

APPENDIX B

BIOLOGICAL ANALYSES

Methods for calculating community parameters including traditional biodiversity measures such as Shannon-Wiener diversity index [$H'(\log_e)$], Margalef's diversity (d), Simpson's Index (c), and Pielou's evenness (J'), Gleason's species richness, and catch per unit effort (CPUE) are presented. Additionally, we present a series of biodiversity measures, called phylodiversity indices, that more accurately reflect taxonomic, and ideally, phylogenetic relationships. These measures include taxonomic diversity (Δ), quantitative taxonomic distinctness (Δ^*), average taxonomic distinctness (Δ^+), total taxonomic distinctness ($S\Delta^+$), variation in taxonomic distinctness (Λ^+), total phylogenetic diversity ($S\Phi^+$), and average phylogenetic diversity (Φ^+). Most of these phylodiversity indices have gained immediate acceptance in the scientific community since their inception due to their favorable features of being independent of sampling effort, relative to the traditional indices employed, and their ability to utilize phylogenetic relationships. All of these concepts and calculations are more thoroughly addressed in Clarke and Gorley (2006), Clarke and Warwick (2001a and 2001b), Warwick and Clarke (1995), and Magurran (1988).

We also explain how biological data using cladistics (most parsimonious distribution of the data) in order to determine relationships of samples based on their taxonomic (species) inventories (Q-analysis) and, conversely, the relationships of taxa based on the samples where they occur (R-analysis). And finally, we briefly explain additional analyses that include non-metric multi-dimensional scaling (NMDS), BEST: BIO-ENV, principal component analysis, and evolutionary principal component analysis (EPCA, Maddison and Maddison, 2005).

Deleting rare species can damage the sensitivity of community-based methods to detect ecological changes (Cao *et al.* 1998 and 2001), and since taxon autochthony may be more informative than their abundance, especially in parsimony analyses (Perochon *et al.* 2001), all species are used in analyses, except those simultaneously meeting three exclusion criteria for non-unique supraspecific taxa, regardless of abundance. The simultaneous exclusion criteria are:

1. The identification is not at the species level;
AND
2. The reported taxon is represented in the sample by other members of the same taxon, which have been identified at lower levels;
AND
3. The taxonomist cannot distinguish the specimen from other members of its taxon in the sample.

TRADITIONAL DIVERSITY INDICES AND COMMUNITY PARAMETERS

SHANNON-WIENER INDEX (H')

An index of diversity commonly used in benthic community analyses is the Shannon-Wiener index, which emphasizes not only the species richness (number of species), but also the apportionment of the numbers of individuals among the species (see Odum 1971 and Reish 1984). These 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 species richness (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.

PIELOU'S 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). Pielou's evenness (or simply 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)

Gleason's species richness is simply a transformed 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.

SIMPSON INDEX

$$\begin{aligned}\lambda &= \sum p_i^2 \\ 1 - \lambda &= 1 - (\sum p_i^2) \\ \lambda' &= \{\sum_i N_i(N_i - 1)\} / \{N_i(N_i - 1)\} \\ 1 - \lambda' &= \{\sum_i N_i(N_i - 1)\} / \{N_i(N_i - 1)\}\end{aligned}$$

where N_i is the number of individuals of species i and p_i is the proportion of the total count arising from the i^{th} species.

CATCH PER UNIT EFFORT

This measure is calculated by simply dividing the total survey abundance of taxa or a particular taxon by the number of sampling events for a given survey.

PHYLOGENETIC DIVERSITY INDICES

Assuming taxonomy reflects phylogeny, which recent systematists have striven to achieve with more confidence through advances in technology (i.e., molecular analyses) and parsimony analysis (cladistics), a sample having five species of the same genus is less biodiverse than another having five species of differing families (see Figure B-1 for illustration). Accepting this to be true, indices integrating both taxonomic distances through a tree, as well as abundances, captures much more information than the traditional diversity indices, and yet most are more robust with respect to independence of samples size/effort.

- *Average taxonomic diversity: quantitative* (Δ) accomplishes these goals by calculating the expected path length between any two individuals chosen at random.

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

- *Average taxonomic distinctness: quantitative* (Δ^*) still captures the phylogenetic relationships, but on the other hand, removes the influence of dominating abundances to produce an index more reflective of taxonomic hierarchy. This is achieved by dividing (Δ) by the Simpson index.

