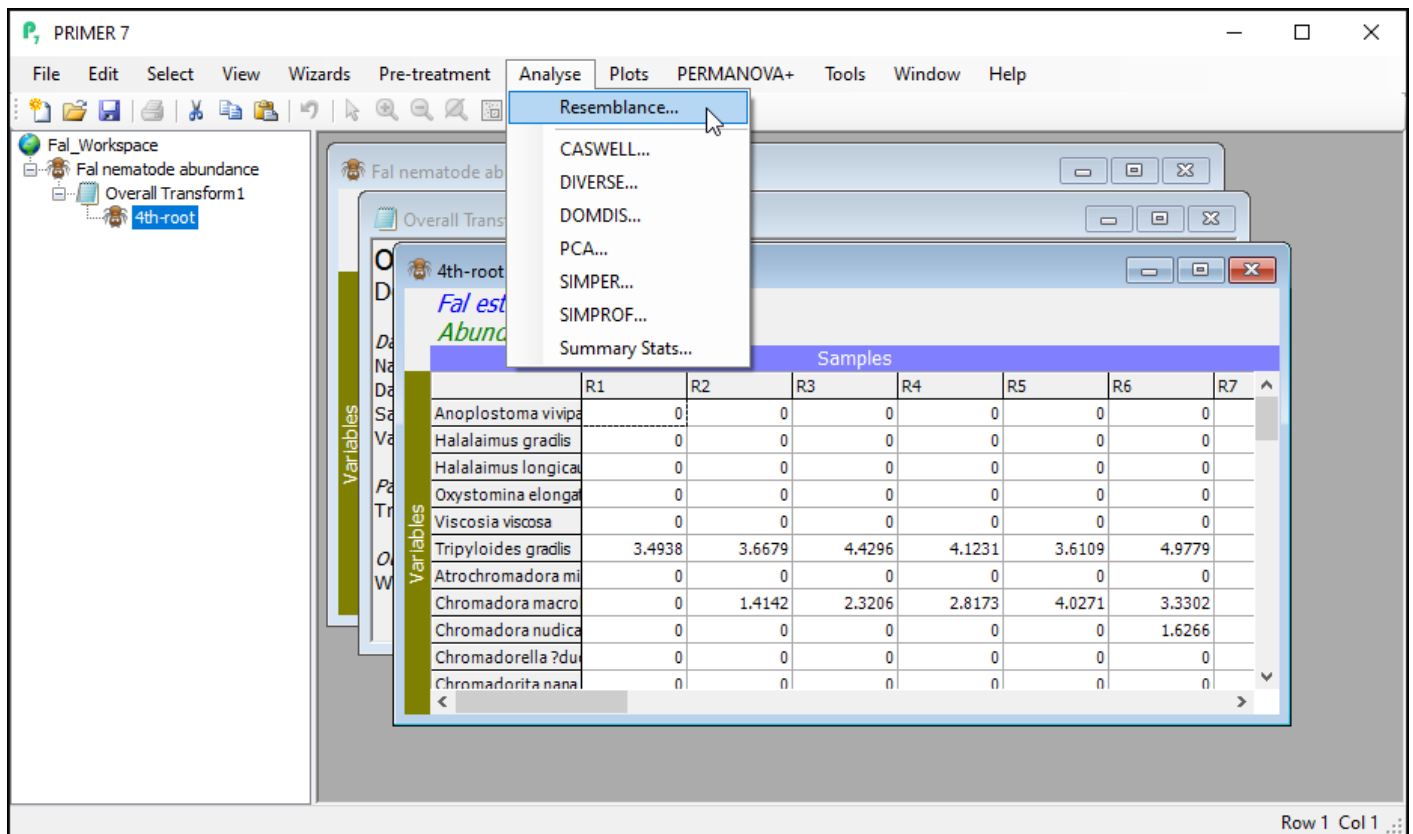


# Step 2: Resemblance

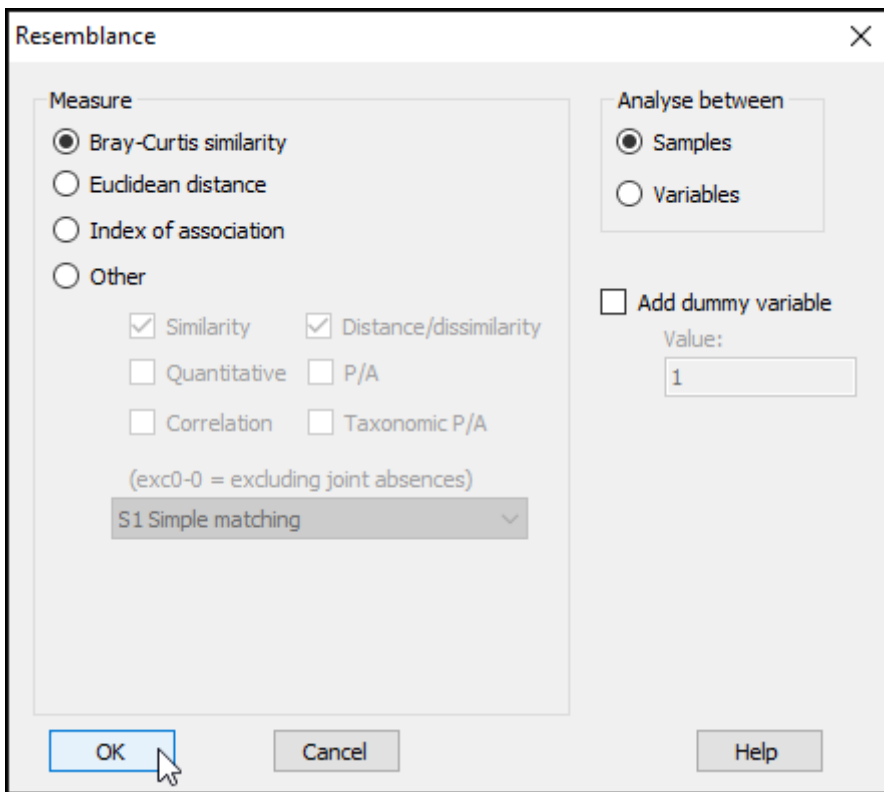
For a description of the Bray-Curtis resemblance measure and the rationale for its use with biotic data, see [Clarke et al. \(2006\)](#) and [Chapter 2](#) in '*Change in Marine Communities*'.

1. With the data sheet named '4th-root' from the previous step as the active window, click on **Analyse > Resemblance...**

