

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

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