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

- *Average taxonomic distinctness: presence/absence* (Δ^+) is merely the taxonomic breadth of a sample event based on presence/absence. This index is most appealing for data with highly variable or unknown sample size and effort.

$$\Delta^+ = [\sum \sum_{i < j} \omega_{ij}] / [S(S - 1)/2]$$

- *Total taxonomic distinctness: presence/absence* ($S\Delta^+$) is the total taxonomic breadth of a sample event based on presence/absence. It is the average taxonomic distance from species i to every other species, summed over all species.

$$S\Delta^+ = \sum_i [(\sum_{j \neq i} \omega_{ij}) / (S - 1)]$$

- *Variation in taxonomic distinctness: presence/absence* (Λ^+) can elicit differences among samples having the same Δ^+ but different taxonomic or phylogenetic tree constructions by focusing on the variance of the taxonomic distances between each pair of species about their Δ^+ value.

$$\Lambda^+ = [\sum \sum_{i < j} (\omega_{ij} - \Delta^+)^2] / [S(S - 1)/2]$$

- *Total phylogenetic diversity: presence/absence* ($S\Phi^+ = PD$, Faith 1992 and 1994) offers comparison of samples based on cumulative branch lengths of their full trees. This measure is incapable of discriminating samples of equal tree length, but differential taxonomic distributions within.
- *Average phylogenetic diversity: presence/absence* (Φ^+), based on presence/absence data and being the quotient of $S\Phi^+ / S$, is the contribution that each species makes on the total tree length. As species numbers increase, the later two indices' values change noticeably, rendering them sample-size/effort dependent.

$$\Phi^+ = PD / S$$

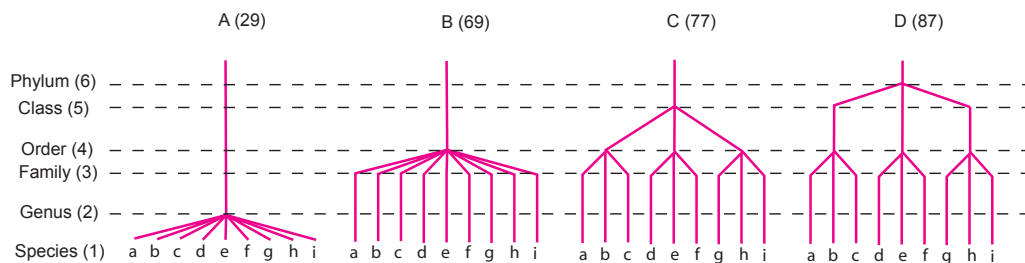


Figure B-1. Simplified schematic diagrams of various possible taxonomic/phylogenetic hierarchical tree structures and associated, relative weighting among levels essential to all phylodiversity indices (adapted from Warwick and Clarke 1995). Samples are designated by uppercase, species by lowercase, and taxonomic level and cumulative weights per sample by numbers in parentheses.

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, S is the total number of species in the sample, and N is the total number of individuals in the sample (Clarke and Warwick 2001a).

The suite of taxonomic distinctness and phylogenetic diversity indices are calculated in Primer v6 (Clarke and Gorley 2006), as well as all graphics derived from them, require the construction of an appropriate 'master species list' from which the given sampling events are compared. The taxonomic hierarchy include species, genus, family, order, class, and phylum. Calculations of indices, based on comparison of a given sample data file with the respective master species list, are executed using 1,000 repetitions and weighted by taxon richness. Graphical representations (funnel plots) of $(\Delta+)$ and $(\Lambda+)$ are allowed 10,000 restarts in order to escape from local optima and also weighted by taxon richness.

CLADISTIC ANALYSES

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 that uses parsimony, and thus, is more economic in assumptions and strictly conforms to Occam's (or Ockham's) razor. In cladistics' infancy, its application was narrowly limited to describing relationships among taxa based on their morphological characters. Although still widely used in this manner, its scope of application has radically expanded (see Deets 1987, Hillis 1998, and CLA, EMD 1996-2006) to warrant more generic terminology where characters are referred to as descriptors and taxa as objects. Figure B-2 illustrates the fundamental features of a cladogram. Cladistics is a general approach to classification which can be used for organizing any comparative information (Scotland 1992, O'Brien and Lyman 2003). 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 (shared derived character) from homoplasy (recurring similarity).
- 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. In a community or ecological analysis application, the topology (elastic geometric structure) of the cladogram reveals several readily identifiable groups or station clades distinguished by dependent data. Additionally, since cladograms are additive trees, branch lengths are indicative of species diversity or the number of species found in a given sample (Figure B-2). Thus, providing an additional dimension of information not available in the conventionally used ultrametric trees derived from overall similarity measures in phenetic approaches.

