

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.

The screenshot shows the PRIMER 7 software interface. The main window displays a project tree on the left with 'Ekofisk ws' as the root, containing 'Ekofisk macrofauna counts', 'Overall Transform 1', 'Square root', 'Shade Plot1', 'Shade Squar', 'Overall Transform2', and 'Fourth root'. The central plot area shows a 'Square root' transformation of 'Ekofisk oilfield Abundance' with a bar chart for 'Abra prismatica'.

The 'Analyse' menu is open, showing options like 'Resemblance...', 'CASWELL...', 'DIVERSE...', 'DOM...', 'PCA...', 'SIMPE...', and 'SIMPE...'. The 'Resemblance...' option is selected, opening the 'Resemblance Matrix Properties' dialog box.

The 'Resemblance Matrix Properties' dialog box has the following settings:

- Title: Ekofisk oilfield macrofauna
- Resemblance type: ☒ Similarity, ☐ Dissimilarity, ☐ Distance, ☐ Distance^2, ☐ Correlation, ☐ R, ☐ Rank
- Between: ☒ Samples, ☐ Variables, ☐ Other
- 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
- History: Transform: Square root, Resemblance: S17 Bray-Curtis similarity

The 'Resemblance' dialog box is also open, showing the following settings:

- Measure: ☒ Bray-Curtis similarity, ☐ Euclidean distance, ☐ Index of association, ☐ Other
- Analyse between: ☒ Samples, ☐ Variables
- Add dummy variable: ☐ (Value: 1)
- Similarity: ☒ Similarity, ☒ Distance/dissimilarity
- Quantitative: ☐ Quantitative, ☐ P/A
- Correlation: ☐ Correlation, ☐ Taxonomic P/A
- (exc0-0 = excluding joint absences)
- S1 Simple matching

The 'Resem1' dialog box is also open, showing a similarity matrix for 'Ekofisk oilfield macrofauna'.

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	

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