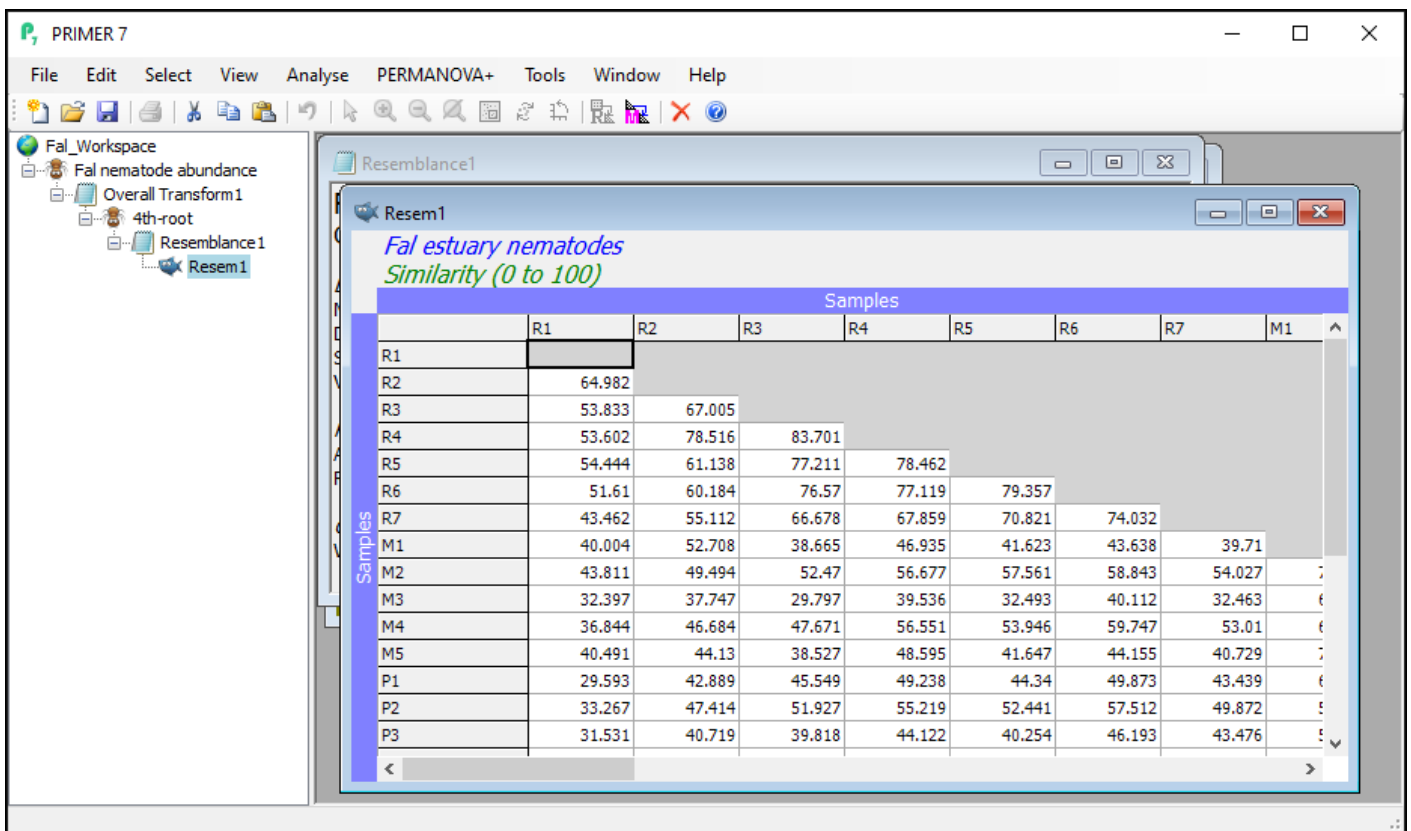


This dialog has a host of choices for you to consider, which you can uncover by clicking on the 'Other' radio button. See [Clarke et al. \(2006\)](#) and chapter 7 in [Legendre & Legendre \(2012\)](#) for more details regarding the available choices here. For this example, however, we are going to use the Bray-Curtis resemblance measure. (This is the default for data of type 'Abundance').

2. In the 'Resemblance' dialog, under 'Measure', click on ☒ Bray-Curtis similarity (the default), then click **OK**.



You will see the resulting (lower triangular form of the) matrix of Bray-Curtis similarities between every pair of samples (called 'Resem1').



Notice that this will inherit relevant properties and also factors that were associated with the dataset from which it was generated. From the 'Resem1' matrix as the active window, click on **Edit** > **Properties** to see the properties associated with this resemblance matrix (shown below); you can also click on **Edit** > **Factors** to see the factors (which have not changed).

Resemblance Matrix Properties

Title:  
Fal estuary nematodes

Resemblance type

☒ Similarity

☐ Dissimilarity

☐ Distance

☐ Distance^2

☐ Correlation

☐ R

☐ Rank

Between

☒ Samples

☐ Variables

☐ Other

History:

Transform: Fourth root  
Resemblance: S17 Bray-Curtis similarity

Number of row/columns: 27

Description:

Abundance of nematodes (counts from identifications in a random sub-sample multiplied up by total nematode count for each sample, so has the statistical properties of density rather than pure count).  