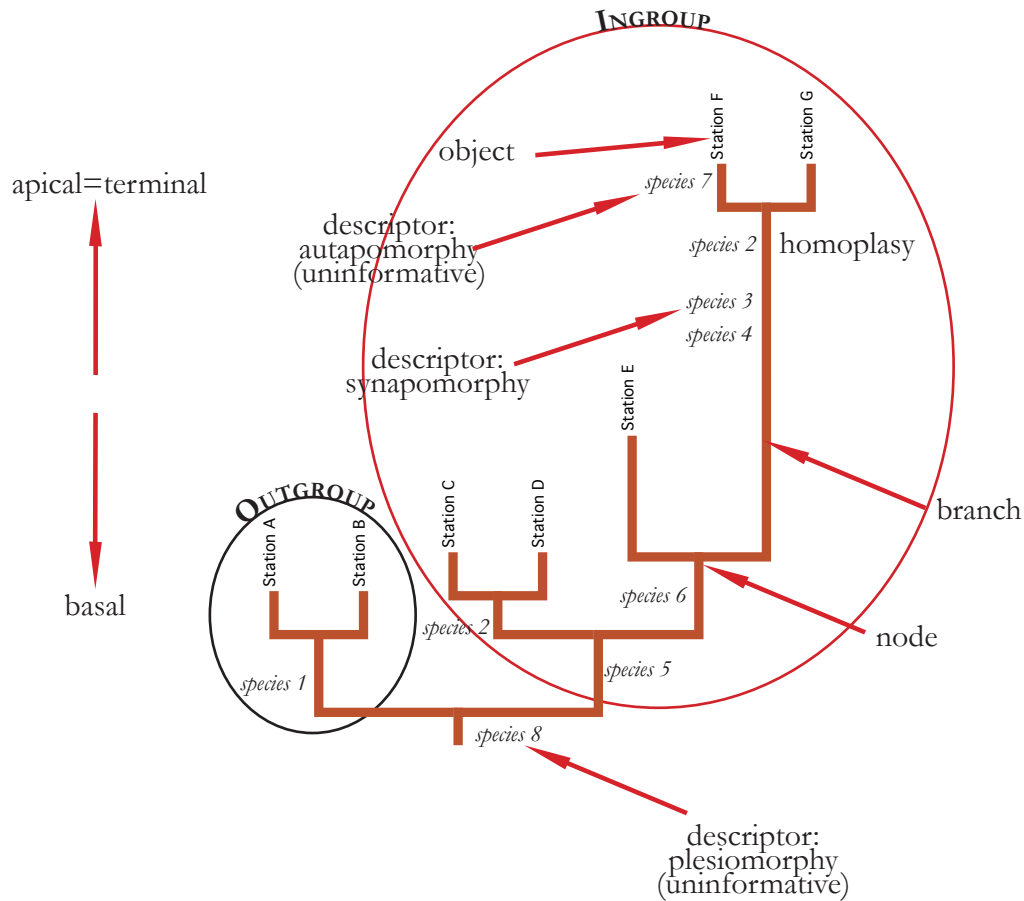


Figure B-2. The fundamental features of a cladogram. The collective of the unique configuration and relationships of the branches, their lengths, nodes, and the objects of a given cladogram are its topology. *Species 2* is homoplastic. Differential branch lengths reflect diversity.

Relatedness is not synonymous with overall similarity. As an analogy, phenetic analyses in the past grouped dinosaurs with lizards, but contemporary classification schemes using parsimony group dinosaurs and birds together with their many unshared unique traits. We have a parallel situation with ecological data sets in which some samples are extremely species-rich (like the bird and its many unique characters) making them appear less similar to less species-rich samples and therefore becoming phenetically more different / dissimilar and thus, grouping more removed or distantly in phenetic space. Hence, this lesser diverse sample appears phenetically more similar to the other lesser species-rich samples, despite sharing more unique species with the species-rich sample, which parsimony analysis captures.

Cladistic, or parsimony, analyses are performed using the heuristic search, Tree-Bisection and Reconnection (TBR) algorithm for large data sets, and the Exhaustive Search algorithm for smaller data sets with the computer program PAUP* Phylogenetic Analysis Using Parsimony (*and other methods) version 4.0b10 (Swofford 2000). Methods for calculating the measure-of-fit indices are presented in Kitching *et al.* (1998). The “new search strategy” developed by Quicke *et al.* (2001) is utilized, which is a heuristic strategy designed to find optimal (parsimonious) trees for data sets with large numbers of taxa (objects) and characters (descriptors). This new strategy uses an iterative searching process of branch swapping with equally weighted characters followed by swapping with reweighted characters. This process increases the efficiency of the search because, after each round of swapping with re-weighted characters, the subsequent swapping with the original or

equal weights will start from a different group (island) of trees that are only slightly, if at all, less optimal. In contrast, conventional heuristic searching with constant equal weighting can become trapped on islands of suboptimal trees. Change lists and species diagnostic tables (calculating various fit indices for each species) are also produced in PAUP*.

For Q-analysis, species and independent abiotic variables are mapped onto the organism-derived cladograms by employing the *trace character history* module in Mesquite version 1.05 (build g24) Maddison and Maddison (2005) for all parsimony analyses.

Scattergram and regression diagnostics from independent contrasts are generated by the PDAP:PDTREE module (Midford *et al.* 2003) within Mesquite. The rationale for the utilization of independent contrast methodology is due to the *lack* of independence that data from a hierarchy possess (see Garland *et al.* 1999, Garland and Ives 2000). The contrasted continuous characters mapped back onto the tree are optimized via calculating the most parsimonious ancestral states at the nodes of the tree assuming a cost of $(x-y)^2$ on a branch if the branch shows a change from state x to state y (this assumption is known as squared-change or least-squares parsimony). This also calculates the cost of a most parsimonious reconstruction. This Brownian motion model of change results in a distribution with a normal variance proportional to time and is equivalent to the maximum likelihood method under this model. Two-tailed probabilities are reported along with the Pearson Product-Moment Correlation Coefficient r -value.

