leaving the other boxes unticked for now. The outcome is a results window, **nMDS1**, and a multi-plot **MultiPlot1** which, if unrolled in the Explorer tree (either by clicking the  in the tree or by clicking on any of the plot components in the multi-plot), shows four plot windows, probably named **Graph3** to **Graph6**. For the first one, remove the spread of symbols with **Graph>Sample labels & symbols**, unchecking (Symbols>By factor), to leave just the labelled default symbols.



Revision #1

Created 26 June 2024 00:53:38 by Arden

Updated 26 June 2024 01:11:33 by Arden