BVStep (Morlaix macrofauna)

Re-open the Morlaix ws workspace in C:\Examples v7\Morlaix macrofauna from earlier in this section, or since this is all that is needed, just open the data file Morlaix macrofauna abundance into a clear workspace. It consists of 21 sampling times and 251 species. Clarke & Warwick 1998 reasoned that many of these species were sufficiently rare (over half have totals across all samples in single figures) that the problem could be scaled down by removing those – so reduce to the *most important* 100 (see Section 3). Thus, **Select>Variables**>(•Use n-most important where n is 100) on Morlaix macrofauna abundance, then fourth-root transform, naming it 4rt data. (A severe transform seems the best choice, otherwise the counts of tens of thousands in a few species will dominate, as can be seen from a shade plot). Generate the *n*MDS ordination from Bray-Curtis similarities on this reduced, transformed data, calling the resemblance matrix B-C on 4rt. This is the active sheet on entry to **Analyse>BEST**, which takes the transformed data matrix 4rt data as its secondary sheet and searches for the smallest possible subset of the 125 species that effectively contains (to within ρ>0.95) the same among-sample information as B-C on 4rt. It is clear that the full enumeration of possibilities in the (•BIOENV) option would never be possible (2^{100} species combinations!) so the stepwise option of (•BVSTEP) is necessary. Even with the reduction of species numbers, it must be realised that many of these 100 species will be highly inter-correlated, and it is inevitable that many marginally different combinations of species will do an almost equally good job as indicators of the full data set (a point also made in Section 13 about linking biotic and abiotic variables). It is desirable therefore to start the search from several random subsets (perhaps 50), and look at all the output results (Detailed) – if only to appreciate that we are very far from having a single ‘correct’ answer! Nonetheless, it is interesting to see that the detailed MDS based on 100 species can be reproduced almost perfectly by several competing selections of only 8 or 9 species, as follows.

Revision #4
Created 28 October 2024 01:11:15 by Arden
Updated 25 February 2025 23:09:02 by Abby Miller