

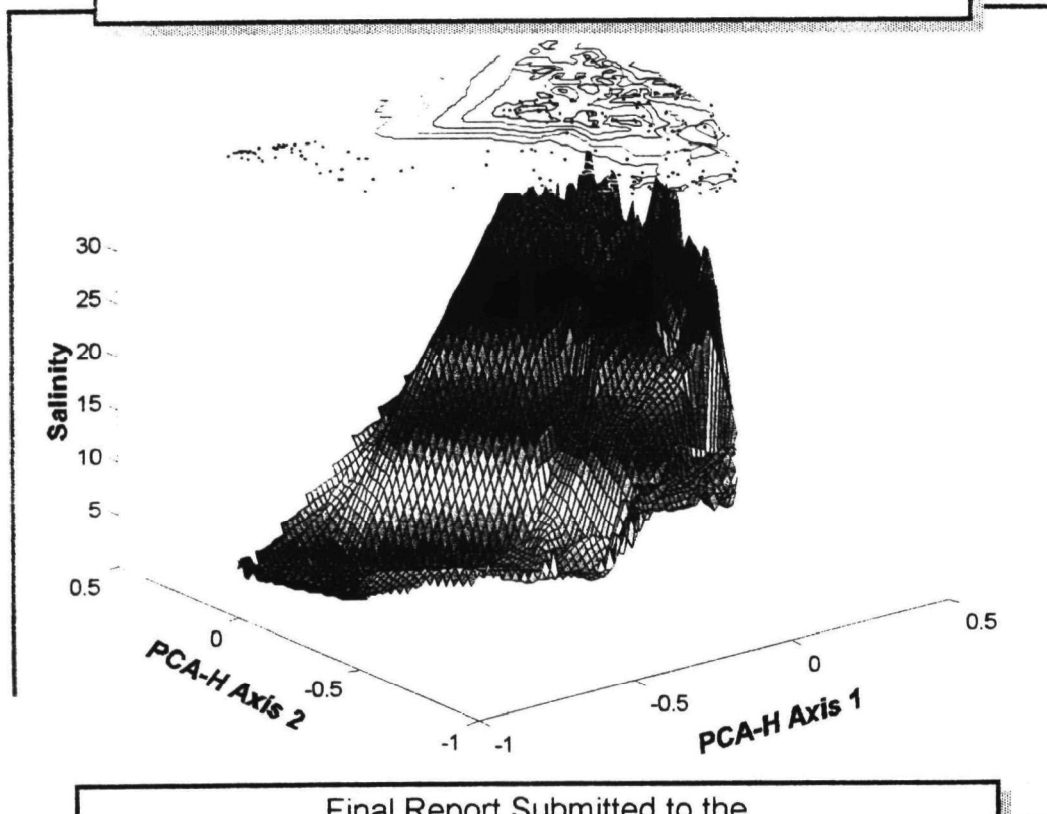
# Virginian Province Macroinfaunal Community Structure: PCA-H Analyses and an Assessment of Pollution Degradation Indices

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United States Environmental Protection Agency  
Atlantic Ecology Division (AED)  
Narragansett, RI 02882  
EPA PROJECT OFFICER: **Brian D. Melzian**

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## EXECUTIVE SUMMARY

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This report describes research done under a cooperative agreement between the EPA and the University of Rhode Island and Rutgers University. The lead author performed this work while on sabbatical leave at Rutgers University in the 1994-1995 academic year. Dr. J. Fred Grassle hosted and assisted Dr. Gallagher in the analysis of the EPA's "Environmental Monitoring and Assessment Program-Estuaries Virginian Province" (EMAP-E VP) data.

The EMAP program set as a goal the identification of degraded biological conditions in the nation's ecosystems. Biotic indicators of degraded conditions were to be developed rather than focusing on the concentrations of pollutants (Messer *et al.* 1991, p. 70-81). Each EMAP program was to design biotic indices to determine the extent of impacted biological conditions. Then, the assessment portion of the EMAP program was to determine whether these adverse effects could be attributed to the effects of pollution. The EMAP program was designed as a multi-decade program. The EMAP-Estuaries program was to assess the status of our nation's near-shore coastal zone, including estuaries. The Virginian and Louisianian Provinces were chosen to be the demonstrations for the EMAP-E program. The EMAP-E Virginian Province (EMAP-E VP) program developed four different indices of benthic degradation. We review each of these indices and offer our assessment of their adequacy as descriptions of impacted benthic communities. The first three benthic indices are no longer used in the EMAP-E VP program. We provide additional reasons to reject these indices. We provide an analysis of the latest EMAP-E VP index, the 1990-1993 index. This index may discriminate between a subset of stations regarded as degraded and non-degraded, but it should not be used as a general index of degraded marine benthos. When reduced to simple terms, this index states that roughly 7000 spionid polychaetes or 17000 oligochaetes per square meter indicates benthic degradation. This index will classify large portions of pristine benthic areas in the Virginian Province and throughout the world as degraded.

We review one of the central assumptions of the development of EMAP-E VP benthic degradation indices: that sediment pollutant concentrations, overlying dissolved oxygen concentrations, and amphipod toxicity are necessary and sufficient conditions for creating test data sets of degraded and reference stations. We do not agree with this assumption. It is possible to have relatively unimpacted benthic sites be classified as degraded using the EMAP-E VP criteria for degradation. Conversely, many impacted sites would fit the EMAP-E VP criteria that define natural or reference sites. The EMAP-E program is based on circular logic. Instead of devising independent criteria to assess the effects of contaminants and low dissolved oxygen on benthic communities, the EMAP-E program has *a priori* assumed that sites having concentrations of contaminants in excess of published thresholds, amphipod survival less than a threshold or low dissolved oxygen in the overlying water must be degraded. Once these criteria were established, two test data sets were created and an equation derived which would separate these two groups. All other EMAP-E VP sites are scored using this function. The EMAP-E VP program did not evaluate whether any of these sites really showed biological impacts indicative of degradation.

We present new analyses of the patterns of benthic community structure in the Virginian Province. The effects of pollution on benthic communities must be assessed relative to natural patterns of variation in community structure. We use both classification and ordination analysis to describe the major patterns in community structure in the EPA's EMAP-E VP benthic data. These analyses use the metric faunal distance metric CNESS, short for Chord-normalized expected species shared (Trueblood *et al.* 1994). This index is a metric version of Grassle and Smith's (1976) NESS or Normalized Expected Species Shared faunal similarity index. The ordination method based on CNESS is called PCA-H, short for principal components analysis of hypergeometric probabilities. We conclude that salinity is the overriding factor controlling natural patterns of Virginian Province community structure. It is the major factor controlling the maximum number and type of



species that occur in an area. Species richness in the Virginian Province is a strong function of salinity, with very low salinity habitats having roughly eight species in three replicate samples and high salinity areas having over forty species.

The EMAP-E VP benthic degradation indices have attempted to account for this habitat factor. Salinity strongly affects degradation indices based on species richness and the abundance of opportunistic taxa, variables which strongly covary with salinity. The use of opportunistic or pollution-indicating taxa is problematic because almost all opportunistic taxa used in marine ecology are natural components of medium and low salinity habitats.

The existing EMAP-E indices indicate that tidal-river habitats have the highest percentage of degraded area, approximately 40%. Tidal river systems, often near urban sources of pollution, are more likely to have degraded benthic communities than large and small estuaries. However, these sites are also the ones most likely to be misclassified as degraded if the effects of salinity are not properly taken into account.

We review the extensive literature on benthic pollution indices. Much of this literature has attempted to find an index to classify pollution-affected vs. natural benthic communities. The Chesapeake Bays Program developed a Restoration Goals Index for the Chesapeake Bay. This index is different from the EMAP-E index. An index similar to the Chesapeake Bay Restorations Goals Index was developed for the Regional EMAP program in the New York/New Jersey harbor system.

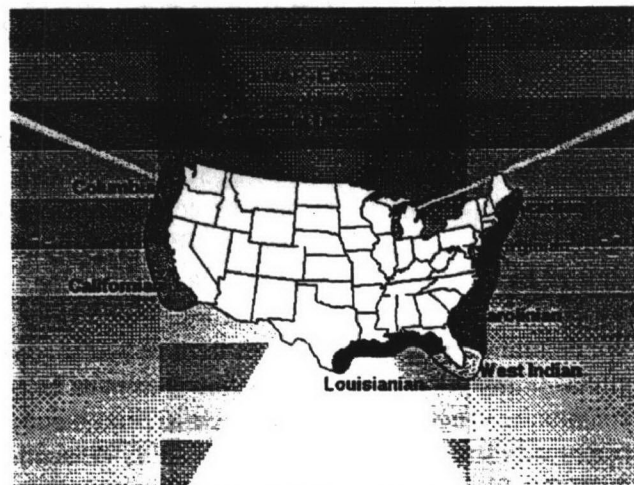
## INTRODUCTION

The Environmental Monitoring and Assessment-Estuaries (EMAP-E) program was designed to be a long-term, multi-decade monitoring plan for the nation's estuaries. EMAP-E is a subset of the nationwide EMAP program, which was to provide answers to the following questions (Weisberg *et al.* 1993):

- What is the status, extent, and geographical distribution of the nation's ecological resources?
- What proportion of these resources is declining or improving? Where? At what rate?
- What factors are likely to be contributing to declining conditions?
- Are pollution control, reduction, mitigation, and prevention programs achieving overall improvement in ecological condition?

The Virginian Province was selected as the demonstration area to implement the sampling and analytic procedures for the EMAP-E program. As a result, it has been sampled over four different years (1990-1993). The Louisianian Province was sampled in 1991. These provinces are shown in Figures 1 and 2.

EMAP-E sampling stations (sites) were chosen using Overton *et al.*'s (1990) probability-based



**Figure 1. The EMAP-E Provinces.** The Virginian Province was sampled each year from 1990-1993 and the Louisianian Province was first sampled in 1991. [Figure from the EMAP-E World-Wide Web page.]

sampling procedure. Probability sampling was applied to three strata in the Virginian Province: large estuaries, small estuaries and tidal rivers. A random selection of small estuaries was selected for probability-based sampling, and all large tidal rivers and large estuaries were sampled. Approximately two thousand benthic grab samples were processed during the four-year duration of EMAP-E VP.

The EMAP-E VP program used patterns of benthic community structure to assess the status of the Virginian Province's near-shore coastal zone. Benthic ecologists throughout the world use benthic community structure to assess the effects of anthropogenic pollution (*e.g.*, Boesch and Rosenberg 1981, Bloom 1980, Chapman *et al.* 1987, Field *et al.* 1982, Gray 1976, 1979a & b, 1989, Jumars 1981, Warwick 1993). Some reasons

for the efficacy of monitoring changes in benthic community structure are that benthic populations are relatively sedentary (*i.e.*, they can't migrate away from a pollution source or source of disturbance), and their typical monthly to annual generation times are such that the populations are adapted to short-term fluctuations in environmental variables but are capable of a strong numerical response to significant long-term environmental changes. Moreover, the populations are sensitive enough to respond to relatively low levels of toxic substances. For example, Grassle *et al.* 1981 observed pronounced community responses to 90 ng/g of #2 diesel oil in the MERL ecosystem tanks). The recovery time of benthic populations is short enough that changes in community structure can be detected in a matter of months, but long enough that the community structure is to some extent a response to the integrated habitat quality over the previous months or even years.

