

Summary of the pathway

A summary of the essential routines in PRIMER that were used to produce the 5-step analysis pathway described above for the nematode (biotic) data from the Fal estuary is given in the table below:

Step	To implement in PRIMER:
1. Fourth-root transformation	<i>From the original data sheet:</i> click Pre-treatment > Transform(overall) > (Transformation: Fourth root), click OK .
2. Bray-Curtis resemblance	<i>From the transformed data sheet:</i> click Analyse > Resemblance > (Measure Bray-Curtis similarity) & (Analyse between Samples), click OK .
3. Hierarchical group-average cluster analysis	<i>From the resemblance matrix:</i> click Analyse > Cluster > CLUSTER... > (Cluster mode Group average) & (Plot dendrogram), click Finish .
4. Non-metric MDS ordination	<i>From the resemblance matrix:</i> click Analyse > MDS > Non-metric MDS (nMDS)... > (see if you are happy with the default settings), click OK .
5. Analysis of similarities (ANOSIM)	<i>From the resemblance matrix:</i> click Analyse > ANOSIM... > Design > (Model: One-Way - A) & Factors > A: Creek) & (Max permutations: 9999) & (Plot histogram), click OK .

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