

# 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  $\sum_i (...)$  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...

Ekofisk ws  
Ekofisk macrofauna counts  
Overall Transform 1  
Square root  
Shade Plot1  
Shade Squar  
Overall Transform2  
Fourth root

Square root  
Ekofisk oilfield  
Abundance  
Abra prismatica

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

Measure  
☒ Bray-Curtis similarity  
☐ Euclidean distance  
☐ Index of association  
☐ Other  
☒ Similarity ☒ Distance/dissimilarity  
☐ Quantitative ☐ P/A  
☐ Correlation ☐ Taxonomic P/A  
 (exc0-0 = excluding joint absences)  
 S1 Simple matching

Analyse between  
☒ Samples  
☐ Variables

Add dummy variable  
Value: 1

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	

OK

OK Cancel Help

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