The EMAP-E VP program developed benthic degradation indices to determine the proportion of the Virginian Province with degraded benthic communities. The EMAP-E VP program selected a set of degraded stations and a set of undegraded, or "reference" stations, and then produced an equation based on biological variables that discriminated between these two groups. The Chesapeake Bay Restorations Goals Index [RGI] (Ranasinghe *et al.* 1993) used a similar approach. The EMAP-E VP and RGI indices differ in the statistical methods used to classify samples into degraded and undegraded classes. The EMAP-E VP uses a parametric linear discriminant function. The RGI index is based on an ordinal ranking of biological variables into the groupings 1 (below expected), 2 (expected), and 3 (greater than expected). A degraded station in the RGI index is one that has an average ranking across biological variables of less than 2.

To demonstrate the utility of alternate methods for assessing the effects of pollution on benthic communities, this report contains detailed analyses of patterns of community structure in the four-year Virginian Province data. These analyses are performed using methods based on CNESS and PCA-H (Gallagher *et al.* 1992, Trueblood *et al.* 1994). CNESS or the chord-normalized expected species shared, is a metric for assessing the faunal similarity among samples. PCA-H, short for principal components analysis of hypergeometric probabilities, is an ordination technique based on CNESS. CNESS is the metric equivalent of Grassle and Smith's (1976) Normalized Expected Species Shared or NESS index. Using either NESS or CNESS, the entire 1918-sample EMAP-E VP data can be clustered using COMPAH96 in about 10 minutes using a desktop PC. COMPAH96 is the latest version of Boesch's (1977a) clustering program. It is available for



Figure 2. Virginian Province EMAP-E sample locations from 1990-1992 [1993 sample locations not shown, Figure downloaded from the EMAP-E web page]

download with documentation on the lead author's World Wide Web page. Boesch's (1977a) EPA report describes many of the methods available in COMPAH and applies them to benthic data from Chesapeake Bay.

## STATISTICAL METHODS USED IN THIS STUDY

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### How the EMAP-E VP benthic data were collected

Samples are taken within the Virginian Province using a probability-based sampling design within pre-defined strata. Weisberg *et al.* (1993, p. 2-4 to 2-5) describe the strata: Large estuaries, Large Tidal Rivers, and Small Estuarine Systems. The specific application of probability sampling to each strata was different. A systematic random two-dimensional grid was applied to the large estuaries. Overton's (1989) sampling grid, designed for the nationwide EMAP program, was scaled down to make these grids. The sampling points were the centers of the hexagonal grids. The five large tidal rivers (*i.e.*, Hudson, Potomac, James, Delaware, and Rappahannock) were sampled using a one-dimensional analog of the two-dimensional grid used for the large estuaries. A list frame was used to select 32 (23%) of the 137 small estuarine systems during the 1990 sampling. All small estuaries were ranked by latitude and grouped into groups of four. One small estuary out of each group was randomly chosen. In the 1990 sampling, Delaware Bay and the Delaware River were sampled more intensively. Subsequent EMAP-E VP sampling used the same basic approach. Strobel *et al.* (1995, p. A-2) summarize all four years of EMAP-E VP sampling. There were 446 sites sampled with probability-based sampling. Several EMAP-E VP sampling sites were sampled repeatedly over the four-year period (*e.g.*, twenty samples from Indian River Bay site No. 150, and eighteen benthic samples from the Potomac River site No. 188). Most sites were sampled only once, with three replicate grabs. A subset of sampling sites from the 1990 sampling, called Index sites, were chosen because they are 'located in depositional environments, where there is a high probability of sediment contamination or low dissolved oxygen conditions.' There were 86 index sites in the EMAP-E VP database. There were a select number of 1990 sampling sites chosen for long-term sampling, the Long-term trend sites. There were twelve Long-term trend (LTT) sites. Strobel *et al.* (1995) describe additional sites that were sampled repeatedly during the EMAP-E VP program.

Typically three Ted Young modified van Veen grab samples (0.044 m<sup>2</sup>) were collected at each sampling station (site) from the Virginian Province (Figure 2). Additional grabs were taken and composited for sediment chemistry, grain size, and amphipod toxicity tests. The benthic infauna retained a 500- $\mu$ m mesh sieve were identified. Most of the sorting and identification in the EMAP-E VP program was done by Cove Associates. Most of the individuals were identified to species. The taxonomy of samples collected in areas with bottom water salinity less than 5 psu (short for practical salinity units, formerly called parts per thousand or abbreviated ‰) is handled differently than the remaining samples. Oligochaetes and chironomids were classified to levels finer than the taxonomic level Class. Many of the oligochaetes and chironomids collected from sites with bottom salinities less than 5 psu were identified to species. The chironomids and oligochaetes from samples collected in areas with salinities above 5 psu were lumped at the level of Family and Class, respectively.

### Preparing the EMAP-E Virginian Province data for community analysis

The unedited EMAP-E VP data cannot be used for traditional community structure analysis. There are 868 taxonomic categories in the full EMAP database. We dropped many taxa and merged others to form a much smaller set of valid taxonomic categories. Some of the EMAP taxa are invalid, some are redundant, and many refer to epifaunal taxa. We arrived at a final list of 551 taxa. We discuss the reasons for dropping and merging categories below. This provide the full and edited list of EMAP-E VP taxa in Appendix II.

## Drop and Merge Rules

There are over 868 taxonomic designations listed in the four-year Virginian Province data set. Two of these 'taxa' include:

NOORGPRS	No Organisms Present
POLYCHAE	Polychaeta: Other - Unidentified & fragments

Of the remaining 866 species codes in the EMAP-E VP database, more than three hundred must be dropped or merged for community structure analyses. We use 551 taxonomic designations (most are species) for our analyses. For more detailed analyses of community structure, we would probably drop many or merge many additional EMAP-E VP taxa. For example, much of the break in community structure at the 5 psu mark is because chironomids and oligochaetes were sorted to levels finer than family and class in the low salinity habitats, but not in the higher salinity habitats. To assess whether 5 psu really marks a key transition in community structure, these taxa would have to be merged or dropped. The existing EMAP-E VP data set flags only a subset of the invalid taxa with the database flag SPEC\_IGN (Ignore this species in calculating total species per event).

The authors of this study developed the first list of "valid EMAP taxa" using two DROP rules and three MERGE rules:

### The drop rules

- Drop Rule 1.** Drop all strictly epifaunal, meiofaunal, and pelagic taxa.
- Drop Rule 2.** Drop all general taxonomic designations at the generic, familial and higher taxonomic levels if there are more than two valid lower-level designations for that group. For example, there are many species of the family Spionidae identified in the EMAP data and three species of the genus *Spio*. Therefore, both the familial level EMAP taxon SPIONIDA and the generic level taxonomic category SPIO must be dropped. Failure to implement this "drop" rule would have the unfortunate effect of greatly enhancing the faunal similarity of samples along environmental gradients. Samples would appear more similar than they really are.

Only a limited number of non-specific designations escaped the drop rule. These are listed below. Several of these higher level taxonomic designations should be dropped in future analyses designed to assess biogeographic patterns (*e.g.*, oligochaetes, Tubificidae with capiliform chaetae, Tubificidae without capiliform chaetae).

<i>Acanthohaustorius</i> spp.	Dolichopodidae
Amphitritinae	Flabelligeridae
<i>Aphelochaeta</i> spp.	<i>Laonice</i> spp.
<i>Bezzia</i> spp.	<i>Magelona</i> spp.
Buccinidae	<i>Microchironomus</i> spp.
<i>Capitella</i> spp.	Nemertinea
Chironomidae	Oligochaeta
<i>Chironomus</i> spp.	<i>Ophryotrocha</i> spp.
<i>Cladotanytarsus</i> spp.	<i>Owenia</i> spp.
<i>Coelotanytus</i> spp.	<i>Palpomyia</i> spp.
<i>Cryptochironomus</i> spp.	<i>Phoronis</i> spp.
<i>Demicryptochironomus</i> spp.	<i>Pisidium</i> spp.
<i>Dicratendipes</i> spp.	<i>Polygordius</i> spp.
Diptera	<i>Polypedium</i> spp.

<i>Procladius</i> spp.	<i>Sphaeromias</i> spp.
<i>Procladius</i> (Holotanypus) spp.	<i>Stictochironomus</i> spp.
<i>Protodrilus</i> spp.	<i>Tanypus</i> spp.
<i>Protohaustorius</i> spp.	<i>Tanytarsus</i> spp.
<i>Pseudochironomus</i> spp.	Thalassinidea
Sipuncula	Tubificidae without capiliform chaetae
Solecurtidae	Tubificidae with capiliform chaetae
<i>Sphaerodoropsis</i> spp.	

## The merge rules

**Merge Rule 1.** Merge all taxa that can not be adequately distinguished taxonomically. The EMAP-E VP data set contains hundreds of taxonomic designations at taxonomic levels higher than the species. For example, in the full EMAP species list, the following eight ampeliscid amphipod categories are found:

AMPEABDI	<i>Ampelisca abdita</i>
AMPEABVA	<i>Ampelisca abdita-vadorum</i> complex
AMPELISC	<i>Ampelisca</i> spp.
AMPEVADO	<i>Ampelisca vadorum</i>
AMPEAGAS	<i>Ampelisca agassizi</i>
AMPEVERR	<i>Ampelisca verrilli</i>
AMPHIPOD	Amphipoda: Other

We consulted with the taxonomists at Cove Associates (Tim Morris and Nancy Mountford) to determine whether *Ampelisca* spp. and 'Amphipoda: Other' were indeed different from the juvenile stages of *Ampelisca abdita* and *A. vadorum*, which can not be identified to species. They stated these categories did not refer to either *A. abdita* or *A. vadorum*, therefore both higher level taxa were dropped using DROP RULE 2 (above). Using Merge Rule 1, the AMPEABDI, AMPEABVA, and AMPEVADO designations were fused, reducing the original seven taxonomic categories used to describe ampeliscid amphipods to three:

AMPEABVA	<i>Ampelisca abdita-vadorum</i> complex
AMPEAGAS	<i>Ampelisca agassizi</i>
AMPEVERR	<i>Ampelisca verrilli</i>

**Merge Rule 2.** If there are a pair of taxonomic designations indicated by *Genus A species x* and *Genus A spp.*, and there is a high probability that the individuals identified only as *Genus A spp.* are indeed *Genus A species x*, then merge the two taxa. This merge usually occurs when there is only one species in addition to the higher level taxonomic designation. Note that Drop Rule 2 would force the deletion of *Genus A spp.* if there were more than one species of *Genus A* in the data set. Our main justification for merging these taxa is that the taxonomists were better able to distinguish species in the later years of the EMAP-E VP sampling.