In addition to the cladograms showing the relationships of the objects or stations (Q-analysis), cladograms of species groups showing the association or co-occurrence of these descriptors or species with one another (R-analysis, Legendre and Legendre 1998) are produced for organisms from a subset of exemplar communities. This parsimony analysis of co-occurring species has been coined “PACOS” herein.

Specifically, the Q-mode data are 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, stemmatic, cultural, archeological, ecological, etc.) data set (O’Brien and Lyman 2003, 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 or descriptors) abundance values were standardized to relative abundance, equally weighting each species. The approach herein is very similar to the step-matrix approach utilized in MANOB (Manhattan Distance, Observed Frequency Arrays) introduced by Berlocher and Swofford (1997), but utilizes a two-column reductive coding approach guaranteeing the logical independence of a species’ absence from its presence, and the associated abundance states represented by a given step-matrix. This approach accommodates continuous data without resorting to coding strategies with problematical coding justifications, reduces impact of sampling error (e.g., the failure to detect or utilize rarely occurring or less abundant species), and utilizes potentially useful frequency or relative abundance data not conventionally used in presence/absence coding (see Berlocher and Swofford 1997).

Parsimony analysis, or cladistics, was developed to generate the most parsimonious ordering of data (Wiley, 1981) minimizing *ad hoc* hypotheses of character distributions and has become the dominant methodology in systematics. The use of cladistics in biogeographical studies is known in the literature as parsimony analysis of endemism or parsimony analysis of distributions, PAE and PAD, respectively. Although richly cited and formalized in the systematic literature by Rosen (1988) and Rosen and Smith (1988), the seminal work ignored

in the systematic literature was in fact applied to marine infaunal data for eco-monitoring purposes from European waters two years earlier (Lamshead 1986, Lamshead and Paterson 1986). Small spatiotemporal-scaled ecological applications have been explored by Lamshead and Paterson (1986), Bellan and Bellan-Santini (1997), Bellan-Santini, Dauvin, and Bellan (1994), Bellan-Santini, Arnaud, and Bellan (1994), Cracraft (1994), Morrone (1994), Morrone and Crisci (1995), EMD with Los Angeles Harbor infauna and trawl data (CLA, EMD 1994, 1995b, 1996, 1997b, 1998, 1999b, 2000, 2001b, 2002, 2003b, 2004, 2006), EMD with Santa Monica Bay infauna and trawl data (CLA, EMD 1995a, 1997a, 1999a, 2001a, 2003a, 2005, 2007), Salen-Picard *et al.* (1996), Watanabe (1998), Masselot *et al.* (1997), Nel *et al.* (1998), Lyons-Weiler and Tausch (1997), Myers and De Grave (2000) with regard to nested species distributions and endemism at all spatial scales, Dauvin and Bellan-Santini (2002 and 2004) using benthic Gammaridea to unravel biogeographic relations along European coastal areas, Porzecanski and Cracraft (2005) studying neotropical bird distributions in South America, and most recently Pellens *et al.* (2005) underscore the powerful advantages of cladistics over the conventionally used phenetic methods in community nestedness and evolution.

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. Indeed, the nested arrangements of co-occurring non-conspecific organisms is one of several hierarchies that form from the direct outcome of the evolutionary process (Eldredge 1985). This segues into Damuth's (1985) conceptual analogy that communities evolve by avatar selection; avatars being the species found in specific communities. Avatars, therefore, are somewhat analogous to genes as they function as both interactors (with other species) and replicators (they produce offspring). Hull (1988) interprets Damuth's avatars as possessing both ecological and genealogical components, being parts of species (genealogical entities), and parts of communities (ecological entities). Thus, the avatar embodies the intersection between the genealogical and ecological hierarchies proposed by Eldredge (1985).

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 Non-Metric Multidimensional Scaling (NMDS) ordinations and parsimony analyses, as did Lamshead *et al.* (1994) with deep-sea nematode assemblages. Rosen (1992) previously argued that PAE be viewed as an alternative to conventional multivariate analyses. Finally, Nihei (2006) summarizes the large increase in the number of publications using PAE or PAD to recognize and identify ecological affinities or relationships among biotas or communities by analyzing species compositions of samples or areas at various spatiotemporal scales. Nihei (2006) is also the first author to recognize or differentiate two distinct classes or approaches to PAE or PAD, namely static (change over space) and dynamic (change over time).

