

# Transform on resemblances;

## Combining resemblances

Transforming resemblances remains in the **Tools** menu in PRIMER 7, since it is not an option for pre-treatment of data matrices prior to resemblance calculation (which characterises the other items on the **Pre-treatment** menu). Although not commonly required, it facilitates at least a couple of interesting analysis concepts. One is really outside the scope of this manual, namely to examine the extent to which the semi-parametric PERMANOVA tests are robust to (monotonic) transformation of the resemblance values, transformations which would not change the ANOSIM test results in any way (since they are based only on the ranks of the resemblances). It is empirically well-known, for example, that the square root of Bray-Curtis (unlike Bray-Curtis itself) does not give negative eigenvalues for the high-d PCO ordination which underpins the approaches in PERMANOVA+. Whether the consequentially poorer low-d PCO representation is a price worth paying for a PCO space without imaginary axes must be open to question, however.

**Tools>Transform** on a single resemblance matrix provides a basic tool to assist in following up such questions. More simply, we have already seen it used (under **Correlation as similarity** in Section 5) to turn a correlation with values in  $(-1, 1)$  into a similarity over  $(0, 100)$  by use of the transform Expression:  $100 * \text{Abs}(V)$ .

Another use of **Tools>Transform** on resemblance matrices is also less esoteric and potentially of substantial practical benefit. It provides an interesting solution to the handling of ecological data matrices from mixed faunal types, e.g. counts of motile organisms and cover of colonial species within the same rocky-shore quadrats. This type of problem was raised earlier (end of Section 8), when two resemblance matrices over the same set of samples were combined in a single MDS, by minimising an average stress function. The difficulty with that approach is that it only generates an MDS, and many of the methods in PRIMER do not work in the approximate low-d space of an ordination but on the full resemblance matrix (or usually its ranks). However, whilst counts and area covers are difficult to scale in relation to each other in a single data matrix, it is not difficult to calculate Bray-Curtis similarities (say) for a count matrix and a cover matrix separately, for the same set of samples, and then simply average the two resemblance matrices over every matching pair of entries using **Tools>Transform**, using a similar worksheet-based transform expression to that previously demonstrated. (Dis)similarity values in the range  $(0, 100)$  for both matrices will stay in  $(0, 100)$  under the arithmetic averaging expression of  $(A+B)/2$  (or a weighted form,  $(3*A+B)/4$ , if the contribution of counts is considered roughly three times as important as that from area cover). Geometric averaging of the type seen above is also possible, e.g.  $(A*B)^{0.5}$  or  $(A^{0.75})*(B^{0.25})$ . If the two resemblance matrices are not on a common scale and direct averaging is not appropriate, a simple solution would be to run both through **Tools>Rank distance**, putting them on a common scale – and fitting well with PRIMER's non-parametric approach – then averaging as above and re-ranking (though the latter is unnecessary for most PRIMER routines, which do their own ranking).

A simple example using two resemblance matrices can be constructed with the Clyde data, namely the Bray-Curtis site similarities averaged over abundance and biomass measures. So, instead of combining the data matrices (as in the earlier  $A^{0.25} B^{0.75}$ ), we average the *A* and *B* resemblances. There is likely already to be a Bray-Curtis similarity matrix based on the square-root transformed biomass data from **Clyde macrofauna biomass** in the workspace (rename it **ResemB**) and you should now also compute Bray-Curtis similarities from **Clyde macrofauna counts**, this time on fourth-root transformed data (there is no reason why a different transform should not be appropriate for abundance than for biomass data). Then with the abundance similarities **ResemA** as the active sheet, take **Tools>Transform>**(Expression:  $(V+WORK("ResemB"))/2$ ), change the title of the result appropriately, and run **Analyse>MDS** to compare this with the earlier (ranked) biomass MDS.

The screenshot displays the PAST software interface with several windows open:

- ResemA**: Shows a similarity matrix for Clyde counts. The title is "Clyde counts Bray-Curtis Similarity (0 to 100)". The data table is as follows:
 

Samples - Sites along transect	S1	S2	S3
S2	47.473		
S3	34.689	64.66	
S4	37.16	55.599	69.675
S5	13.91	28.433	43.456
S6	13.493	0	7.906
- ResemB**: Shows a dissimilarity matrix for Clyde biomass. The title is "Clyde biomass Bray-Curtis Dissimilarity (0 to 100)". The data table is as follows:
 

Samples - Sites along transect	S1	S2	S3	S4
S2	40.824			
S3	25.38	58.404		
S4	28.169	56.367	59.458	
S5	2.4851	17.126	31.306	42.126
S6	0	0	1.1949	1.6058
- TRANSFORM**: The "Expression" field contains  $(V+WORK("ResemB"))/2$ . The "Worksheet" option is selected under the "Pick" section.
- Resem8**: The result of the transform, titled "Clyde - average of A and B similarities Similarity (0 to 100)". The data table is as follows:
 

Samples - Sites along transect	S1	S2	S3	S4	S5	S6
S2	44.149					
S3	30.035	61.532				
S4	32.665	55.983	64.566			
S5	8.1976	22.78	37.381	46.532		
S6	6.7463	0	4.5505	6.5497	18.356	
S7	5.6715	5.2659	16.637	22.703	44.581	29.687
- Transform6**: A dialog box for the transform operation. It shows the expression  $(V+WORK("ResemB"))/2$  and indicates that all samples were transformed.
- Graph20**: An MDS plot titled "Clyde - average of A and B similarities Non-metric MDS". The plot shows 12 samples (S1-S12) plotted in a 2D space with a stress of 0.07. The points are connected by lines, showing a clear separation between S1-S12 and S3-S4.

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