The following groups of EMAP taxa refer to single species and should be merged:

LUMBHEBE	<i>Scoletoma hebes</i>	(These refer to the same species, but were listed as separate species in the EMAP data)
SCOLHEBE	<i>Scoletoma hebes</i>	

MELINNA	<i>Melinna</i> spp.	MICRATRA	<i>Microphiophotis</i>
MELIMACU	<i>Melinna maculata</i>		<i>atra</i>
NOTOMAST	<i>Notomastus</i> spp.	OPHIUROI	Ophiuroidea
NOTOSPA	<i>Notomastus</i> sp. A Ewing	MUSCTRAN	<i>Musculium</i> <i>transversum</i>
OWENFUSI	<i>Owenia fusiiformis</i>	MUSCULIU	<i>Musculium</i> spp.
OWENIA	<i>Owenia</i> spp.	ORCHMINU	<i>Orchomenella</i> <i>minuta</i>
PECTGOUL	<i>Pectinaria gouldii</i>	ORCHOMEN	<i>Orchomenella</i> spp.
PECTINAR	<i>Pectinaria</i> spp.	PANDGOUL	<i>Pandora</i> <i>gouldiana</i>
PERAFFI	<i>Pherusa affinis</i>	PANDORA	<i>Pandora</i> spp.
PERUSA	<i>Pherusa</i> spp.	PANDORID	Pandoridae
ASYCELON	<i>Sabaco elongatus</i>	SOLEMYA	<i>Solemya</i> spp.
ASYCHIS		SOLEMYID	Solemyidae
SABAELO	<i>Sabaco elongatus</i>	SOLEVELU	<i>Solemya velum</i>
(All 3 designations refer to the same malacostrachan species, but different codes were used in different years in the EMAP database [The genus name had changed from <i>Asychis</i> to <i>Sabaco</i> ])		TELLAGIL	<i>Tellina agilis</i>
		TELLINA	<i>Tellina</i> spp.
		(Note: the EMAP taxon TELLINID Tellinidae is dropped)	
EUDOPUSI	<i>Eudorella pusilla</i>	YOLDIA	<i>Yoldia</i> spp.
EUDORELL	<i>Eudorella</i> spp.	YOLDLIMA	<i>Yoldia limatula</i>

**Merge Rule 3.** On occasion, a merge could occur between a higher level category and a species, even if more than one species in a genus were present. If the taxonomists at Cove Associates were reasonably certain that individuals identified as *Genus* spp. belonged to a valid species designation, these taxa were fused rather than dropping the higher level designation.

For example, the EMAP species list contains the following three taxa:

LEITFRAG	<i>Leitoscoloplos fragilis</i>
LEITOSCO	<i>Leitoscoloplos</i> spp.
LEITROBU	<i>Leitoscoloplos robustus</i>

DROP Rule 2 would dictate that LEITOSCO (*Leitoscoloplos* spp.) should be dropped. However, Cove Associates is reasonably certain that the individuals identified as LEITOSCO are *Leitoscoloplos robustus*, so these two categories are merged, forming 2 valid taxa:

LEITFRAG	<i>Leitoscoloplos fragilis</i>
LEITROBU	<i>Leitoscoloplos robustus</i>

## Methods to analyze community structure

### Converting EMAP-E VP data from SAS™ to Matlab™

The EMAP-E VP data are stored in a SAS database. We adapted a SAS program, provided by S. Weisberg and A. Ranasinghe (VERSAR, Columbia MD) to convert the SAS EMAP-E VP database to

COMPAH input format. COMPAH reads data in a number of accepted formats and will convert to other formats, including the binary form used by MATLAB™.

Most of the analyses performed in this report were done with MATLAB™ programs written by the lead author. Many of these programs are available on the lead author's World-Wide Web page.

### ***Diversity analyses***

We used the following diversity indices to analyze the EMAP-E VP data: Brillouin's  $H$ , Shannon's  $H'$ , Hurlbert's  $E(S_n)$ , Pielou's  $J'$  Evenness, Simpson's diversity, total number of species, and Gleason's  $D$ . The first six indices are described in Pielou (1969, 1975, 1977), Peet (1974) and Magurran (1988). Smith and Grassle (1977) describe the statistical properties of Hurlbert's (1971)  $E(S_n)$  and Simpson's unbiased diversity indices. Hurlbert's (1971)  $E(S_n)$  is based on Sanders' (1968) rarefaction method for analyzing species diversity. Gleason's  $D$  diversity index, the number of species divided by the logarithm of number of individuals, is described in Washington (1984).

### ***Cluster analysis***

COMPAH was used to cluster samples and species. Both the sample and species cluster analyses follow methods described in Trueblood *et al.* (1994). Sample clustering uses CNESS ( $m=25$ ) as the distance measure and unweighted pair group (UPGMA) sorting. For clustering species, we used Pearson's  $r$  of the normalized hypergeometric probability matrix with single-linkage clustering. The lead author distributes full documentation, source, and executable codes for COMPAH on his web page.

### ***PCA-H Analysis***

Trueblood *et al.* (1994) describes the methods used to perform an ordination using CNESS faunal distances. This ordination uses a principal components analysis of hypergeometric probabilities, which is abbreviated as PCA-H. Programs to perform PCA-H are available on the lead author's web page. Appendix I provides background information on CNESS and PCA-H.

## **RESULTS & DISCUSSION**

### **The What, Why and Where of benthic monitoring**

#### ***What is monitoring and assessment?***

Chapman *et al.* (1987a) provided this definition of monitoring:

*"Monitoring consists of repetitive data collection for the purpose of determining trends in the parameters [sic] monitored."*

According to Chapman *et al.* (1987a), monitoring must be based on three questions:

- What beneficial uses should be protected?
- What water-quality problems have been identified in the past or at present that need to be monitored?

■ What major natural and anthropogenic factors affect the ecosystem?

The first question is difficult to answer. Chapman *et al.* (1987a) urge ecologists to consider which changes are meaningful ecologically or for regulatory purposes. O'Connor and Dewling (1986) argued that ecological significance is different from statistical significance. An ecologically significant, or perhaps environmentally significant, result is one that is important enough for ecologists to warn regulators about and important enough for environmental regulators to consider regulatory action. Using O'Connor and Dewling's (1986) criteria, we might assess whether the EMAP-E VP benthic degradation indices be used now to assess whether estuarine sediments are sufficiently 'clean' for oceanic dredge disposal.

Green (1979, p. 68) divides the broad field of ecological survey sampling into three categories: baseline studies, monitoring studies, and impact studies. A baseline study is a sampling program that determines the present state of the system (*e.g.*, estimates of biological and chemical variables). An impact study assesses the effects of an impact such as an oil spill. In a monitoring study, the goal is merely to detect change from the present state. Baseline data must be available in an impact study to provide a standard against which to detect a change.

One of the goals of the EMAP-E VP program is not only to establish baseline monitoring data, but also to measure a wide variety of habitat and sediment pollutant variables. The habitat factors include water depth, temperature, salinity, pH, stratification, total suspended solids, water clarity, and sediment grain size. The pollutant variables include most of the EPA priority pollutants including heavy metals, pesticides, PCB's, PAH's and pesticides. The assessment portion of the EMAP-E VP program, based on analyses of the covariation of physical and biological variables, should allow the assessment of which factors might be responsible for changes in community structure.

### ***Statistics and sampling designs***

A monitoring plan should be based on established principles of statistics. All variables, hypotheses and statistical models should be specified in advance. The use of sample statistics in the broad sense should be an essential part of almost all monitoring plans. Unfortunately, despite token references to the contrary, hypothesis testing using valid sampling designs is rarely incorporated in most monitoring studies. A strong case could be made for the view that hypothesis testing need not be an essential feature of monitoring. Just as museum collections of bird shells provided essential baseline data for documenting the effects of DDT in the 1960s, some might feel that data collection *per se* has intrinsic value. However, when funds for monitoring are scarce and the potential array of variables that might be monitored is large, data collection without a rigorous sampling design can no longer be justified. A monitoring program should attempt to link changes in the environment with the variables that account for that change.

There are three types of error involved in an experimental or survey design. The first two are well known: Type I and Type II error. These well-known statistical errors in a monitoring program involve finding change when there is none and not detecting a change in the environment. Underwood (1981) called a third major source of error model misspecification. Model misspecification is caused by using an inappropriate statistical model to perform the analyses. Model misspecification can result in either failing to detect important patterns in the data, or detecting patterns and attributing the result to the wrong cause. This third source of error subsumes much of what Hurlbert (1984) has called pseudoreplication. Monitoring should attempt to minimize this third source of error by insuring that the assumptions of the tests being used are met, and that the appropriate covariates are either measured or randomized out of the design.



### Type I & II error and model misspecification

The following table shows the relationship between Type I and Type II error:

		Null Hypothesis	
		True	False
Decision Based on Statistical Test	Reject $H_0$	Type I error	Correct decision "Science Advances"
	Accept $H_0$	Correct Decision "No Advance"	Type II error

In environmental monitoring, the traditional null hypothesis is that of 'no change' (e.g.,  $H_0: \mu_1 = \mu_2$ ). The probability of Type I error, symbolized as  $\alpha$ , is the probability of rejecting a true null hypothesis; its magnitude is set through the choice of the critical value of the underlying statistical distribution against which the value of the test statistic is to be judged. Conventionally, the probability of Type I error is set at 0.05 or 0.01, so that the odds of rejecting a true null hypothesis are only 1 in 20 or 1 in 100. The choice of a significance level is merely convention, and there is justification for choosing a relatively large  $\alpha$ -level (e.g., Probability (Type I error)=0.10) for environmental monitoring studies. Committing a Type II error by accepting a false null hypothesis of no change in the environment may have serious regulatory consequences. For example, the depletion of atmospheric ozone is of such immediate world-wide concern that sampling programs for Antarctic ozone levels should be designed to minimize the probability of Type II error. If the null hypothesis is 'the percentage of benthic area containing few animals, e.g., less than 1000 per square meter) is not changing, the environmental consequences of a large Type II error could be extremely serious. For a given sample size, increasing the probability of Type I error (e.g., testing at the  $\alpha=0.10$  rather than  $\alpha=0.05$  level) leads to a decrease in the probability of Type II error. Increasing sample size reduces the probabilities of both Type I and Type II error. However, if sample size can not be increased, then many scientists would argue for  $\alpha$ -levels larger than the conventional 0.05 level to reduce the probability of Type II error.

The EMAP-E VP program is one of the few benthic monitoring programs that has included explicit power analyses in its statistical summaries. The EMAP-E VP program is designed so that a 2% annual change in the percentage of area classified as degraded can be detected with high statistical power over a 10-year period.

### Trend analysis

Chapman *et al.* (1987) state that the goal of monitoring is not merely to detect a change in environmental variables, but a trend. 'Trend' usually implies a non-random temporal pattern in the data. It would be possible to take enough samples so that a change in an environmental variable could be detected between each and every sampling period; roughly half of these changes would be positive and half negative. It is not sufficient to merely find significant results in a monitoring program. If that was the goal, by increasing the sample size and program cost, a monitoring program could detect even slight changes in variables. If there was no long-term trend in the variable, half of these significant changes would be positive and half negative.

As O'Connor and Dewling stress, applied ecologists must move beyond minimizing Type I and Type II error and determine what magnitude of change is significant ecologically. Year-to-year fluctuations about the mean can be detected with a large enough sample size (*i.e.*, more replicate samples), but these fluctuations are not good indicators of the long-term changes in the ecosystem. However, the demonstration of a significant trend in an environmental variable cannot be achieved by simply increasing the number of samples and solves this dilemma. Increasing the number of replicates will not produce a trend if none exists.

