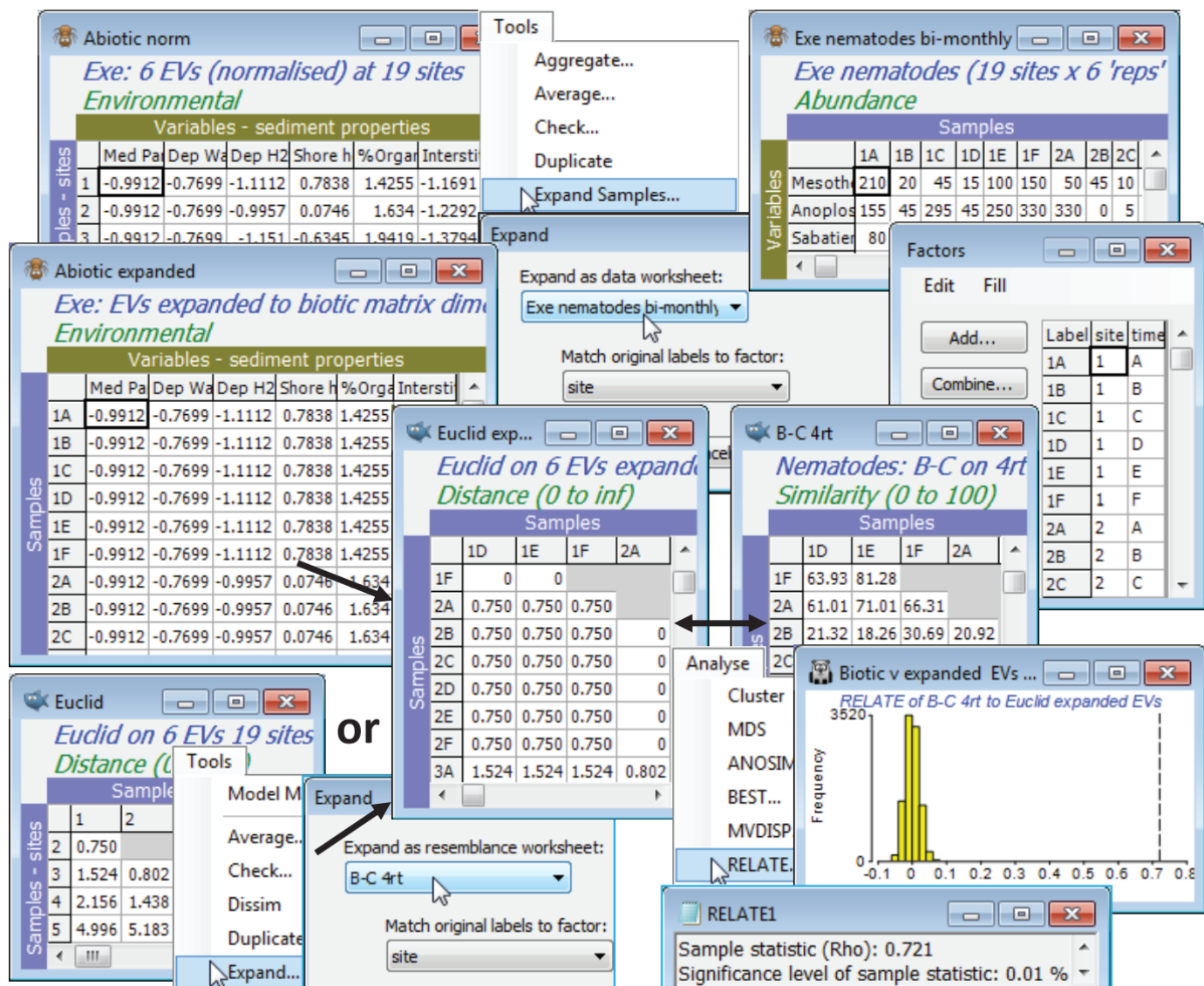


Expand Samples or Expand resemblances

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.



Revision #1

Created 15 October 2024 21:48:29 by Arden

Updated 15 October 2024 21:59:06 by Arden