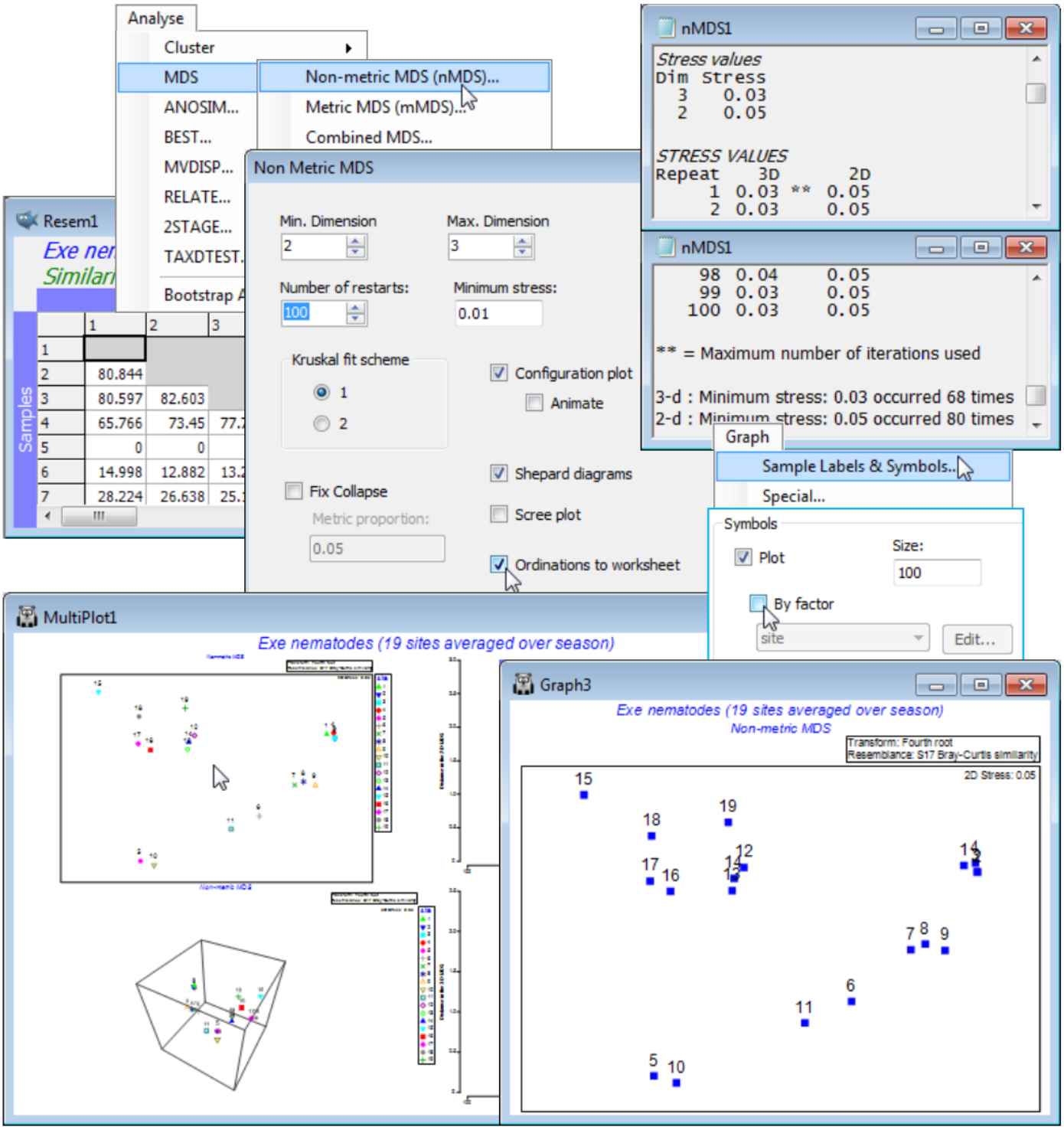
Running an nMDS (Exe nematodes)

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 [image] 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.



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