The EMAP-E VP program is designed to detect trends in environmental degradation over the decade time scale. The EMAP-E VP sampling program has been curtailed after only four sampling periods. The detection of a significant temporal trend in a variable (at an  $\alpha$ -level of 0.05) requires at least six sampling periods. The probability of observing five straight increases (or decreases) in an environmental variable sampled six times is  $(0.5)^5$  or 0.03125. In order to be assured of detecting a trend, far more sampling periods are needed. In trend analyses there is one null hypothesis, 'No trend', but there are many alternate hypotheses:

- A short-period cycle plus a unidirectional trend.
- Unidirectional trend.
- Unidirectional trend confounded with a long-term cyclic trend.
- Cyclic trend.

Distinguishing between increasing or decreasing trends and cycles requires long time series. Nichols (1988) discovery of a long-term cyclic trend with an apparent twenty-year period in the benthic infaunal community structure of the 200-m main basin of Puget Sound should give pause to any benthic ecologist who assumes that a 4-year trend is due to a degradation of the marine environment. The deepest part of Puget Sound, at 200-m depth in Elliot Bay was first sampled by Ulf Lie in the early 1960s (Lie 1968, Lie and Evans 1973). Fred Nichols sampled this station in the late 1960s for his masters and doctoral dissertations (Nichols 1975). During the 1960s and 1970s, this site ("the 100-fathom hole") was dominated by a subsurface deposit-feeding polychaete *Pectinaria californiensis*. Nichols continued to monitor this area every year throughout the 1970s and 1980s. The *Pectinaria* population, which had reached abundances of 1000 per m<sup>2</sup> 1969, had nearly disappeared from the main Basin of Puget Sound by 1976. The new numerical and biomass dominants were surface deposit feeding bivalves and polychaetes. Nichols (1985) thought that the changes he observed in benthic community structure at his 200-m station were due to degradation of the Sound environment due to anthropogenic pollutants (Seattle METRO's West Point Sewer Outfall). The pattern fit Pearson and Rosenberg's (1978) paradigm which predicts that organic enrichment will lead to the replacement of subsurface feeders by surface deposit feeders. Shortly after Nichols published his 20-year data set in 1985, *P. californiensis* returned to the main basin of Puget Sound. Annual monitoring shows that *Pectinaria* abundances are now as high as they were in the early 1960s. Nichols (1988) rejected his hypothesis of a long-term unidirectional trend (alternate 2 above) in favor of 20-year cyclic trend driven by long-term hydrographic changes in the Sound. The flushing characteristics of the deep portion of Puget Sound change on a twenty-year time scale, and this pattern may have led to changes in larval recruitment to the site. Gray and Christie (1983) document other long-term trends in benthic populations, driven presumably by allogenic trends, especially hydrography.

Mistaking long-term trends and cycles in benthic communities for changes in pollutant loading is an example of model misspecification. Detecting significant ecological changes in benthic communities is not the problem. The major problem is connecting those changes to changes in pollutant loading.

## **Analysis of the EMAP-E VP Benthic Degradation Indices**

### ***The 1990, 1991-1992, and 1990-1993 Benthic Degradation Indices***

To date, there have been at least four different benthic degradation indices applied to EMAP-E VP benthic community structure data: the 1990 index (Weisberg *et al.* 1993), the 1991 Louisianian Index: (Summers *et al.* 1992), the 1991 Virginian Province index (Schimmel *et al.* 1994), and the 1990-1993 Index (Strobel *et al.* 1995). Strobel *et al.* (1994) used the 1991 Index to summarize the 1992 EMAP-E VP Virginian Province data. All of these indices are based on a one-dimensional discriminant function, developed to distinguish between a selected group of degraded and non-degraded stations.

The abiotic data from the EMAP-E VP program are used to classify benthic samples into degraded and non-degraded "reference" groups. Weisberg *et al.* (1993), Summers *et al.* (1992), Schimmel *et al.* (1994), Strobel *et al.* (1994), and Strobel *et al.* (1995) describe the protocol for the creation of these indices. A set of degraded stations is chosen based on low dissolved oxygen, sediment contaminant concentrations, and amphipod survival. The absolute values of these thresholds have changed from year to year. For example, in 1990, to be classified as "degraded" due to low dissolved oxygen, oxygen concentrations had to be less than 0.3 mg/L at any time, or 10% of measurements less than 1 mg/L or 20% of continuous measurements < 2 mg/L or less than 2 mg/L for 24 consecutive hours. Strobel *et al.* (1995, p. A-12) state that a site could be classified as a degraded test site if the bottom dissolved oxygen was less than 2 mg/L. The 1990-1993 index used the recent Long *et al.* (1995) ER-L and ER-M values to divide samples into degraded and reference data sets. These stations were selected from three salinity regimes (<5 psu, 5-18 psu, and >18 psu).

Reference, or non-degraded, stations were also selected. None of these stations could have significant *Ampelisca* mortality, DO less than 1 mg/l, and no pollutants could exceed Long and Morgan's (1990) ER-M value. Strobel *et al.* (1995) used the newer Long *et al.* (1995) ER-L and ER-M contaminant thresholds. In the latest 1990-1993 index, to be considered a "reference" site, no more than three sediment contaminant concentrations could exceed the Long *et al.* (1995) ER-L value and none could exceed the ER-M concentration.

Once these two groups of test stations were chosen, Student's t-tests were used to find variables that significantly differed between groups. In all years, the effects of habitat factors on species richness were evaluated. In the 1990 index, the EMAP-E VP diversity measure, Total Species per Event, was calculated relative to the expected species richness at each salinity. A similar analysis was performed for the 1991 index, including organic carbon as well, but salinity was not included in the final 1991 index, because the "salinity-normalized" variable was poorer at discriminating degraded and undegraded sites than the unnormalized species number. These variables, including those adjusted for salinity, are then entered into a set of step-wise discriminant analyses to find the linear combination of variables that best discriminates between groups. The 1990 Benthic Index from Weisberg *et al.* (1993) is shown below:

### 1990 Benthic Index

Weisberg *et al.* (1993)

$$BI =$$

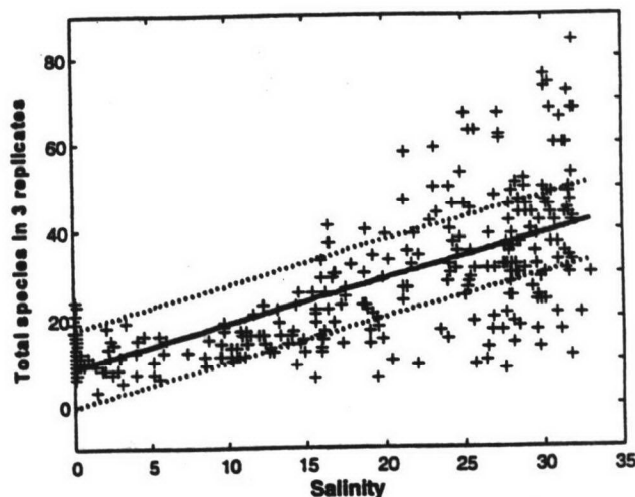
- + 0.011 \* Percent Expected Species (mean number)
- + 0.817 \* Number of amphipods per 0.044-m<sup>2</sup> grab
- + 0.671 \* Percent of total abundance as bivalves
- + 0.465 \* Number of capitellids per 0.044-m<sup>2</sup> grab
- + 0.577 \* Average weight per individual polychaete.

***BI < 3.40 INDICATES DEGRADED.***

This 1990 Benthic Index was based on only the first year of EMAP-E VP sampling. The expected species included normalization for salinity. Weisberg *et al.* (1993) found a very strong positive correlation between the number of species collected in a grab and salinity. At the lowest salinities in estuaries, only about eight to ten species will be found per grab (Figure 3). With each additional psu salinity, about one additional species is added. Weisberg *et al.* (1993) used a three-point running average to fit a polynomial curve to the top of the cluster of points in a plot of total species sampled vs. salinity.

Weisberg *et al.* (1993) compared their 1990 Benthic Index with Rhoads & Germano's (1986) Organism-Sediment Index. The OSI™ is based on the photographs of the sediment-water interface. Figure 4 shows the values of the 1990 Benthic Index and the OSI™ for a subset of the 1990 samples. The two indices are weakly correlated. However, if the indices are converted to their binary "degraded-nondegraded" form, the statistical association is no greater than one might expect by chance alone.

Schimmel *et al.* (1994) tested the 1990 Biotic Index on the EMAP-E VP data collected in 1991. Following the procedures developed by Weisberg *et al.* (1993), they identified a set of degraded and "reference" sites based on pollutant concentration (pollutants > Long & Morgan's ER-M), amphipod toxicity, and dissolved oxygen concentration. New reference and degraded stations were added to the list of stations used in 1990. Schimmel *et al.* (1994) identified thirteen new stations in the 1991 dataset as being degraded using their established criteria. The 1990 index classified 7 of these 13 (54%) as degraded and 6 (46%) as non-degraded. Based on this high rate of misclassification of presumably degraded stations, Schimmel *et al.* (1994) developed the 1991 index (shown below). In



**Figure 3.** Total species per sampling event (species in all 3 replicate grabs) is strongly correlated with salinity. At 0 psu salinity, 8.5 species are expected and roughly 1 species is added for every psu of salinity. The variance increases at salinities greater than 15 psu. This plot is similar to Weisberg *et al.* (1993, Fig. 4-2) but is based on an additional three years of data and a much reduced list of valid taxa. The  $R^2$  is 48.3%. 95% Confidence limits for the mean value of the dependent variable are based on three replicates.

developing the 1991 index, Schimmel *et al.* (1994) analyzed the effect of salinity on species richness. They performed their discriminant analyses using both unnormalized species number and species number normalized by both organic carbon and salinity. Figure 5 plots the second order polynomial equation, used to normalize simultaneously for organic carbon and salinity (2 minor typographic errors in the original equation on Page B-3 of Schimmel *et al.* 1993 have been corrected):

$$\begin{aligned} \text{Expected number of species} = & 8.25 + 3.87 \times 10^{-4} (\text{TOC}) \\ & - 1.9 \times 10^{-8} (\text{TOC})^2 \\ & + 0.784 (\text{salinity}) - 0.00125 (\text{salinity})^2 \\ & - 2.031 \times 10^{-5} (\text{TOC}) (\text{salinity}). \end{aligned}$$

Schimmel *et al.* (1993, B-3) divided the observed number of species by the expected number of species predicted by this equation.

Schimmel *et al.* (1994) created a test data set and ran a series of discriminant analyses. The TOC/salinity adjusted species richness measure was less effective at discriminating between degraded and reference conditions than unadjusted species number.

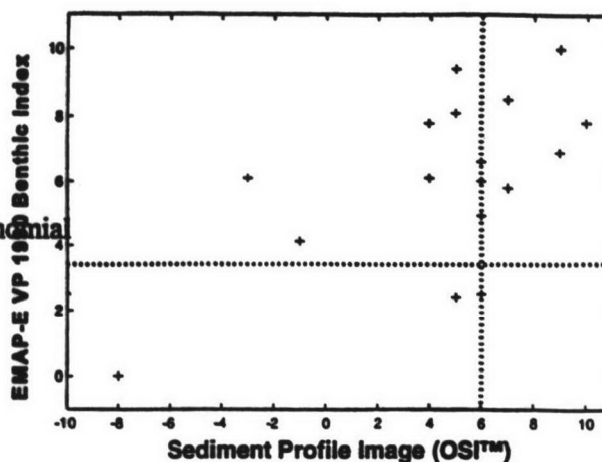


Figure 4. The value of the 1990 EMAP-E VP benthic index vs. that calculated using Rhoads and Germano's (1986) Sediment-Profile-Image Organism-Sediment Index. The thresholds between degraded and non-degraded are indicated. The two indices are correlated (Kendall's  $\tau=0.326$ ,  $\text{prob}<0.044$ ). However, when these ordinal data are converted to nominal "good-bad", or "degraded-nondegraded" classes, the concordance between indices is non-significant.

