

Bray-Curtis similarity

The most commonly-used similarity coefficient for biological community analysis, because it obeys many of the 'natural' biological guidelines in a way that most other coefficients do not (see CiMC), is the Bray-Curtis similarity, defined between samples 1 and 2 as:

$$S_{17} = 100 \left[1 - \frac{\sum_i |y_{i1} - y_{i2}|}{\sum_i y_{i1} + \sum_i y_{i2}} \right] \equiv 100 \frac{\sum_i \min(y_{i1}, y_{i2})}{\left(\sum_i y_{i1} + \sum_i y_{i2} \right) / 2} .$$

The two forms may not look identical but they are! Here y_{i1} is the count (or biomass, % cover, ...) for the i th (of p) species from sample 1, and $\sum_i(\dots)$ denotes summation over those species. Original references to coefficient definitions are not given here (nomenclature is always a source of debate!) – see [L&L](#), whose numbering scheme is followed where possible, hence S_{17} for Bray-Curtis.

Open the workspace C:\Examples v7\Ekofisk macrofauna\Ekofisk ws from earlier, and click on the Square root counts sheet (obtained earlier with **Pre-treatment>Transform(overall)>Square root**). Take **Analyse>Resemblance>(Measure•Bray-Curtis similarity) & (Analyse between•Samples)**, which are the defaults for this data type. A lower triangular matrix is produced, Resem1, which you should rename B-C on sq rt. **Edit>Properties** (or right-clicking over the matrix to get **Properties**) shows it is of Resemblance type•Similarity from 39 samples. The History box carries through the knowledge of how it was created to a subsequent Cluster or MDS ordination plot. This box is not user-editable, though the Title and Description boxes can be altered; changes to the Title are carried forward to a subsequent plot but not backward to the data sheet Square root.

Now repeat **Resemblance** directly on the original Ekofisk macrofauna counts, without the **Pre-Treatment** transformation. PRIMER tries to help – a warning message appears that no transform has been applied; community matrices usually require some transformation before calculating Bray-Curtis (though you can happily ignore this warning if you are interested in the pattern of the few most dominant species only). **Cancel** the calculation and resave the Ekofisk ws workspace.

PRIMER 7

File Edit Select View Wizards Pre-treatment Analyse Plots PERMANOVA+ Tools Window Help

Resemblance...

CASWELL...
DIVERSE...
DOM...
PCA...
SIMPE...
SIMPE...

Sort...
Properties...
Labels...

Resemblance Matrix Properties

Title: Ekofisk oilfield macrofauna

Resemblance type:
☒ Similarity
☐ Dissimilarity
☐ Distance
☐ Distance^2
☐ Correlation
☐ R
☐ Rank

Between:
☒ Samples
☐ Variables
☐ Other

History:
 Transform: Square root
 Resemblance: S17 Bray-Curtis similarity

Number of row/columns: 39

Description:
 39 sites in an approximately 5-spoke radial design, re-arranged in order of increasing distance from the centre of drilling activity (S30, S36, ..., S5) and with species in alphabetic order.
 The factor 'Distance Groups' categorises the sites into 4 groups (to

Resemblance

Measure:
☒ Bray-Curtis similarity
☐ Euclidean distance
☐ Index of association
☐ Other

Analyse between:
☒ Samples
☐ Variables

Add dummy variable:
 Value: 1

Similarity ☒ Distance/dissimilarity ☒
 Quantitative ☐ P/A ☐
 Correlation ☐ Taxonomic P/A ☐
 (exc0-0 = excluding joint absences)
 S1 Simple matching

Resem1

Ekofisk oilfield macrofauna
 Similarity (0 to 100)
 Samples - Sites (increasing distance from)

	S30	S36	S37	S31
S36	69.586			
S37	57.901	53.141		
S31	66.507	81.873	58.864	
S3	52.929	71.757	49.111	

Revision #27

Created 30 May 2024 01:35:49 by Arden

Updated 15 January 2025 01:04:05 by Abby Miller