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

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

RETENTION INDEX (RI)

The retention index, a measure of branch support, is used to express the amount of shared derived characters (synapomorphies) in the data set. It is the amount of similarity in a character that can be interpreted as synapomorphy on a given cladogram. The retention index is calculated as the ratio of $(g - s)$ to $(g - m)$, where g is the greatest number of steps a character can exhibit on any cladogram, m is the minimum number of steps a character can exhibit on any cladogram, and s is the minimum number of steps the same character can exhibit on the cladogram in question (Kitching *et al.* 1998).

$$\text{Retention Index} = \frac{\text{Actual Homoplasy}}{\text{Maximum Possible Homoplasy}} \quad ri = \frac{(g - s)}{(g - m)}$$

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:

$$RC = CI \times RI$$

NON-METRIC MULTI-DIMENSIONAL SCALING

Non-metric multidimensional scaling (NMDS) is a highly recommended multivariate ordination method that works on any similarity or distance matrix (Warwick and Clarke 1995, Quicke 1993). Non-metric MDS is applied to patristic distance (branch-length) matrices derived from the cladistic analyses (the cladogram). Patristic distances were chosen as it has been shown that pairwise similarity or distance is underestimated by the conventionally used phenetic distance methods (e.g., Bray-Curtis). Pairwise comparisons using cladistic methods, which include all changes (including homoplasy or lack-of-fit), along the branches is a better estimator or representation of the data (Smith 1994). The lower the stress value, the better the correspondence between the NMDS map or plot and the rank order of dissimilarities amongst the samples.

Patristic distance matrices and pairwise homoplasy matrices (the incongruence, convergence, parallelism, or residual within the data) derived from the cladograms generated in PAUP*, are imported into Primer v. 6 (Clarke and Gorley 2006) for subsequent multivariate NMDS and BIO-ENV treatments. All NMDS analyses are carried out with at least 1000 restarts in order to keep from being trapped in local sub-optimal minima.

BEST: BIO-ENV

The matching of biotic patterns to environmental or abiotic patterns is carried out via the BEST: BIO-ENV procedure in Primer *v6* Clarke and Gorley (2006). This method attempts to calculate a measure of agreement between the patristic distance matrix derived from the cladogram and a worksheet of the abiotic parameters from which a large number of similarity matrices will be calculated. The best matches between the biotic and abiotic matrices are measured by weighted Spearman rank correlations (ρ_w).

PRINCIPAL COMPONENT ANALYSIS AND EVOLUTIONARY PRINCIPAL COMPONENT ANALYSIS

Principal component analyses (PCA) is used for ordination of objects or samples are based on either a dispersion matrix or a correlation matrix if the analysis demands standardized descriptors (Legendre and Legendre 1998). A novel and prototypical multivariate ordination method, evolutionary principal components analysis (EPCA) functions by reconstructing shared states via squared-change parsimony, then performing Principal Components Analysis (PCA) on the vectors of change along each branch of the cladogram. Hence, the ordination acts directly upon the tree or cladogram. Most ordination techniques are based on phenetic similarity or dissimilarity indices. However, using the information from a parsimony or cladistic analysis to guide an ordination allows the ordination to maximize the shared-derived or synapomorphic differences among objects, rather than some arbitrary static property of the data such as variance, which is conventionally used in PCA. This approach (EPCA) gives insight, by capturing the most change in the system, not available using standard multivariate ordinations. EPCA and PCA calculations are carried out in the Rhetenor module within Mesquite 1.05 (Maddison and Maddison 2005).

GLOSSARY

apical: Referring to the terminal area of a cladogram (see terminal).

apomorphy: A derived character or character state. Derived from (and different from) a generalized condition; used of characters, e.g. apomorphic characters.

autapomorphy: A derived character or character state (apomorphy) that is restricted to a single terminal taxon (object) in a data set. An autapomorphy at a given hierarchical level may be a synapomorphy at a less-inclusive level. One form of uninformative character.

basal: Referring to the root area of a cladogram.

branch: A line on a cladogram connecting two nodes (internal branch), a node and the root (basal branch), or a node and a terminal taxon (terminal branch). Also known as an internode.

branch-swapping: A procedure for moving clades around a cladogram in an effort to find a more parsimonious topology.

character (descriptor): An observable feature of an object used to distinguish it from another.

character state: One of two or more alternative manifestations of a character.

node: A point on a cladogram where three or more branches meet.

outgroup: A taxon (object) used in a cladistic analysis for comparative purposes, usually with respect to character (descriptor) polarity determination.

phenetics: A method of systematics that groups taxa on the basis of overall similarity.

pleisiomorphy: An apomorphy of a more inclusive hierarchical level than that being considered. An ancestral or primitive character or character state.

sister-clade: Two subclades that are more closely related to each other than either is to a third subclade.

sub-clade: Clades nested within the larger study-group clade.

synapomorphy: An apomorphy that unites two or more taxa into a monophyletic group. A shared derived character (descriptor).

taxon (object): an entity that is compared by characters (descriptors) to other entities.

terminal: The area of a cladogram opposite the root.

topology: the elastic structure or geometric configuration of a cladogram.