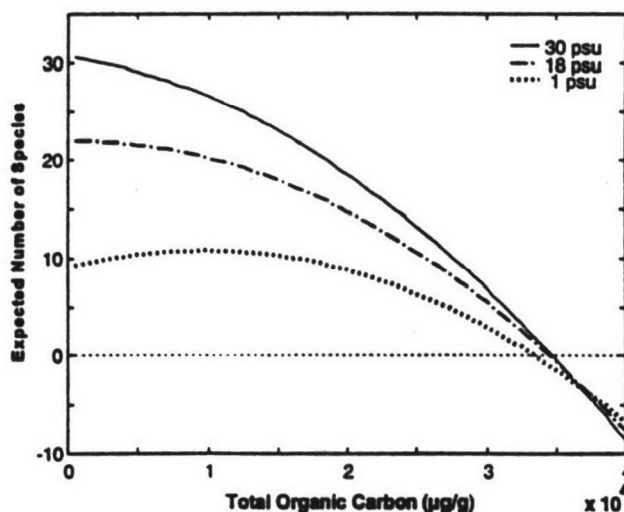


Figure 5 The salinity and Total Organic Carbon normalization used by Schimmel *et al.* (1994) in developing the 1991 EMAP-E biotic index is plotted. The expected number of species continues to decline, reaching about -150 expected species at  $8 \times 10^4$  µg/g (8%) Total Organic Carbon.

Schimmel *et al.*'s (1994) EMAP-E VP 1991 benthic degradation index is shown below. The only negative term in the 1991 benthic index is the abundance of a set of opportunistic species. The list of opportunistic species is not provided.

### 1991 Benthic Index

Schimmel *et al.* (1994)

$$BI =$$

$$\begin{aligned} & - 0.68 * \text{Mean Abundance of Opportunistic Species} \\ & + 0.36 * \text{Biomass / Abundance Ratio for all Species} \\ & + 1.14 * \text{Mean Number Infaunal Species per Grab.} \end{aligned}$$

**BI < -0.5 INDICATES DEGRADED**

Strobel *et al.* (1994) used the 1991 Benthic Index to analyze the 1992 EMAP-E VP data. The only change made in the 1992 Benthic Index was to add 0.5 so that a BI score less than 0 indicated degraded.

Summers *et al.* (1993) developed a benthic index for the EMAP-E Louisianian Province (EMAP-E LP). Their index included a correction for the effects of salinity on species richness

### EMAP-LP's 1992 Benthic Index

$$\begin{aligned} BI = & + 2.3841 * \text{Proportion of Expected Diversity} \\ & - 1.6728 * \text{Percent of Tubificid Abundance} \\ & + 0.6683 * \text{Percent of Brvalve Abundance.} \end{aligned}$$

**BI < 4.1 INDICATES DEGRADED.**

Strobel *et al.* (1995) reevaluated Schimmel *et al.*'s (1994) 1991 Index in their statistical analysis of all four years of EMAP-E VP benthic data. Strobel *et al.*'s (1995) rejected the Schimmel *et al.* (1994) benthic index. Their new 1990-1993 Index, shown at the right is based on all four years of EMAP-E VP sampling. It is based on a set of thirty degraded and thirty reference sites. They do not list these sites in their report. Presumably, many of these degraded and reference sites are the same as those listed in Schimmel *et al.* (1994).

The 1990-1993 index includes two forms of salinity normalization. Salinity must be entered in psu for the polynomial fit (e.g., 0 to 30 psu) and must be entered in decimal form for the tubificid normalization (0 to 0.030). Gleason's D diversity is

### 1990-1993 Benthic Index

Strobel *et al.* (1995)

$$BI =$$

$$\begin{aligned} & + 1.389 * \frac{\% \text{ Expected Gleason's D} - 51.5}{28.4} \\ & - 0.651 * \frac{\text{Normalized tubificid abundance} - 28.2}{119.5} \\ & - 0.375 * \frac{\text{Spionid abundance} - 20.0}{45.4} \end{aligned}$$

where,

$$\% \text{ expected Gleason's D} = \frac{\text{Gleason's D}}{\text{Gleason's D}}$$

$$(4.283 - 0.498 * \text{salinity} + 0.0542 * \text{salinity}^2 - 0.00103 * \text{salinity}^3) * 100.$$

$$\text{Gleason's D} = \frac{S}{\ln N}$$

$S$  = Number of species.

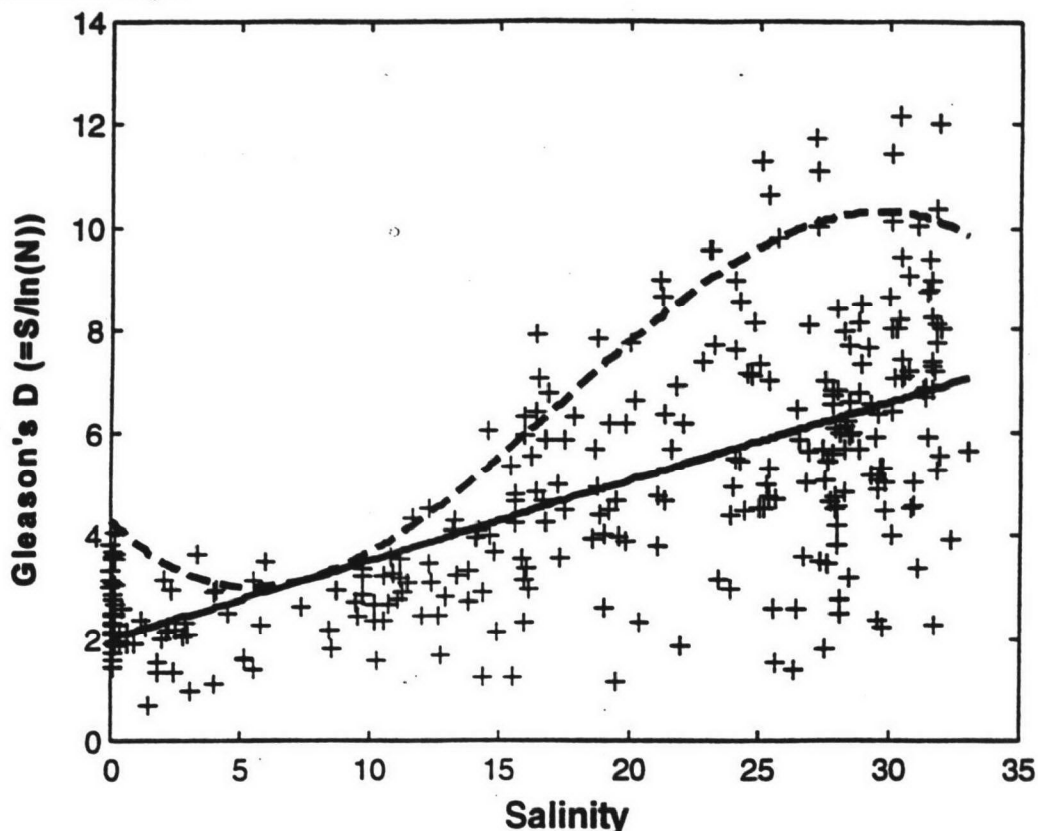
$N$  = Number of individuals.

Normalized tubificid abundance =

$$\text{Tubificids} - 500 * e^{-15 * \text{salinity}}$$

**BI < 0 INDICATES DEGRADED.**

fit to a polynomial equation. Figure 6 shows a display of the Gleason's D diversity per three grabs vs. salinity. The lack of fit isn't too surprising. We deleted hundreds of invalid taxa from the EMAP-E VP data set, including perhaps one hundred taxa included in the EMAP-E VP analyses. Also, it is not clear from Strobel *et al.* (1995) how they were calculating Gleason's D. Gleason's D can be calculated several different ways.



**Figure 6** Gleason's D species diversity vs. salinity plotted with Strobel *et al.*'s (1995) salinity normalization used in the 1990-1993 EMAP-E VP degradation index. The solid line is a linear regression fit; the dotted line is the 2nd order polynomial fit from Strobel *et al.* (1995). The  $R^2$  for the linear regression is 47.2%. Note that we use only a subset of species used by Strobel *et al.* (1995) and we deleted many individuals used by Strobel *et al.* (1995).

### ***Are these benthic indices adequate?***

Are the benthic communities of the Virginian Province being properly assessed by the EMAP-E VP degradation indices? In the four major statistical summaries of the EMAP-E VP data, there are statistical summaries of the percentage of the area in the province that is degraded. Table 1 shows these values with 95% confidence limits

**Table 1.** Percentage of the Virginian Province classified as "degraded" using biotic indices. Also shown for the 1990-1993 data are percentages of the Province with low bottom dissolved oxygen ( $\leq 2$  mg/L), toxicity (amphipod survival less than 80% of controls), and sediment contaminant levels (any inorganic or organic contaminant  $>ER-M$ , using Long *et al.* 1995).

INDEX		LARGE ESTUARIES	LARGE TIDAL RIVERS	SMALL ESTUARINE SYSTEMS	OVERALL
1990 Index Weisberg <i>et al.</i> (1993, p. 5-16)		20 ± 8	46 ± 32	23 ± 14	23 ± 7
1991Index (Combined 1990-1991 data) Schimmel <i>et al.</i> (1994, p. 18, 71)		6 ± 7	27 ± 14	32 ± 17	14 ± 6
1992 Index Strobel <i>et al.</i> (1994, p. 59)		10 ± 10	37 ± 22	23 ± 12	14 ± 6
1990-1993 Summary Strobel <i>et al.</i> (1995)	Biotic Index < 0	18 ± 4	33 ± 14	35 ± 6	23 ± 3
	Bottom DO≤2 mg/L	6 ± 2	10 ± 6	0.2 ± 1.3	5 ± 2
	Toxicity (<80% control)	10 ± 3	3 ± 4	12 ± 6	10 ± 2
	Any analyte (organic or inorganic) > ER-M	5 ± 2	14 ± 6	5 ± 2	6 ± 2

How are we to interpret the results in Table 1? First, a comparison of the final four rows indicates that the biotic condition index is identifying degraded conditions in a much higher percentage of the Province than the abiotic condition indicators (DO, toxicity, and sediment contaminants). Also, the major biotic condition indices have produced significantly different estimates of the proportion of the Province that has degraded benthos. For example, Schimmel *et al.* (1994) concluded using the first two years of EMAP-E VP data that  $14 \pm 6\%$  of the Virginian Province was degraded. Strobel *et al.* (1995) used the same data plus two additional years of data to conclude that  $23 \pm 3\%$  of the Virginian Province was degraded. What could account for this large, significant increase in degradation in such a short period? As noted by Strobel *et al.* (1995), the indices used to evaluate the 1990-1991 data are very different from those used to evaluate the 1990-1993 data set. The definition of 'degradation' hasn't changed much in any of the EMAP-E VP indices. Strobel *et al.* (1995) used the newer Long *et al.* (1995) ER-M levels to define degraded stations for the test data set and noted that the new ER-M values were higher for metals resulting in a significant reduction in the percent area of the Province in exceedence. The differences in the estimates must be based on the differences in the equations used to determine degradation. The success of the EMAP-E program must be judged, in part, on the accuracy of the biotic indices. Is nearly one quarter of the Province's benthos degraded, even though no more than 8% of the Province has contaminant levels in excess of Long *et al.*'s (1995) ER-M values? There are major problems with the three major benthic indices developed in the EMAP-E VP program. We list the problems and discuss them in the following subsections. These problems are:



- ▶ **The validation problem.** The indices appear to work with the test data sets on which they are based, but fail when new sets of degraded and reference stations are added.
- ▶ **The “good-bad” dichotomy.** The degradation indices are based on a linear discriminant function derived from test data sets that are supposed to represent degraded and reference benthic communities. Some of the degraded benthic stations may not be degraded and some of the reference benthic stations may be impacted. The EMAP-E VP benthic degradation indices begs one of the major questions that the entire EMAP program was designed to assess: Is impacted benthic community structure a result of pollution?
- ▶ **Inconsistencies with basic benthic ecology.** Many of the variables used in the EMAP-E VP degradation indices are inconsistent with basic principles of benthic ecology.
- ▶ **Inadequate data and documentation.** All but the 1990 benthic index are inadequately documented. The list of opportunistic taxa used in the 1991 and 1992 biotic indices is not provided. One of the three terms in the 1990-1993 biotic index is based on a taxon which was not identified in most of the EMAP-E VP data.

