Supplementary Material

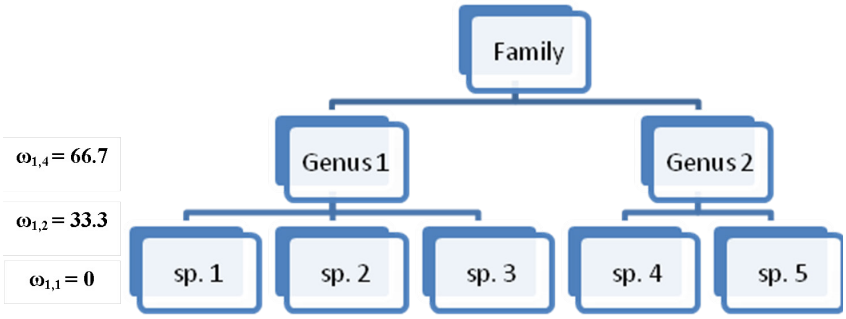
Explanation of Statistical Routines Using Primer

1. SIMPROF

The SIMPROF routine in Primer 6 is a series of similarity profile permutation tests run on biotic data which looks for statistically significant evidence of genuine clusters of sites which are *a priori* unstructured (e.g., single samples from each of a number of sites). While MDS can also show these clusters if they are strong, where the stress of the MDS is high, SIMPROF routine run at the same time or independently of CLUSTER can strengthen the determination of site groupings (Clarke and Warwick 2001).

2. Average Taxonomic Distinctness AvTD (Δ+)

One of the distinctions of Primer is its inclusion of a suite of biodiversity measures based on the relatedness of the species within a given dataset. Average taxonomic distinctness (*i.e.*, the average 'distance apart' of any two species or individuals chosen at random from the samples) captures an axis of variation in the sites not reflected by the standard diversity measures (e.g., S) independent of sampling effort. This index is based on the taxonomic distances through the classification tree, or the expected path length between every pair of individuals chosen at random. For a standard Linnean classification tree these are discrete distances, with individuals from the same species being ascribed a distance of $\omega = 0$, one step if the individuals are in the same genus but are different species and two steps if they are in different genera. Clarke and Warwick (1999) advocate a simple linear scale whereby the largest step is set to 100. Thus for a sample consisting of only 5 species, two Genus' and one Family (as shown below), the distance between two individuals of the same species 1 $\omega_{1,1} = 0$, between individuals in species 1 and 3 $\omega_{1,3} = 33$, between individuals in species 1 and 4 $\omega_{1,5} = 66.7$ *etc.*



Determination of AvTD requires a species aggregation file (which aggregates the species abundance data into lower taxonomic resolution, e.g., presence/absence of individuals in a coral Genus or Family depending on the desired taxonomic resolution). In this study, genus presence/absence data were investigated using this routine as species within a genus are likely to have similar functionality and because previous studies have used this level of taxonomic resolution to resolve regional patters of coral communities (Done 1982). Mean values for average taxonomic distinctness and variation in

taxonomic distinctness remain unchanged over variable sampling times and area sizes (Gage and Coghill 1977).

Table 1. Branch lengths and weights used in the assessment of average taxonomic distinctness (Δ+) (relatedness) of the coral communities from 19 sites the Keppels.

Taxon	Branch	Weight
Species	1	33.33
Genus	1	66.67
Family	1	100

Average taxonomic distinctness Δ* is a quantitative measure of relatedness derived by comparing the path length (weight) between every species in the taxonomic tree of all species or 'master list' of all species found in the study. The path or branch lengths refer to the weights given to the various branch lengths in the taxonomic tree. In this case, equal weight is given to branch lengths between species and species and a higher weight was given to comparisons between genus and species. There is potential to specify decreasing step lengths which places more weight on the branch length between species and less weight on branches between say, species and Genus or Family (Clarke and Warwick 1999).

