16.4 Further extensions

Both BEST Bio-Env and BVStep routines can be generalised to accommodate possibilities other than their ‘defaults’ of selecting abiotic variables to optimise a match with fixed biotic similarities, and selecting subsets of species to link to the sample patterns of the full species set. In fact, the only distinction between the two options in BEST is simply one of whether a full search is performed (Bio-Env) or a stepwise search is adopted (BVStep), the latter being essential where there are many variables to select from (e.g. >16) so that a full search is prohibitive ($> 2 ^ {16} $ combinations).

The fixed similarity matrix can be from species (e.g. Bray-Curtis), environmental variables (e.g. Euclidean), or even a *model matrix*, such as the equally-spaced inter-point distances in the seriation matrix of Chapter 15. The secondary matrix, whose variables are to be selected from, can also be of biotic or abiotic form. Some possible applications involve searching for:¶

1. species within one faunal group that ‘best explain’ the pattern of a different faunal group (‘Bio–Bio’), e.g. key macrofaunal species which are structuring (or are correlated with environmental variables that are structuring) the full meiofaunal assemblages;

2. species subsets which best respond to (characterise) a given gradient of one or more observed contaminants (‘Env–Bio’);

3. species subsets which match a given spatial or temporal pattern (‘Model–Bio’), e.g. the model might be the geographic layout of samples, expressed literally as inter-sample distances, or a linear time-trend (equal-spaced steps, as with seriation), or a circular pattern appropriate to a single seasonal cycle, etc;

4. subsets of environmental variables which best characterise an *a priori* categorisation of samples (‘Model-Env’), e.g. selecting quantitative beach morphology variables which best delineate a given classification of beach types (Valesini, Clarke, Eliot *et al.* (2003)).

¶ *All these combinations are possible in the PRIMER BEST routine with either Bio-Env (full search) or BVStep (stepwise) options. In v7, the fixed resemblance matrix (biotic, abiotic or model) is the active sheet from which the BEST routine is run, and determines the samples to be analysed. The secondary data matrix supplied to the routine, from which variables are to be selected, can be a ‘look-up table’ of a larger set of samples (e.g. from an environmental database for that region) but all sample labels in the resemblance matrix must have a matching sample label in the data matrix. (In v6, the active sheet was the data matrix and not the resemblance matrix but the v7 structure is more logical, and consistent with the analogous DISTLM routine in PERMANOVA+).*

Revision #5
Created 10 March 2022 11:03:35 by Arden
Updated 13 November 2024 01:37:12 by Abby Miller