### **The validation problem**

The first problem, noted in EMAP-E VP reports, is that the indices developed for one year of data misclassify too high a percentage of new stations that are added in subsequent years. The 1990 index failed to discriminate between reference and degraded sites sampled in 1991. The 1991-1992 indices failed to successfully discriminate between reference and degraded sites identified in the full four-year EMAP-E VP data. The only EMAP-E VP index that was used in more than one annual statistical report was the 1991 EMAP-E VP biotic index (Schimmel *et al.* 1993). This index was used by Strobel *et al.* (1994) to describe the 1992 EMAP-E VP data. Strobel *et al.* (1995) rejected the 1991 index in their analysis of all four years of EMAP-E VP data. The only index that has not been rejected within the EMAP-E VP program is the Strobel *et al.* (1995) 1990-1993 biotic index.

### **The “good-bad” dichotomy.**

The major weakness in the EMAP-E VP macroinfaunal analyses is the reliance on the assumption that benthic samples can be unambiguously classified using only two classes: degraded and reference. A review panel, convened by the Estuarine Research Foundation (Schubel *et al.* 1992, p. 5), raised this concern at an early stage of the EMAP-E program, stating that the EMAP-E program needed to modify “the ‘black’ and ‘white’, ‘good’ and ‘bad’, binary characterization of ecological/environmental conditions.” This review panel concluded:

*“We are concerned that EMAP-E may have unnecessarily compromised its ability to achieve its goals by an overly simplistic (binary) approach to defining environmental quality as either “good” or “bad.” Environmental quality is a continuum and society’s definitions of “good” and “bad”, “acceptable” and “unacceptable”, “nominal” and “subnominal” may -- and indeed do -- change as knowledge of natural conditions increases, as management approaches and philosophies become more sophisticated and as society’s priorities change.” Schubel *et al.* (1992, p. 28)*

The EMAP-E VP degraded vs. reference dichotomy is poorly defined. An EMAP-E VP site is degraded if it is more similar to a set of degraded sites than it is to a set of reference sites. This similarity is based on the value of three variables in the latest 1990-1993 benthic index.. The EMAP-E VP program selected degraded and non-degraded reference sites using three criteria: dissolved oxygen concentration, sediment contaminant level, and short-term amphipod survival. As Table 1 shows, even

though abiotic indices (ER-M, DO, and amphipod survival) were used to define the "degraded" test data set, the biotic indices identified a much larger percentage of the Virginian Province as being degraded than the abiotic indices. The major reason for this is the black-white dichotomy inherent in the linear discriminant function. The 1990-1993 index chose an equal number of impacted and reference sites for the test data set (Strobel *et al.* 1995, p. A-12) and the classification of other sites was based on their 'nearness' to one of these two endpoints. If only 10% of the Virginian Province had pollutant concentrations or low dissolved oxygen that could impact benthic communities, and yet 50% of the test data set was composed of these stations, then the discriminant function would tend to classify too many sites as being degraded even if the assumptions of the discriminant analysis were set. For example, a discriminant analysis could be performed with one group consisting of thirty NBA All-Stars, and another group of equal size drawn randomly from the general population. The EMAP-E VP discriminant function was based on twenty-eight variables measured from the two groups (Weisberg *et al.* 1993, p. 4-17; Schimmel *et al.* 1994, p. B-3). If a similar number of variables were measured on the NBA All-Stars and on the general public, a linear discriminant function would undoubtedly identify some of the properties necessary to play in the NBA (*e.g.*, height, jumping ability, reflexes, and big hands). This discriminant function could then be used to divide the US population into two groups: NBA caliber, and not-NBA caliber. It is obvious that such a good-bad approach would produce a tremendous overestimate of the percentage of the US population that might be of NBA caliber. A similar problem may exist in the EMAP-E VP linear discriminant function. If the degraded stations are greatly overrepresented in the test data sets, then the function will overestimate the percentage of area that is impacted. The EMAP-E VP investigators can set the *a priori* Bayesian expectations for the classification frequencies expected from the discriminant analysis to reduce the probability of misclassification, but there is no documentation that they have done so.

The major assumption of discriminant analysis is the equality of variance-covariance matrices. What does this mean? It means that the variables used in the discriminant analysis should have the same scale of variation in the groups being discriminated. Discriminant analysis is designed to classify by differences in the mean values of discriminating variables, not their variance. Many of the variables used in the EMAP-E VP indices clearly violate this assumption. In the 1990-1993 index the first term is expected Gleason's D, adjusted for salinity. As shown in Figure 6, the variance in this species richness index will be much higher in the high salinity areas of the EMAP-E VP province.

There is another serious problem with the existing EMAP-E VP indices. There is no independent evidence that the degraded and reference groups in the EMAP-E VP data are really degraded or non-degraded. Sediment contaminant level is judged by ER-M and ER-L concentrations (Long & Morgan 1990, Long *et al.* 1995). These ER-M concentrations, which represent the concentrations at which 50% of the studies demonstrated some adverse biological effect are tabulated for a wide variety of organic and inorganic pollutants. There was little theoretical justification for these ER-M and ER-L concentrations. Long and Morgan (1990) and Long *et al.* (1995) determine their ER-M values by simply sorting existing environmental and biological data to find the median pollutant concentration at which any biological effect was observed. They considered a number of biological effects, including changes in benthic community structure. Thus, only half the samples containing a given pollutant at or above the ER-M level showed some kind of biological effect indicative of degradation. Long and Morgan (1990) did not assess the covariation among environmental variables or formally analyze the causal connection between a given pollutant variable and the biological effect observed. Other branches of the EPA and state agencies have been reluctant to codify the ER-M levels into regulations. DiToro *et al.* (1990, 1991, 1992) review alternate approaches for establishing sediment pollutant criteria. Strobel *et al.* (1995, p. 48-51) provide a nice summary of alternate approaches to estimated sediment contaminant levels. If the sediment acid volatile sulfide concentrations or organic carbon concentrations are high, a metal in excess of the ER-M level may have little significant biological

effect. Thus, only about 50% of the sites in the Virginian Province with pollutant concentrations in excess of ER-M are predicted to have significant biological effects, and this percentage might be lower if the SEM/AVS ratios are used (Strobel *et al.* 1995, p. 48).

The EMAP-E VP program does not provide an assessment of degraded community structure due to pollutants independent of the abiotic indicators. One of the stated goals of the EMAP program in all ecosystems was to develop indices of impacted community structure or biological effects independent of toxic loads or abiotic stressors. Ecologists were to identify samples or areas showing impacted patterns of community structure, and the assessment portion of the EMAP program was to determine whether these impacts could be due to pollution. The EMAP-E VP program begged this vital question, by assuming that sites with sediment contaminants in excess of ER-M, low dissolved oxygen, or significant amphipod toxicity, must have degraded benthic communities. The EMAP-E VP program did not develop an independent set of criteria to determine whether the patterns of community structure in the degraded sites were indeed degraded. It is entirely possible, and likely, that sites in the Virginian Province could have multiple sediment contaminants in excess of the ER-M thresholds and yet have no significant departures from 'reference' patterns of benthic community structure. The contaminants might be unavailable (*e.g.*, bound to sulfides or organic carbon), and dissolved oxygen concentrations of 2 mg/L in the overlying water might be more than adequate for benthic respiration.

More importantly the EMAP-E VP investigators chose "reference" sites using dissolved oxygen concentration, ER-L concentrations and amphipod toxicity. Again, toxicologists and environmental regulators, including the EPA have been reluctant to embrace the Long and Morgan ER-L levels as indicators of 'clean' sediments. The dissolved oxygen concentration one meter above the bottom does not mean that the sediments are adequately oxygenated. In fact, due to the physics of the benthic boundary layer, anoxic sediments can be associated with very high oxygen levels even centimeters above the bed. Finally, benthic communities with adequate dissolved oxygen one meter above the bed and low pollutant concentrations can still have patterns of community structure indicating recent disturbance or impact. Physical disturbance by other processes — storms, predators, disruption by fishing nets, and red tides, drifting macroalgae — can all produce patterns in community structure that indicate recent disturbance. Many of these patterns of disturbance mimic the effects of pollution. For example, the frequencies of opportunistic taxa increase, species richness declines, species evenness declines, and infaunal abundance levels change. The EMAP-E VP program developed no independent criteria to detect these 'natural' impacts.

### Inconsistencies with basic benthic ecology

The third problem with the indices is that they are inconsistent with basic benthic community ecology. The 1990 index (Weisberg *et al.* 1993) predicts that the more capitellid polychaetes, the more likely a site is to be classified as non-degraded. Members of the genus *Capitella* spp. are generally regarded as pollution indicators (*e.g.*, Grassle & Grassle 1974, Pearson and Rosenberg 1978, Grassle and Grassle 1985). Grassle and Grassle (1976) showed that the species formerly known as *Capitella capitata* is a sibling species complex. Most if not all of these sibling species are found in areas high concentrations of utilizable organic carbon. However, the genus *Capitella* is rare in the EMAP-E VP data. *Capitella* is found in only about ninety of the nearly two thousand EMAP-E VP samples. Moreover, it is not particularly abundant in any of those samples.