Data from meiofauna cores of the sediments of 27 sites over 5

OK Cancel Help

- It is (once again) good practice to re-name the sheet containing the resulting resemblance matrix (currently called 'Resem1') something that would be more useful for future reference. Click on the 'Resem1' sheet, then click on **File > Rename Resem** and call it 'BC\_4th-root' for clarity in ensuing analyses.

PRIMER 7

File Edit Select View Analyse PERMANOVA+ Tools Window Help

New... Ctrl+N  
Open... Ctrl+O  
Undo Workspace  
Close Workspace  
Save Workspace Ctrl+S  
Save Workspace As...  
Save Resem As...  
Rename Workspace...  
Rename Resem F2  
Delete Resem  
Recent Workspaces  
Recent Items  
Exit

Resem1

*Fal estuary nematodes*  
*Similarity (0 to 100)*

	R1	R2	R3	R4	R5	R6	R7
R1							
R2	64.982						
R3	53.833	67.005					
R4	53.602	78.516	83.701				
R5	54.444	61.138	77.211	78.462			
R6	51.61	60.184	76.57	77.119	79.357		
R7	43.462	55.112	66.678	67.859	70.821	74.032	
M1	40.004	52.708	38.665	46.935	41.623	43.638	39.
M2	43.811	49.494	52.47	56.677	57.561	58.843	54.0
M3	32.397	37.747	29.797	39.536	32.493	40.112	32.4
M4	36.844	46.684	47.671	56.551	53.946	59.747	53.
M5	40.491	44.13	38.527	48.595	41.647	44.155	40.7
P1	29.593	42.889	45.549	49.238	44.34	49.873	43.4
P2	33.267	47.414	51.977	55.219	52.441	57.517	49.8

Row 1 Col 1

PRIMER

Rename

BC\_4th-root

OK Cancel Help

Revision #20

Created 13 February 2024 03:50:09 by Marti

Updated 12 April 2024 03:43:27 by Marti