LITERATURE CITED

- Bellan, G., and D. Bellan-Santini. 1997. Utilizzazione delle analisi di parsimonia (cladistica) in sinecologia bentonica: esempi in una zona inquinata. S.It.E. Atti 18: 247-250.
- Bellan-Santini, D., J.C. Dauvin, and G. Bellan. 1994. Analyse de données en écologie benthique: utilisation de la méthode de l'analyse de parcimonie. Oceanologica Acta. 17:331-340.
- Bellan-Santini, D., P.M. Arnaud, and G. Bellan. 1994. Affinités entre peuplements méditerranéens benthique avec et sans *Caulerpa taxifolia*. Second International Workshop on *Caulerpa taxifolia*. November 1994, Barcelona, Spain: 1-4 pp.
- Berlocher S. H. and D. Swofford. 1997. Searching for phylogenetic trees under the frequency parsimony criterion: An approximation using generalized parsimony. Systematic Biology. 46(1): 211-215.
- Cao, Y., D.D. Williams, and N.E. Williams. 1998. How important are rare species in aquatic community ecology and bioassessment? American Society of Limnology and Oceanography, Inc. 43 (7): 1403-1409.
- Cao, Y., D.P. Larsen, and R.St-J. Thorne. 2001. Rare species in multivariate analysis for bioassessment: some considerations. Journal of the North American Benthological Society. 20 (1): 144-153.
- City of Los Angeles, Environmental Monitoring Division. 1994. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period March, 1993 through December, 1993. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 9-4 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 1995a. Marine Monitoring in Santa Monica Bay: Annual Assessment Report for the Period July, 1993 through December, 1994. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Hyperion Treatment Plant, Playa del Rey, California, pp. 1-1 to 9-24 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 1995b. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 1994 through December, 1994. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 9-8 + appendices.

- City of Los Angeles, Environmental Monitoring Division. 1996. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 1995 through December, 1995. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 9-8 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 1997a. Marine Monitoring in Santa Monica Bay: Biennial Assessment Report for the Period July, 1995 through December, 1996. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Hyperion Treatment Plant, Playa del Rey, California, pp. 1-1 to 8-32 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 1997b. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 1996 through December, 1996. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 9-8 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 1998. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 1997 through December, 1997. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 9-8 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 1999a. Marine Monitoring in Santa Monica Bay: Biennial Assessment Report for the Period July, 1997 through December, 1998. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Hyperion Treatment Plant, Playa del Rey, California, pp. 1-1 to 8-32 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 1999b. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 1998 through December, 1998. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 9-8 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2000. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 1999 through December, 1999. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 9-8 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2001a. Marine Monitoring in Santa Monica Bay: Biennial Assessment Report for the Period July, 1999 through December, 2000. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Hyperion Treatment Plant, Playa del Rey, California, pp. 1-1 to 8-37 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2001b. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 2000 through December, 2000. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 8-12 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2002. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 2001 through December, 2001. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 8-15 + appendices.

- City of Los Angeles, Environmental Monitoring Division. 2003a. Marine Monitoring in Santa Monica Bay: Biennial Assessment Report for the Period January, 2001 through December, 2002. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Hyperion Treatment Plant, Playa del Rey, California, pp. 1-1 to 8-38 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2003b. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 2002 through December, 2002. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 7-30 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2004. Marine Monitoring in the Los Angeles Harbor: Annual Assessment Report for the Period January, 2003 through December, 2003. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, pp. 1-1 to 7-30 + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2005. Marine Monitoring in Santa Monica Bay: Biennial Assessment Report for the Period January, 2003 through December, 2004. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Hyperion Treatment Plant, Playa del Rey, California, 192 pp. + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2006. Marine Monitoring in the Los Angeles Harbor: Biennial Assessment Report for the Period January, 2004 through December, 2005. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Terminal Island Treatment Plant, San Pedro, California, 135 pp. + appendices.
- City of Los Angeles, Environmental Monitoring Division. 2007. Marine Monitoring in Santa Monica Bay: Biennial Assessment Report for the Period January, 2005 through December, 2006. Report submitted to EPA and RWQCB (Los Angeles). Department of Public Works, Bureau of Sanitation, Hyperion Treatment Plant, Playa del Rey, California, 204 pp. + appendices.
- CLA, EMD. See City of Los Angeles, Environmental Monitoring Division.
- Clarke, K.R. and R.N. Gorley. 2006. *PRIMER v6: User Manual/Tutorial*. PRIMER-E: Plymouth, England, 190 pp.
- Clarke, K.R. and R.M Warwick. 2001a. Change in Marine Communities: An Approach to Statistical Analysis and Interpretation, 2nd Edition. PRIMER-E: Plymouth, England, pp. 0-1 to 17-18 + appendices.
- Clarke, K.R. and R.M Warwick. 2001b. A further biodiversity index applicable to species lists: variation in taxonomic distinctness. *Marine Ecological Progress Series*, 216: 265-278.
- Cracraft, J. 1994. Species diversity, biogeography, and the evolution of biotas. *American Zoologist* 34: 33-47.
- Damuth, J. 1985. Selection among species: a formulation in terms of natural functional units. *Evolution* 39:1132-1146.
- Dauvin, J-C. and D. Bellan-Santini. 2002. Les crustacés amphipodes Gammaridea benthiques des côtes Françaises métropolitaines: Bilan des connaissances. *Crustaceana* 75 (3-4): 299-340.
- Dauvin, J-C. and D. Bellan-Santini. 2004. Biodiversity and the biogeographic relationships of the Amphipoda: Gammaridea on the French coastline. *Journal of the Marine Biological Association of the United Kingdom*. 84: 621-628.

