

14.4 General conclusions and recommendations

General conclusions

Three general conclusions emerge from these examples:

1. The similarity in community structure between sites or times based on their univariate or graphical/distributional attributes is different from their clustering in the multivariate analysis.
2. The species-dependent multivariate method is much more sensitive than the species-independent methods in discriminating between sites or times.
3. In examples where more than one component of the fauna has been studied, univariate and graphical methods may give different results for different components, whereas multivariate methods tend to give the same results.

The sensitive multivariate methods are essentially geared towards detecting *differences* in community composition between sites. Although these differences can be correlated with measured levels of stressors such as pollutants, the multivariate methods so far described do not in themselves indicate *deleterious* change which can be used in value judgements. Only the species-independent methods of data analysis lend themselves to the determination of deleterious responses although, as we have seen in [Chapter 8](#) (and will do so again in [Chapter 17](#)), even the interpretation of changes in diversity is not always straightforward in these terms. There is a need to employ sensitive techniques for determining stress which utilise the full multivariate information contained in a species/sites matrix, and three such possibilities form the subject of the next chapter.

Recommendations

It is important to apply a wide variety of classes of data analysis, as each will give different information and this will aid interpretation. Sensitive multivariate methods will give an 'early warning' that community changes are occurring, but indications that these changes are deleterious are required by environmental managers, and the less sensitive taxa-independent methods will also play a role. Amongst the latter are the newly-devised biodiversity measures based on taxonomic (or phylogenetic) distinctness of the species making up a sample – see the discussion in [Chapter 17](#) of their advantages over classical diversity indices.

