

APPENDIX B

DIVERSITY & MULTIVARIATE ANALYSES

INTRODUCTION

In this appendix, methods are presented for the calculation of community parameters, i.e., diversity (H'), evenness (J'), species richness, and taxonomic distinctness. The biological data were cladistically (most parsimonious distribution of the data) analyzed in order to determine relationships between species assemblages at their respective monitoring stations.

COMMUNITY PARAMETERS

Diversity (H')

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.

Evenness (J')

As mentioned above, two components of the Shannon-Wiener index (H') are species richness, expressed by a ratio between total number of species and total number of individuals, and evenness (or equitability), which accounts for the number of individuals apportioned to each of the species (Odum 1971). Evenness, therefore, takes into consideration the dominance or lack of dominance of one or a few organisms in the community. For example, if the numbers of individuals are evenly apportioned among all the species present in the community, the species assemblage exhibits maximum evenness ($J' = 0$): there are no dominant organisms. The evenness is calculated by the following formula:

$$J' = \frac{H'}{\log s}$$

where H' is the Shannon-Wiener index of diversity and s is the number of species.

Gleason's Species Richness (d)

Species richness is a measure of the number of species in a sample. It is calculated by the following equation:

$$d = \frac{S - 1}{\ln N}$$

where S is the number of species and N is the number of individuals.

Consistency Index (CI)

Consistency index is the fit of the data to the resultant tree topology (distribution of the character over the tree). It is calculated by the following equation:

$$CI = \frac{m}{s}$$

where m is the minimum amount of change possible for the character; therefore, m is equal to the number of states minus one, and is the actual number of changes in the character observed on the tree. The ensemble CI for the tree is calculated by the summation of m and s, (M and S), over the suite of characters in the data set:

$$CI = \frac{M}{S}$$

Retention Index is used to express the amount of shared derived characters (synapomorphy) in the data set.

$$\text{Retention Index} = \frac{\text{Actual Homoplasy}}{\text{Maximum Possible Homoplasy}}$$

Hence, the amount of synapomorphy is measured as the complement of the measure of homoplasy.

The rescaled consistency index (RC) utilized in the successive approximations technique is calculated by the following equation:

$$RC = CI \times RI$$

Taxonomic Distinctness

Average taxonomic diversity

$$\Delta = [\sum_{i < j} \omega_{ij} x_i x_j] / [N(N-1)/2]$$

where ω_{ij} is the taxonomic distance between every pair of individuals from species i and species j , x_i is the abundance of species i in the sample, and N is the total number of individuals in the sample (Clarke and Warwick 2001).

Average taxonomic distinctness

$$\Delta^* = [\sum_{i < j} \omega_{ij} x_i x_j] / [\sum_{i < j} x_i x_j]$$

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 principle 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.

LITERATURE CITED

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