In calculating multiple univariate species indices, draftsman's plots are used to inspect the influence of each diversity measure on the others. Where diversity measures are strongly influenced by another measure or two diversity measures are correlated, only one of these is included in further standard univariate statistical analyses [ANOVA, mean, 95% CI, (Rogers, Clarke *et al.* 1999)].

3. Observed *vs* Expected AvTD

The presence of a statistical testing framework for Δ+ enables a comparison to be made between an observed taxonomic distinctness measure and its expected range of variation. Histograms were first constructed of the expected range of average taxonomic distinctness (Δ+) following random drawings of 's' species and the true values for each site were compared to these expected values. Values outside the 95% confidence limits were considered to have departed significantly from expectation.

4. SIMPER

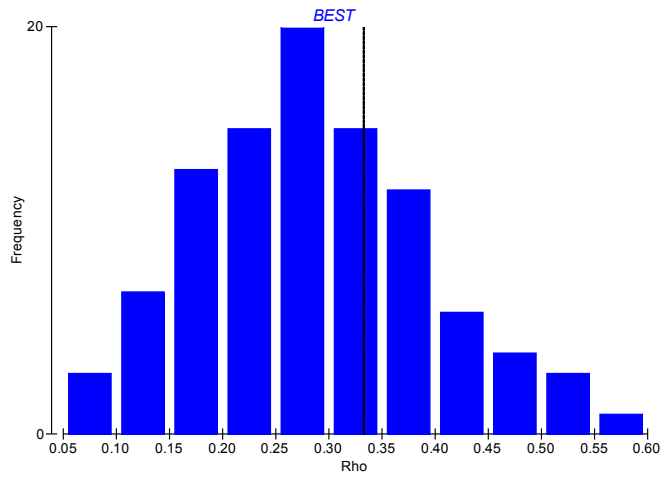
In the case of a convincing clustering of samples using CLUSTER and MDS, the data was re-examined and individual species contributions to the separation of the four groups determined using the SIMPROF were determined using the similarity percentages or SIMPER routine. This routine indicates which species were principally responsible for the site groups. The limitation of this method is that it compares two groups of sites at a time and does not adequately represent continuums of community change. However, in the context of this study SIMPER is appropriate. The routine decomposes the average Bray-Curtis similarities between all pairs of site groups into percentage contributions from each species, listing the species in decreasing order of such contributions (Clarke and Warwick 2001).

5. BEST

The BEST (BIO-ENV is the method of the BEST routine in Primer) routine aims to find the 'best' match between the MDS site patterns and the environmental data. The extent to which these two patterns match reflects the degree to which the MDS of sites based on environmental data 'explains' the MDS coral community structure. The routine carries out a full search for high rank correlations between the species similarity matrix and the resemblance matrices generated from different subsets of the environmental variables (Clarke and Ainsworth 1993; Clarke and Warwick 2001).

BIO-ENV calculates rank correlations (in this case Spearman's) between the similarity matrix derived from the coral species presence/absence data and matrices derived from subsets of environmental variables, thereby defining suites of variables which 'best explain' the biotic structure. The statistical significance of the BEST routine results are tested by the global BEST match permutation test whereby each set of samples is randomly permuted relative to the other. Then the best match correlation coefficient is determined 99 times and displayed in a histogram with represents the null hypothesis case (*i.e.*, no relationship between the species and any of the possible resemblance matrices of subsets of the environmental variables). The real rank correlation coefficient is compared with the permuted null hypothesis values in the histogram and if it is larger than any of them then the null hypothesis can be rejected at $p < 1\%$ (*i.e.*, there is a significant match between the species community structure and the subset of environmental variables determined using BIO-ENV, Figure 1).

Figure 1. An example of a histogram of 99 permutations of Spearman's correlation coefficient (ρ) shows the normal distribution of bins of randomly permuted values of ρ and the real value (dotted line) lying within the 95% confidence limit. In this case, the null hypothesis of no relationship between the best subset of environmental variables and the species community structure would not be rejected.



References

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