One reason why 'capitellid polychaetes' may have been important in the 1990 index is that the capitellid *Mediomastus ambiseta* is the most abundant and wide-spread taxon in the entire Virginian Province. *Mediomastus ambiseta* can be found in salinities ranging from 10 psu through 35 psu. Diaz and Schaffner's (1990) summarized the benthic species characteristic of different salinity and grain

size habitats in Chesapeake Bay. They found that *M. ambiseta* reaches peak abundance in high mesohaline (10-18 psu salinity) muds and mixed mud and sand habitats. However, *M. ambiseta* is often the numerical dominant in high salinity coastal waters. Fuller *et al.* (1988) found *M. ambiseta* was the numerical dominant in Buzzards Bay, reaching abundances of 720,000 m<sup>-2</sup> in outer New Bedford Harbor. This species would be a poor choice as an indicator of pristine, unpolluted sites. Grassle & Grassle (1985) review the use of *M. ambiseta* as a pollution indicator. Grassle *et al.* (1986) observed *M. ambiseta* increase dramatically in response to eutrophication. Grassle *et al.* (1988) added sewage-sludge to the MERL tanks and again observed substantial increases in the abundance and frequency of *M. ambiseta*. Grassle *et al.* (1981) observed that *M. ambiseta* was the taxon that declined most sharply with the addition of 90 ng/g #2 fuel oil in the MERL ecosystem tanks. Using *M. ambiseta* as an indicator of high petroleum hydrocarbon concentrations in sediments is unwise, since *M. ambiseta* increased dramatically in abundance in heavily oiled offshore stations after the West Falmouth oilspill (Grassle and Smith 1976, Sanders *et al.* 1980). It is very difficult to provide any ecological basis for assuming that more capitellids indicates a lower probability of degradation.

There are two major problems with the Schimmel *et al.* (1994) 1991 biotic index. They used the mean number of species per grab as a discriminating variable. As Weisberg *et al.* (1993, Fig. 4-2) showed, salinity has a profound effect on species richness. We show the strong effect of salinity on species richness in Figure 3 (p. 13). Any index based on species richness which fails to take salinity into account will classify many non-degraded low-salinity sites as degraded. Strobel *et al.* (1995, p. A-12) noted this, stating that the 1991 Index is "highly correlated with salinity and appeared to misclassify good sites in the oligohaline [ $<5$  psu] and impacted sites in the meso- [5-18 psu] and polyhaline [ $>18$  psu]."

The 1991 and 1992 biotic indices failed to incorporate a correction for the effects of salinity on species richness because they combined salinity with total organic carbon concentration (TOC) in the normalization. This was not a proper way to assess the covariation of salinity and diversity. Figure 5 (p. 14) shows the expected species at different TOC concentrations predicted by that function at three different salinities (1 psu, 18 psu, 30 psu). All EMAP-E VP samples with greater than 3.5% TOC are expected to have less than 0 species. Dividing observed by expected species number can produce high adjusted species richness values in the range 3 to 3.5% or negative species richness numbers if TOC is greater than 3.5%. Simultaneously normalizing TOC and salinity together was not a good idea.

Total organic carbon concentration in sediments is one of the best indicators of both contamination and eutrophication. It is not a natural environmental factor like salinity, temperature, or depth. Wallace *et al.* (1991) have shown that sediment total organic carbon concentration is tightly coupled with sediment heavy metal concentrations in Boston Harbor. The correlation is often 0.9 or higher. In Boston's Inner Harbor, sediments with TOC concentrations of about 3.3 % are either anoxic in the late summer or contain about six species per grab. Figure 5 (p. 14) shows that these sites would have 100% or more of the expected species richness expected at these organic carbon concentrations. Strobel *et al.* (1995, Figure 3-27) shows that TOC in the Virginian Province ranged from 0 to 7%, with roughly 10% of the Province having TOC concentrations greater than 3% organic carbon. By not adding a proper normalization for salinity, the 1991 and 1992 indices would be highly likely to classify non-degraded oligohaline sites as degraded, as Strobel *et al.* (1995) noted.

The 1990-1993 Index, shown on p. 15, was developed by Strobel *et al.* (1995). This index has three terms: salinity-normalized Gleason's D species richness, spionid abundance, and salinity-adjusted tubificid oligochaete abundance. We will discuss each term of the equation.

The 1990-1993 index, like Weisberg *et al.*'s (1993) Index, normalizes species diversity by salinity. Species diversity is calculated using Gleason's D (Gleason 1922). We show the relationship between Gleason's D and salinity in Figure 6 (p. 16). Washington (1984, p. 661) included Gleason's D for historical purposes only, noting that it "has not been used extensively in the recent literature, being replaced by Margalef's." Gleason's D has some very poor statistical properties (as does Margalef's index). Imagine a situation where all of the individuals in the sediments are independently Poisson distributed (*i.e.*, randomly placed). Gleason's D, the number of species divided by the natural log of the number of individuals, is one of the only diversity indices listed in Washington (1984) that declines as larger samples (either by area or numbers) are collected. Margalef's index also declines with increasing sample size. Most other indices either remain the same ( $H$ ,  $H'$ ,  $E(S_n)$ ) or increase (total species) with increasing sample size. Even with a fixed sample area, this sample-size dependence is a serious problem. In two grabs containing an identical number of species, with identical frequencies, Gleason's D will find that the sample with the lowest abundance has the highest diversity.

The final two terms of the 1990-1993 index are based on spionid abundance and tubificid oligochaete abundance, the latter scaled by salinity. It is difficult to assess this index using the existing EMAP-E VP publications. Oligochaetes were never identified below Class Oligochaeta in samples collected from areas where bottom salinity was greater than 5 psu. We are assuming that Strobel *et al.* (1995) are following Weisberg *et al.* (1993, p. 2-12) in assuming that most oligochaetes in habitats with salinities > 5 psu are tubificids. This is not true, but given the assumption that most marine oligochaetes are tubificids, we can calculate how many tubificids and spionids per m<sup>2</sup> are sufficient to produce a classification of "degraded" if the Gleason's D diversity is 100% of the expected value. Figure 7 plots this relationship. If a sample has 100% of the expected Gleason's D diversity, then observing more than 7000 spionids per m<sup>2</sup> at 30 psu salinity indicates that a sample is degraded. Observing 17,000 tubificids per m<sup>2</sup> at 30 psu indicates degradation. Fewer tubificids are required to indicate degradation at lower salinities.

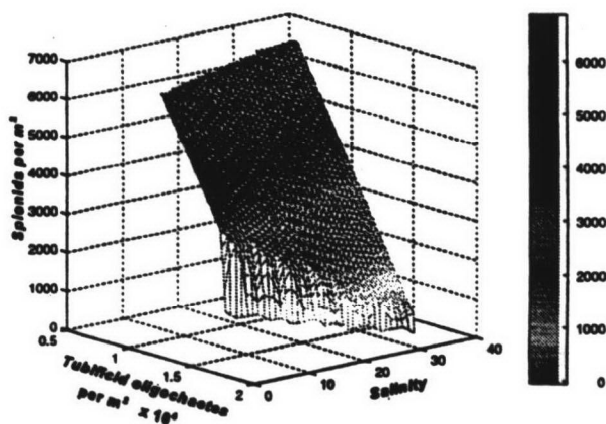


Figure 7 The 1990-1993 EMAP-E VP index (p. 15) was recast to predict the number of tubificid oligochaetes and spionid polychaetes necessary to equal 100% of the expected Gleason's D diversity at salinities from 0 to 35 psu (plotted in Fig. 6, p. 16). A sample with 100% Gleason's D diversity that plots to the right or above this veil would be classified as degraded. At 30 psu, 7000 spionids per m<sup>2</sup> or 17,000 tubificids per m<sup>2</sup> indicates degradation.

Spionid polychaetes are a species-rich successful family of polychaete worms. There are a handful of spionid polychaete species that have been used as pollution indicators, most notably *Streblospio benedicti* and *Polydora cornuta*. However, both of these species are natural components of shallow or mesohaline habitats in the Virginian province. Dauer *et al.* (1981) reviews the factors controlling the distribution and abundance of the six major spionid species in Chesapeake Bay. Members of the polychaete family Spionida are among the most important members of the Chesapeake Bay benthos in all sediment types and most salinities. The family Spionidae cannot be used as a pollution indicator. Spionids are among the most abundant surface deposit and suspension feeding organisms in habitats ranging from the intertidal zone to the deep sea. The abundance of individuals belonging to this polychaete family does not indicate either pollution or disturbance. The 1990-1993 index sets a 5000-

7000 spionid per  $\text{m}^2$  threshold for degradation (Fig. 7) and would classify many pristine areas as degraded.

### Inadequate taxonomic data and documentation

One of the three terms in the 1990-1993 Index is based on the abundance of tubificid oligochaetes. This family of organisms was never identified in samples collected in areas with more than 5 psu. The only variable in the EMAP-E VP for these samples is the number of individuals of Class Oligochaeta. In evaluating this index, we assumed that Strobel *et al.* (1995) followed Weisberg *et al.* (1993) in arguing that most oligochaetes in marine waters are tubificids. This assumption may not be true. If only individuals properly identified as tubificids are used, then all marine samples automatically have 0 tubificid abundance and after scaling, the second term in the 1990-1993 benthic degradation index (p. 15) becomes positive. We would not recommend basing one of the three terms of the biotic index on a variable that was not measured in the majority of stations.

It is difficult to evaluate the 1991 index, because it is based on the abundance of opportunistic polychaetes. The list of species considered to be opportunistic is not provided in any of the EMAP-E reports.

### Community Structure Analyses of Virginian Province

The 1918 samples in the full EMAP data set were analyzed using COMPAH and PCA-H. A subset of the full data set was created. This subset contained all samples for which salinity data existed and which had infaunal abundances greater than 25 individuals. Replicate grabs from each sampling event were summed and used only if the maximum CNESS distance among the three replicates was less than 0.7. We used only base sampling sites represented by three replicate grabs in this analysis. A CNESS value of 0.7 indicates tremendous differences in community structure. Only 371 'sampling events' in the full EMAP data set met both the CNESS cutoff and salinity criteria.

### Diversity analyses

In this section we will evaluate the correlations among diversity indices using the EMAP-E VP data, and the covariation of diversity with salinity. Of the diversity indices that might be used in the EMAP-E VP program, the two with the richest body of theory are Shannon's  $H'$  and Hurlbert's expected number of species  $E(S_n)$ .  $E(S_{10})$  is the expected number of species if 10 individuals are drawn at random from a sample. Peet (1974) and Smith *et al.* (1979a) showed that Hurlbert's  $E(S_{10})$  is highly correlated with the Shannon's  $H'$  diversity index. Figure 8 shows this relationship.

Either  $E(S_{10})$  or  $H'$  would provide an assessment of diversity of EMAP-E VP samples. However, both of these indices are

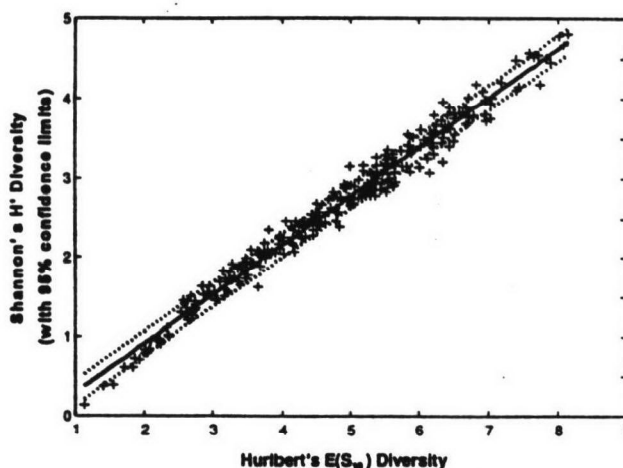


Figure 8. At a random size of 10 individuals, the Sanders-Hurlbert expected number of species  $E(S_n)$  is highly correlated with Shannon's  $H'$  diversity. The above shows the association with EMAP-E data (all 4 years, replicates combined). The  $R^2$  is 97.8%. The 95% confidence limits are based on 3 replicate grabs.



sensitive to the evenness component of diversity and neither one is particularly sensitive to species richness. At a larger random sample size,  $E(S_n)$  becomes increasingly sensitive to species richness. The relationship between  $E(S_{10})$  and total species per event is shown in Figure 9. A nearly identical pattern (but with a different scale) is found when Shannon's  $H'$  is plotted versus total species.  $E(S_{10})$  is correlated with Total species per event (Figure 9), but the two diversity indices are obviously measuring different components of species diversity. It is possible to have a sampling site with over 60 species collected in 3 grabs that would have a species diversity much lower than the median ( $E(S_{10}) < 5$ ). This pattern would be expected if one or a few species made up most of the individuals in a sample.

