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

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