RELATE on resemblance matrices

The BEST routine in the previous section introduced the concept of measuring how closely related two sets of multivariate data are, for a matching set of samples, by calculating a rank correlation coefficient (Spearman's ρ, Kendall etc.) between all the elements of their respective (dis)similarity matrices. Thus, if the among-sample relationships agree, in exactly the same way in both data sets (e.g. the two closest samples are 3 and 5, the next two closest are 7 and 15, …, and the furthest apart are 6 and 11), then the rank correlation ρ = 1, a perfect match. (These element-by-element correlations of two resemblance matrices are known as *matrix correlations* or *Mantel coefficients*, though Mantel – working in epidemiology – defined them with standard Pearson correlations, a less flexible option than rank correlations for our purposes but one which PRIMER now provides). The two resemblance matrices to be compared in this way need not be of biotic and environmental data respectively, but can come from any source: biotic compared with biotic, abiotic with abiotic, biotic with a *model matrix*, etc. – it is only necessary that they refer to matching sample labels.

PRIMER performs the calculations by the **Analyse>RELATE** routine, with active window as one of the resemblance matrices to be compared. In fact, RELATE allows the user either to supply the second matrix as another triangular resemblance sheet (the general case) or to specify one of two special cases of simple model matrices, which the routine then constructs for itself. The first is referred to as *seriation*, where the data is compared to a linear sequence, either in space or time, i.e. the matching coefficient ρ assesses the extent to which samples follow a simple trend: adjacent samples being the closest in species composition, samples two steps apart the next closest, and so on, with assemblages from the first and last samples differing the most. Chapter 15 of CiMC gives more detail on model matrix construction, and draws the clear link between the RELATE test for seriation and the *ordered ANOSIM* test seen in Section 9 (and described in Chapter 6 of CiMC). RELATE, however, is able to accommodate more complex hypothesised models than the simple serial trends of ordered ANOSIM (with or without replication), e.g. the other model RELATE constructs automatically is simple *cyclicity*, with the sample relationships thought of as matching those of distances between points placed equidistantly around a circle. A possible context could be monthly samples taken over a full year. With a seasonal signal one might expect adjacent months to be the most similar, months two steps apart less similar etc., but the assemblage structure for later months gradually returns to that at the start, so that Dec and Jan are only one step apart, not 11.

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