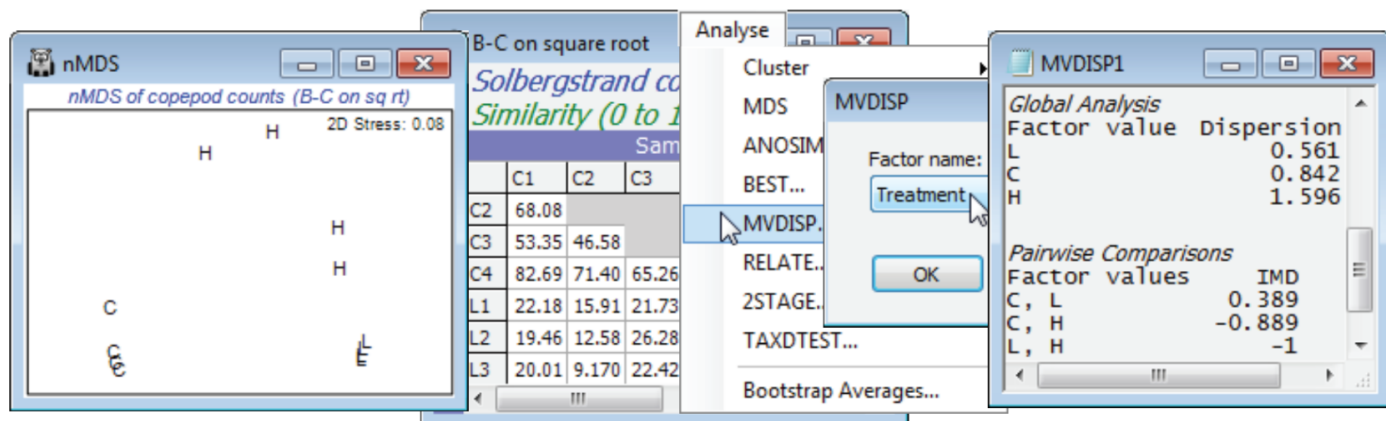


(Mesocosm experiment, Solbergstrand copepods)

The illustration used here is a simple 1-way design of 3 mesocosm treatments: Control (C), Low (L) and High (H) dose of organic enrichment applied to the surface of 12 intact sediment cores, taken from the same location into a mesocosm system, and randomly allocated to the treatments (with 4 replicates in each). Data are from Gee JM *et al* 1985 *J Exp Mar Biol Ecol* 91: 247-262, as analysed in a multivariate way by Warwick RM & Clarke KR 1993 "Increased variability as a symptom of stress in marine communities" *J Exp Mar Biol Ecol* 172: 215-226. Chapter 15, CiMC shows analysis of the resulting meiofaunal communities in the sediment cores (nematodes and copepods) after several weeks' exposure, but here we open just the copepod data, **Solbergstrand copepod counts** in C:\Examples v7\Solberg copepods. For square-root transformed data and Bray-Curtis similarities, plot the *n*MDS and note the apparently much larger dispersion within the High dose treatment (as well as the obvious differences between treatments, which would be tested, validly, by 1-way **ANOSIM**). This is indicated more reliably, i.e. not in the low-d approximation of an ordination plot, by running **Analyse>MVDISP>**(Factor name: **Treatment**) on the resemblance matrix. The dispersion sequence of 0.56, 0.84, 1.60 for L, C, H shows that the average rank dissimilarity is almost three times higher within H than L (comparable dispersions result in a sequence of 1's), and the pairwise comparisons show that all the lowest dissimilarities (within a group) are in L and all the highest in H (thus *IMD* = -1 for that pair of treatments). The result, however, is of limited usefulness since an exact permutation test of these dispersion differences is not possible under the non-parametric framework in PRIMER, for much the same reason as interaction tests in a two-way crossed layout are not possible, see the comments at the end of Section 9 and Chapter 6 of CiMC. [No permutation procedure exists under a null hypothesis that the dispersions are the same for each group, but that the 'locations' – in so far as they are defined for rank-based dissimilarities – may differ. If the primary interest is in testing for differences in multivariate dispersion of groups, for a given resemblance measure, you should use the (approximate, semi-parametric) permutation test given by the PERMDISP routine in PERMANOVA+ – see the Anderson *et al* 2008 manual. The parameters defining centroids of each group in the high-d PCO space are estimated and each centroid is moved to the same point, justifying permutation of the samples across groups under the null hypothesis – if location differences have been removed, and the null hypothesis specifies no dispersion differences, then sample labels again become interchangeable.]



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