

Expand Samples or Expand resemblances

The **Exe environment** matrix does not seem (from **Plots>Draftsman Plot** or **Histogram Plot**) to contain notable outliers and can safely be used without transformation of individual variables. It does however need **Pre-treatment>Normalise Variables** - rename it **Abiotic norm**. To expand this data matrix to the dimensions of 108 samples \times 6 variables, with **Abiotic norm** as the active sheet take **Tools>Expand Samples>**(Expand as data worksheet: **Exe nematodes bi-monthly**) & (Match original labels to factor: **site**). The fourth-root form of the biotic data matrix could equally well have been used in place of the original nematode sheet - what is needed from it is the size of expanded matrix needed, and the structure of samples over the sites, from the factor **site** whose levels 1, ..., 19 are matched up with the labels 1, ..., 19 of the normalised environmental sheet. The expanded environmental matrix is then entered to a Euclidean distance resemblance calculation, to give **Euclid expanded**. The same construction can be achieved by first taking Euclidean distance on the **Abiotic norm** data matrix, to give a resemblance matrix renamed **Euclid**, and then entering this as the active matrix in **Tools>Expand>**(Expand as resemblance worksheet: **B-C 4rt**) & (Match original labels to factor: **site**) to obtain exactly the same model (abiotic) matrix **Euclid expanded**.

Now with active sheet **B-C 4rt** a further run of **Analyse>RELATE>**(Secondary data•Resemblance /model matrix: **Euclid expanded**) gives a much larger ρ of 0.72 (highly significant, of course, at $p < 0.01\%$ for the 9999 permutations of this run), indicating the very good fit of the individual bi-monthly samples to the alternative model of sites differences, structured by these abiotic variables.

The screenshot illustrates a workflow in PAST software for expanding environmental variables and calculating a RELATE statistic. The process involves several windows and data tables:

- Abiotic norm**: Shows environmental variables for 19 sites. Example: 6 EVs (normalised) at 19 sites. Environmental variables include Med Pa, Dep Wa, Dep H2, Shore h, %Orga, and Intersti.
- Abiotic expanded**: Shows the same 6 EVs expanded to a biotic matrix dimension. Environmental variables are the same as in the 'Abiotic norm' window.
- Exe nematodes bi-monthly**: Shows abundance data for 19 sites x 6 'reps'. The 'Samples' table is as follows:

	1A	1B	1C	1D	1E	1F	2A	2B	2C
Mesoth	210	20	45	15	100	150	50	45	10
Anoplos	155	45	295	45	250	330	330	0	5
Sabatier	80								
- Euclid exp...**: Shows Euclid distance on 6 EVs expanded. The 'Samples' table is:

	1D	1E	1F	2A
1F	0	0		
2A	0.750	0.750	0.750	
2B	0.750	0.750	0.750	0
2C	0.750	0.750	0.750	0
2D	0.750	0.750	0.750	0
2E	0.750	0.750	0.750	0
2F	0.750	0.750	0.750	0
3A	1.524	1.524	1.524	0.802
- B-C 4rt**: Shows Nematodes: B-C on 4rt Similarity (0 to 100). The 'Samples' table is:

	1D	1E	1F	2A
1F	63.93	81.28		
2A	61.01	71.01	66.31	
2B	21.32	18.26	30.69	20.92
2C				
- Euclid**: Shows Euclid distance on 6 EVs 19 sites. The 'Samples - sites' table is:

Sample	1	2
2	0.750	
3	1.524	0.802
4	2.156	1.438
5	4.996	5.183
- Factors**: Shows a table for matching original labels to factors:

Label	site	time
1A	1	A
1B	1	B
1C	1	C
1D	1	D
1E	1	E
1F	1	F
2A	2	A
2B	2	B
2C	2	C
- RELATE1**: Shows the result of the RELATE analysis:

Sample statistic (Rho): 0.721
Significance level of sample statistic: 0.01 %

The workflow involves expanding the 'Abiotic norm' data into a biotic matrix ('Abiotic expanded') and then calculating Euclid distance ('Euclid exp...') and B-C 4rt similarity ('B-C 4rt'). The 'Euclid' window shows the distance between samples, and the 'RELATE1' window shows the result of the RELATE analysis, which is a histogram of the frequency of the sample statistic (Rho) and its significance level.

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