Model matrix construction

Model matrices corresponding to more complicated structures than simple seriation or cyclicity need first to be constructed by the user and then entered to RELATE in the same way as any other resemblance matrix being matched to the active sheet. There are at least three ways of obtaining such model matrices. Firstly, they can be read in directly as a triangular matrix, e.g. as an existing physical distance matrix between the sampling points – there the idea would be to judge how well the community dissimilarities match geographical layout. Secondly, they can be produced from simple *x* (or *x*, *y* or *x*, *y*, *z*) co-ordinates of the sample points by running this 1- (or 2- or 3-) variable data sheet through **Analyse>Resemblance**, choosing Euclidean distance. For example, if simple seriation (perhaps for an inter-annual time trend) was not already catered for directly in **Analyse> RELATE**, it could be handled by creating a data sheet with one variable and *n* samples, of entries 1, 2, ..., *n*, and calculating Euclidean distances – producing a lower triangular matrix with 1's on the diagonal, 2's on the first off-diagonal, ..., down to *n*–1 in the lower left corner. And a model distance matrix corresponding to a monthly season cycle would result from the *x*, *y* co-ordinates of numbers on a clock face being input to Euclidean distance (again, non-normalised). This will not give model entries which are integers but the distances will be in the correct rank order – which is all that matters for RELATE's rank correlations). For a geographical layout, enter the metric form of lat/long co-ordinates to Euclidean distance. Thirdly, however, PRIMER helps you to construct model matrices directly from specified factors using **Tools>Model Matrix**, which is run when the active sheet is the biotic resemblance matrix to be compared with the model. An example given below is of *seriation with replication*, namely four groups of samples considered to be at points 1, 2, 3, 4 along a line (thus dissimilarity between group 1 and 2 is less than that for 1 and 3, or 2 and 4, and that for 1 and 4 is larger still). This cannot be handled by choice of the *seriation* option in **RELATE** because that is only appropriate to single samples at each space (or time) point – here there are replicates in each group, considered to be at distance 0 from each other. **Tools>Model Matrix**, specifying a numeric factor with appropriate levels 1, 2, 3, 4, will create the correct model.

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