- Deets, G.B. 1987. Phylogenetic analysis and revision of *Kroeyerina* Wilson, 1932 (Siphonostomatoida: Kroyeriidae), copepods parasitic on chondrichthyans, with descriptions of four new species and the erection of a new genus, *Prokroyeria*. *Canadian Journal of Zoology* 65: 2121-2148.
- Eldredge, N. 1985. *Unfinished Synthesis: Biological hierarchies and modern evolutionary thought*. Oxford University Press. Oxford. 237 pp.
- Faith, D.P. 1992. Conservation evaluation and phylogenetic diversity. *Biological Conservation*, 61: 1-10.
- Faith, D.P. 1994. Phylogenetic pattern and the quantification of organismal biodiversity. *Philosophical Transactions of the Royal Society of London: Series B. Biological Sciences*, 345: 45-58.
- Garland, T., P.E. Midford, and A.R. Ives. 1999. An introduction to phylogenetically based statistical methods, with a new method for confidence intervals on ancestral values. *American Zoologist*. 39: 374-388.
- Garland, T. and A.R. Ives. 2000. Using the past to predict the present: confidence intervals for regression equations in phylogenetic comparative methods. *The American Naturalist*. 155(3): 346-364.
- Hillis, D.M. 1998. Phylogenetic analysis of frequency data in molecular ecological studies. Pp. 25-38, *in* *Advances in Molecular Ecology*. Proceedings of the NATO Advanced Study Institute on Molecular Ecology. G. R. Carvalho ed.. IOS Press, 313 pp.
- Hooper, J. N. A., J. A. Kennedy, and R. J. Quinn. 2002. Biodiversity “hotspots”, patterns of richness and endemism, and taxonomic affinities of tropical Australian sponges (Porifera). *Biodiversity and Conservation*, 11: 851-885.
- Hull, David L. 1988. *Science as a Process : An Evolutionary Account of the Social and Conceptual Development of Science* . The University of Chicago Press, Chicago, 586 pp.
- Kitching, I.J, P.L. Forey, C.J. Humphries, and D. M. Williams. 1998. Measures of character fit and character weighting Pp. 92-116 *in* *Cladistics: the theory and practice of parsimony analysis*. 2nd edition. Oxford University Press, New York, 228 pp.
- Lamshead, P.J.D. 1986. Sub-catastrophic sewage and industrial waste contamination as revealed by marine nematode faunal analysis. *Marine Ecology - Progress Series* 29: 247-260.
- Lamshead, P.J.D. and G.L.J. Paterson. 1986. Ecological cladistics – an investigation of numerical cladistics as a method for analysing ecological data. *Journal of Natural History* 20: 895-909.
- Lamshead, P.J.D., B.J. Elce, D. Thistle, J.E. Eckman, and P.R.O. Barnett. 1994. A comparison of the biodiversity of deep-sea marine nematodes from three stations in the Rockall Trough, Northeast Atlantic, and one station in the San Diego Trough, Northeast Pacific. *Biodiversity Letters* 2: 95-107.
- Legendre P. and L. Legendre. 1998. *Numerical ecology*, second English edition. Elsevier, Amsterdam. 853 pp.
- Lyons-Weiler, J. and R.J. Tausch. 1997. The demarcation of historical from ecological variance in species diversity patterns. Pp. 209-221, *in* *Conservation and management of native plants and fungi*. A. Liston, R.M. Love, D.L. Luoma, R.J. Meinke, and M.V.Wilson, eds. Native Plant Society of Oregon, Corvallis, Oregon, 296 pp.
- Maddison, W.P. & D.R. Maddison. 2005. *Mesquite: A modular system for evolutionary analysis*. Version 1.05. <http://mesquiteproject.org>.

