

# Steps in a PERMANOVA analysis

The two essential steps required to run a PERMANOVA analysis in PRIMER are always:

- *first*, **specify the design**; and
- *then*, **run the PERMANOVA analysis**, given the design, on a chosen resemblance matrix (arising from the data of interest).

Generally, we first need to get our data in to PRIMER, perform appropriate pre-treatment(s), if any, then calculate a resemblance matrix from this. A resemblance matrix will always serve as the starting point for any PERMANOVA analysis.

An analysis of only the mollusc species from the holdfasts in accordance with the three-factor hierarchical design, based on Jaccard resemblances, will follow the following steps:

1. **Open the example data file** in the PRIMER workspace. Select a subset of the variables corresponding to only the mollusc species for what follows.
2. Calculate **Jaccard similarities\*** among the sampling units (individual holdfasts).
3. **Specify the experimental/sampling design** (creating a design file).
4. **Run the PERMANOVA routine** (partitioning and p-values *via* permutation for each term in the model).
5. Do an **ordination of distances among centroids** to visualise the effects and the relative importance of the factors.

*(\*Note: the Jaccard resemblance measure utilises only presence/absence information, so we do not need to perform a pre-treatment transformation step for this example.)*

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