



# 5.11 Recommendations

1. Non-metric MDS can be recommended as the best general ordination technique available (e.g. [Everitt \(1978\)](#) ). Important early studies comparing ordination methods for community data gave nMDS a high rating (e.g. [Kenkel & Orloci \(1986\)](#) ) and improvements in computing power since those early studies have made it even more attractive. In comparison with (even) older techniques such as PCA, nMDS has a number of practical advantages stemming from its flexibility and lack of assumptions.  

2. When the inter-sample relationships are relatively simple, e.g. there are some strong clusters or strong gradient of change across all samples, several ordination methods will perform adequately and give comparable pictures. The main advantage of nMDS is its greater ability, by comparison with projection-based methods such as PCA or PCO to better represent relations accurately in low-dimensional space. It outcompetes its metric form, mMDS, and also PCO, especially in cases where biological coefficients such as Bray-Curtis are used and there is a strong turnover of species across the sites, times, treatments etc, such that a fair number of samples have few or no species in common. Then, the dissimilarity scale becomes strongly compressed in the region of 100% (with many values at 100, perhaps, as can be seen for the Exe Shepard plot in Fig. 5.2) and the ability of the monotonic regression to expand this tight range of dissimilarities to wider-spaced distances is the key to a successful ordination. In contrast, where the Shepard diagram is fairly linear through the origin, nMDS, mMDS and PCO will often produce similar ordinations.  

3. If the stress is low (say  $<0.1$ ), an MDS ordination is generally a more useful representation than a cluster analysis: when the samples are strongly grouped the MDS will reveal this anyway, and when there is a more gradual continuum of change, or some interest in the placement of major groups with respect to each other, MDS will display this in a way that a cluster analysis is quite incapable of doing. For higher values of stress, the techniques should be thought of as *complementary* to each other; neither may present the full picture so the recommendation is to *perform both and view them in combination*. This may make it clear which points on the MDS are problematic to position (examining some of the local minimum solutions can help here<sup>¶</sup>, as can animation of the iterative procedure), and an ordination in a higher dimension may prove more consistent with the cluster groupings. Conversely, the MDS plots may make it clear that some groups in the cluster analysis are arbitrary subdivisions of a natural continuum.

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<sup>¶</sup> For example, run the PRIMER MDS routine several times, with a single random starting position on each occasion, and examine the plots that give a higher stress than the 'optimal' one found. In PRIMER7, run the MDS animation for a number of restarts. Also, outliers on the Shepard diagram can be identified by clicking on the appropriate point on the plot.

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