- Magurran, A.E. 1988. Ecological diversity and its measurement. Princeton University Press, Princeton, New Jersey, 179 pp.
- Masselot, G, A. Nel, A. Thomas, and J. Nel. 1997. Parcimonie de Wagner et biomonitoring de cours d'eau: Application au bassin de la Risle (Normandy, France). *Annales de la Societe Entomologie* . 33 (3): 237-258.
- Midford, P. E., T. Garland Jr., and W. P. Maddison. 2003. PDAP Package.
- Morrone, J.J. 1994. On the identification of areas of endemism. *Systematic Biology* 43 (3): 438-441.
- Morrone, J.J. and J.V. Crisci. 1995. Historical biogeography: Introduction to methods. *Annual Review of Ecology and Systematics*. 26: 373-401.
- Myers, A.A., and S. De Grave. 2000. Endemism: origins and its implications. *Vie et Milieu*. 50 (4): 195-204.
- Nel, A., J. Nel, G. Masselot, and A. Thomas. 1998. An investigation into the application of the Wagner parsimony method in synecology. *Biological Journal of the Linnean Society*. 65: 165-189.
- Nihei, S.S. 2006. Misconceptions about parsimony analysis of endemism. *Journal of Biogeography*. 33: 1-8.
- O'Brien, M.J. and Lyman, R.L. 2003. *Cladistics and Archaeology*. University of Utah Press, Salt Lake City, Utah, 280 pp.
- Odum, E.P. 1971. *Fundamentals of Ecology*. Third edition. W.B. Saunders Company, Philadelphia, London, Toronto, 574 pp.
- Pellens, R., P. Grandcolas, and E. Guilbert. 2005. Phylogenetic algorithms and the evolution of species communities in forest fragments. *Cladistics*. 21: 8-14.
- Perochon, E., G. Masselot, and Andre Nel. 2001. Freshwater macroinvertebrates sampling problems in synecological analyses and biomonitoring. A concrete example. *Annales Societe de Entomologie Francais*. (N.S.). 37 (3): 341-346.
- Porzecanski, A. L., and J. Cracraft. 2005. Cladistic analysis of distributions and endemism (CADE): using raw distributions of birds to unravel the biogeography of the South American aridlands. *Journal of Biogeography*. 32: 261-275.
- Quicke, D.L.J., J. Taylor, and A. Purvis. 2001. Changing the landscape: a new strategy for estimating large phylogenies. *Systematic Biology* 50(1): 60-66.
- Quicke, D.L.J. 1993. *Principles and techniques of contemporary taxonomy*. Blackie Academic and Professional, Glasgow, Scotland. 311 pp.
- Reish, D.J. 1984. Domestic Wastes. Pp. 1719-1767 *in* O. Kinne, ed., *Marine Ecology*. John Wiley and Sons, New York, Volume V, part 4.
- Rosen, B.R. 1988. From fossils to earth history: applied historical biogeography. Pp. 437 - 481 *in* A. A. Myers and P. S. Giller, eds. *Analytical biogeography: An integrated approach to the study of plant and animal distributions*. Chapman and Hall, Glasgow, Scotland.

- Rosen B.R. and B. Smith. 1988. Tectonics from fossils? Analysis of reef-coral and sea-urchin distributions from late Cretaceous to Recent, using a new method. Pp. 275-36 *in* M.G. Audeley-Charles and A. Hallam, eds. Gondwana and Tethys. Geological Society Special publication 37. London, England.
- Rosen, B.R. 1992. The biogeographical black box: concepts and methods in marine palaeobiogeography. *Palaeogeography, Palaeoclimatology, Palaeoecology*, 92: 171-205.
- Salen-Picard, C., G. Bellan, D. Bellan-Santini, D. Arlhac, and R. Marquet. 1996. Long-term changes in a benthic community of a Mediterranean gulf (Gulf of Fos). *Oceanologica Acta* 20: 299-310.
- Sankoff, D. and R.J. Cedergren. 1983. Simultaneous comparison of three or more sequences related by a tree. Pp. 253-263, *in* D. Sankoff and J.B. Kruskal eds. Time warps, string edits, and macromolecules: The theory and practice of sequence comparison. Addison-Wesley, Reading, Massachusetts.
- Sankoff, D. and P. Rousseau. 1975. Locating the vertices of a Steiner tree in arbitrary space. *Mathematics Progress*. 9: 240-246.
- Scotland, R.W. 1992. Cladistic theory. Pp. 3-13 *in* Cladistics: a practical course in systematics. P.L. Forey, C.J. Humphries, I.J. Kitching, R.W. Scotland, D.J. Seibert, and D.M. Williams, contributing authors. Oxford University Press, New York, 191 pp.
- Swofford, D. 2000. PAUP*. Phylogenetic analysis using parsimony (* and other methods) version 4.0b10, National Museum of Natural History, Smithsonian Institution, Washington, D.C.
- Swofford, D.L., G.L. Olsen, P.J. Waddell, and D.M. Hillis. 1996. Phylogeny reconstruction. Pp. 407-514 *in* Molecular systematics, 2nd ed. D.M. Hillis, C. Moritz, and B.K. Mable, eds., Sinauer Sunserland, Massachusetts, 655 pp.
- Trejo-Torres, J. C. and J.D. Ackerman. 2002. Composition patterns of Caribbean limestone forests: Are parsimony, classification, and ordination analyses congruent? *Biotropica*. 34(4): 502-515.
- Warwick, R.M. and K.R. Clarke. 1995. Multivariate measures of community stress and their application to marine pollution studies in the east Asian region. *Phuket Marine Biological Center Research Bulletin*. 60: 99-113.
- Watanabe, K. 1998. Parsimony analysis of the distribution pattern of Japanese primary freshwater fishes, and its application to the distribution of the bagris catfishes. *Ichthyological Research* 45 (3): 259-270.
- Wiley, E.O. 1981. Phylogenetics, the theory and practice of phylogenetic systematics. Wiley-Interscience, New York. 439 pp.