

## APPENDIX B

### DIVERSITY & MULTIVARIATE ANALYSES

#### Diversity Indices

An index of diversity commonly used in benthic community analyses is the Shannon-Wiener's index, which emphasizes not only the number of species (richness or variety), but also the apportionment of the numbers of individuals among the species (see Odum 1971 and Reish 1984). The simple community parameters are reduced to a single number using the following equation:

$$H' = - \sum_{j=1}^s \frac{n_j}{N} \ln \left( \frac{n_j}{N} \right)$$

where  $n_j$  is the number of individuals in the  $j$ th species,  $s$  is the total number of species, and  $N$  is the total number of individuals. Although the  $H'$  value can range from 0 in a highly degraded area to 5-6 in a pristine environment (see Reish 1984), this index is applicable to more general ecological phenomena and need not be restricted to pollution impact studies. Simpson's dominance was also utilized.

#### Measures of Taxonomic Diversity

Assuming taxonomy reflects phylogeny, which recent systematists have striven to achieve with more confidence through advances in technology (i.e., molecular analyses) and cladistics, a sample having five species of the same genus is less biodiverse than another having five species of

differing families. Accepting this to be true, indices integrating both taxonomic distances through a tree as well as abundances captures much more information than those indices that have been abandoned in this report, and hence are more robust with respect to independence of samples size/effort (Clarke and Warwick 2001a). Therefore, the suite of taxonomic diversity measures used in Chapters 6 and 7 [taxonomic diversity ( $\Delta$ ), quantitative taxonomic distinctness ( $\Delta^*$ ), average taxonomic distinctness ( $\Delta^+$ ), variation in taxonomic distinctness ( $\Delta^+$ ), total phylogenetic diversity ( $S\Phi^+$ ), and average phylogenetic diversity ( $\Phi^+$ )] were employed (Clarke and Warwick 2001a, Clarke and Warwick 2001b).

#### Cladistic Analysis

Systematics underpins all of biology. It is the discipline through which comparative biology progresses, whether the subdiscipline of interest is ecology, biogeography, evolution, or physiology. Cladistics is a method of systematics. It is also a general approach to classification, which can be used for organizing any comparative information (Scotland, 1992). The axioms of this powerful systematic discovery procedure are:

- 1) Nature's hierarchy is discoverable and effectively represented by a branching diagram (cladogram).

2) Characters change their status at different hierarchical levels. Characters (species) within a study group that are either present in all members of the study group or have a wider distribution than the study group (plesiomorphies) cannot indicate relationships within the study group.

3) Character congruence is the decisive criterion for distinguishing synapomorphy from homoplasy.

4) The principal of parsimony maximizes character congruence.

Hence, the most parsimonious cladogram represents the best fit of the data and becomes the accepted hypothesis for the relationships of the entities under study.

The species assemblages were analyzed via parsimony or cladistic analyses. Parsimony analysis of endemicity (PAE) uses a parsimony algorithm in order to obtain area or site cladograms based on the taxa (species) inhabiting the areas under scrutiny (monitoring stations). In PAE, the relative amount of species loading or loss is indicated by the length of the branches or internodes of the cladogram. Interestingly, Podani *et al.* (2000) advocates the more extensive use of additive trees (which cladograms are) in community ecology, as branch lengths usually approximate species richness, a feature not possible with ultrametric trees, conventionally used in phenogram construction.

Specifically, the data were analyzed via a “generalized parsimony” or “step-matrix” approach (Sankoff and Rousseau 1975, Sankoff and Cedergren 1983, Swofford *et al.* 1996). Generalized parsimony is an efficient and highly adaptable approach for systematic analyses, as the parsimony criterion is easily applied to virtually any comparative (frequency, behavioral, ecological, etc) data set (Hillis 1998). This computationally intensive, “brute force” approach enumerates all possible combinations of character state assignments at every node, calculating partial costs (relative abundance of a given species) and

converging on the most parsimonious tree. Species (characters) abundance values were standardized to relative abundance equally weighting each species (character).

Although, richly cited and formalized in the systematic literature by Rosen (1988), and Rosen and Smith (1988), the seminal work ignored in the systematics literature was in fact applied to marine infaunal data for eco-monitoring purposes from European waters two years earlier (Lamshead and Paterson 1986, Lamshead 1986).

Further justification for the use of PAE is the fact that communities and the species they contain are typically nested and cladistics is the dominant method in systematics for parsing out nested subsets of character distributions. Contemporary work by Trejo-Torres and Ackerman (2002), conclude that the methodological, theoretical, and interpretive advantages of PAE make it an attractive and complementary method for ecological studies of fine-scale species assemblage composition patterns. Comparing methodologies, Hooper *et al.* (2002) show congruent groupings of Australian sponge communities between phenetic NMDS ordinations and parsimony analyses, as did Lamshead *et al.* (1994) with deep-sea nematode assemblages.

Indeed, the literature is becoming rich utilizing parsimony analyses applied at various spatiotemporal scales in biogeographic studies. Recently, Porzecanski and Cracraft (2005) used CADE, a derivative of PAE, to study neotropical bird distributions in South America, and most recently Pellens *et al.* (2005) underscored the powerful advantages of cladistics over the conventionally used phenetic methods in community nestedness and evolution. Other references of conceptual interest include: Dauvin and Bellan-Santini 2004, Bellan-Santini *et al.* 1994, Cracraft 1994, Costa *et al.* 2000, Legendre 1986, Lyons-Weiler and Tausch 1997, Masselot *et al.* 1997, Morrone 1994, Nel *et al.* 1998, Salen-Picard *et al.* 1996, and Watanabe 1998.

Much literature has shown that deleting rare species can damage the sensitivity of community-based methods to detect ecological changes (Cao *et al.* 1998 and 2001), and that taxon autochthony (endemism) may be more informative than their abundance, especially in parsimony analyses (Perochon *et al.* 2001). Additionally, recent work underscores that it is the rare species, not the common and abundant taxa, which respond to or are affected by varying aspects of habitat change or modification (Goodsell and Connell 2002). Hence, all species (operational equivalent for character) were included in the analyses.

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