Neither  $E(S_{10})$  nor Shannon's  $H'$  are strongly correlated with Gleason's  $D$  diversity (Figure 10).

We have performed an analysis that shows at a glance the correlations among the major diversity indices and Hurlbert's  $E(S_n)$  with increasing sample size. The diversity of the 371 EMAP-E VP event data set was analyzed using four different diversity indices. The nonparametric correlation between the ranked diversity was compared with the  $E(S_n)$  diversity with  $n$  ranging from 2 to 200.  $E(S_2)$  is Simpson's diversity+1. At larger random sample sizes,  $E(S_n)$  becomes more strongly correlated with both Gleason's  $D$  and total number of species per sampling event (Figure 11). Figure 11 clearly shows that there is no universal index of diversity. Gleason's  $D$  clearly falls in the class of indices that are more heavily influenced by species richness.

Shannon's  $H'$  is sensitive to species richness, but it is also strongly influenced by species evenness. In a later section we will review the effects of pollution on diversity. Pollution and disturbance can affect both the richness and diversity components of diversity. One virtue of analyzing the effects of pollution in the EMAP-E Virginian Province using the evenness component of diversity is that it shows virtually no statistical association with salinity (Figure 12).

Sanders-Hurlbert  $E(S_{10})$  is positively correlated with salinity (Figure 13), but this relationship is much weaker than either the correlation between total species and salinity (Figure 3, p. 13) or Gleason's  $D$

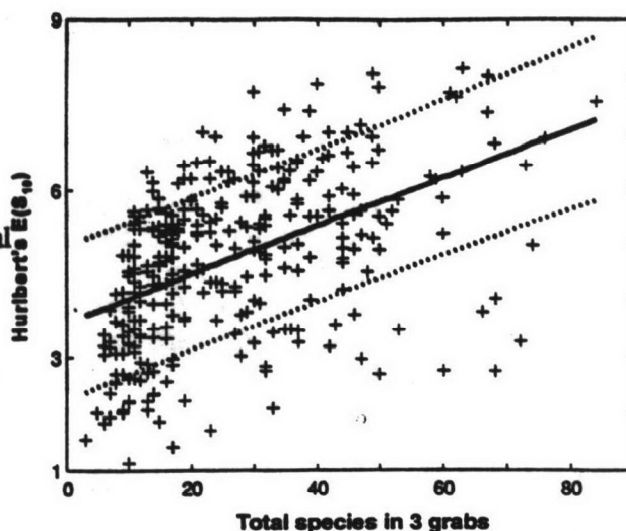


Figure 9. Sanders-Hurlbert diversity  $E(S_n)$  at  $n=10$  is only weakly correlated with species per sampling event ( $R^2=23.1\%$ ). The 95% confidence limit is based on 3 replicates.

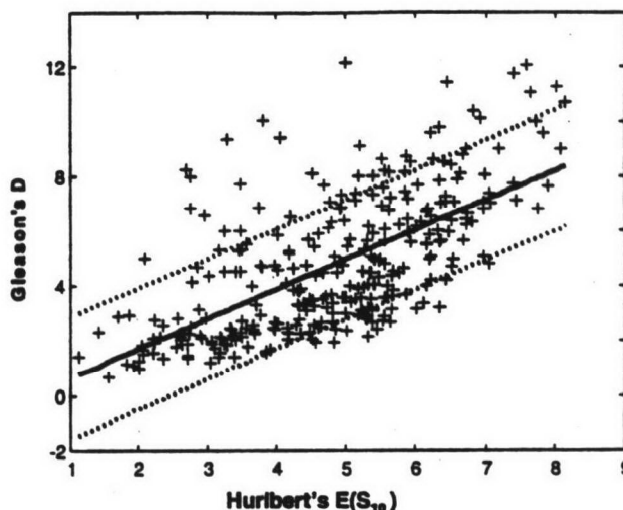


Figure 10 Gleason's  $D$  species diversity vs. Hurlbert's  $E(S_{10})$ . The 95% confidence limits for 3 replicates are shown.

and salinity (Figure 6, p. 16). At this random sample size,  $E(S_{10})$  is sensitive to both the species richness and evenness components of diversity.

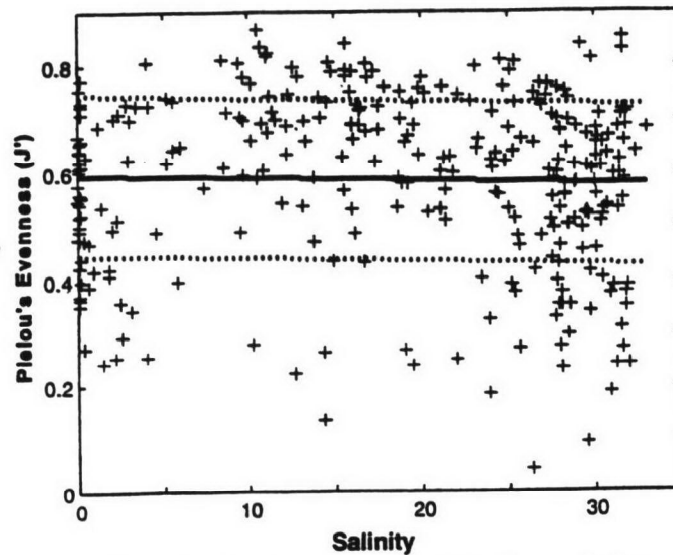


Figure 11. There is virtually no statistical association between species evenness, as estimated by  $J'$ , the evenness measure for Shannon's  $H'$ , and salinity ( $R^2=0.2\%$ ).

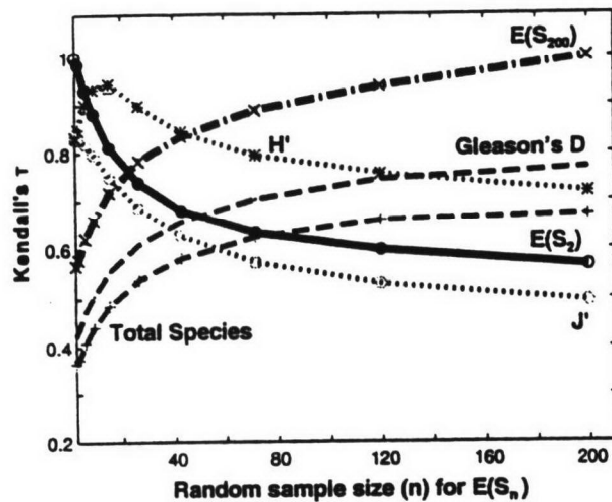


Figure 12. The nonparametric Kendall's  $\tau$  correlation between Sanders-Hurlbert diversity  $E(S_n)$  at various random sample sizes,  $n$ , is plotted versus other diversity indices. Brillouin's  $H$  (not shown) plots just below the line for Shannon's  $H'$ .  $E(S_{200})$  is the largest  $n$  shown. At small  $n$ ,  $E(S_n)$  is sensitive to both species richness and evenness. At high  $n$ ,  $E(S_n)$  is more strongly associated with species richness.  $E(S_n)$  is highly correlated with  $H'$  at  $n=10$  (see Figure 8).



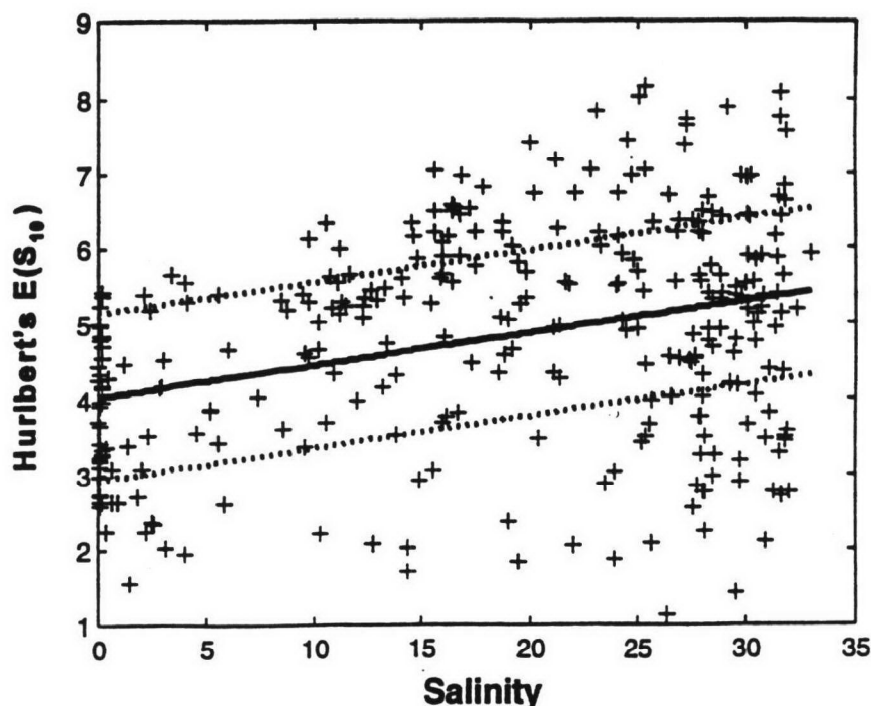


Figure 13.  $E(S_{10})$  is only weakly correlated with salinity.

## Cluster analysis

### Sample clusters

The large sample cluster analysis of all four years of EMAP-E VP data is found in Appendix IV. The major pattern in the data set is the clear break between all samples taken in the 0-5 psu salinity regime from the other mesohaline and oligohaline samples (5 to 35 psu). There is a further break among the higher salinity samples corresponding to a salinity of roughly 15 psu (not the 18 psu used in the stratification of degraded and clean reference sites in the creation of EMAP-E VP degradation indices).

There is a considerable amount of within-site, among-season and among-year variation in the EMAP-E VP data. In Appendix IV, two degraded and two clean reference sites are colored to show the extent of this variation. On a qualitative level, there appears to be as much variation among samples taken at the same site during different seasons (*e.g.*, New Bedford Harbor 099 sampled on August 15, 1990 and September 4, 1990) as there is between any difference between degraded vs. clean (using the criteria in Weisberg *et al.* 1993 and Schimmel *et al.* 1994). There appears to be as much variation at New Bedford site 099, sampled during the same year but 3 weeks apart, as between any pair of estuarine stations (salinity > 5 psu) in the entire data set. It was impossible to analyze the full extent of within site variation relative to the degraded vs. non-degraded dichotomy since most of the 'degraded' samples, especially in the oligohaline and mesohaline portions of the Virginian Province, had fewer than 25 individuals per grab and were dropped from the analysis.

### Species clusters

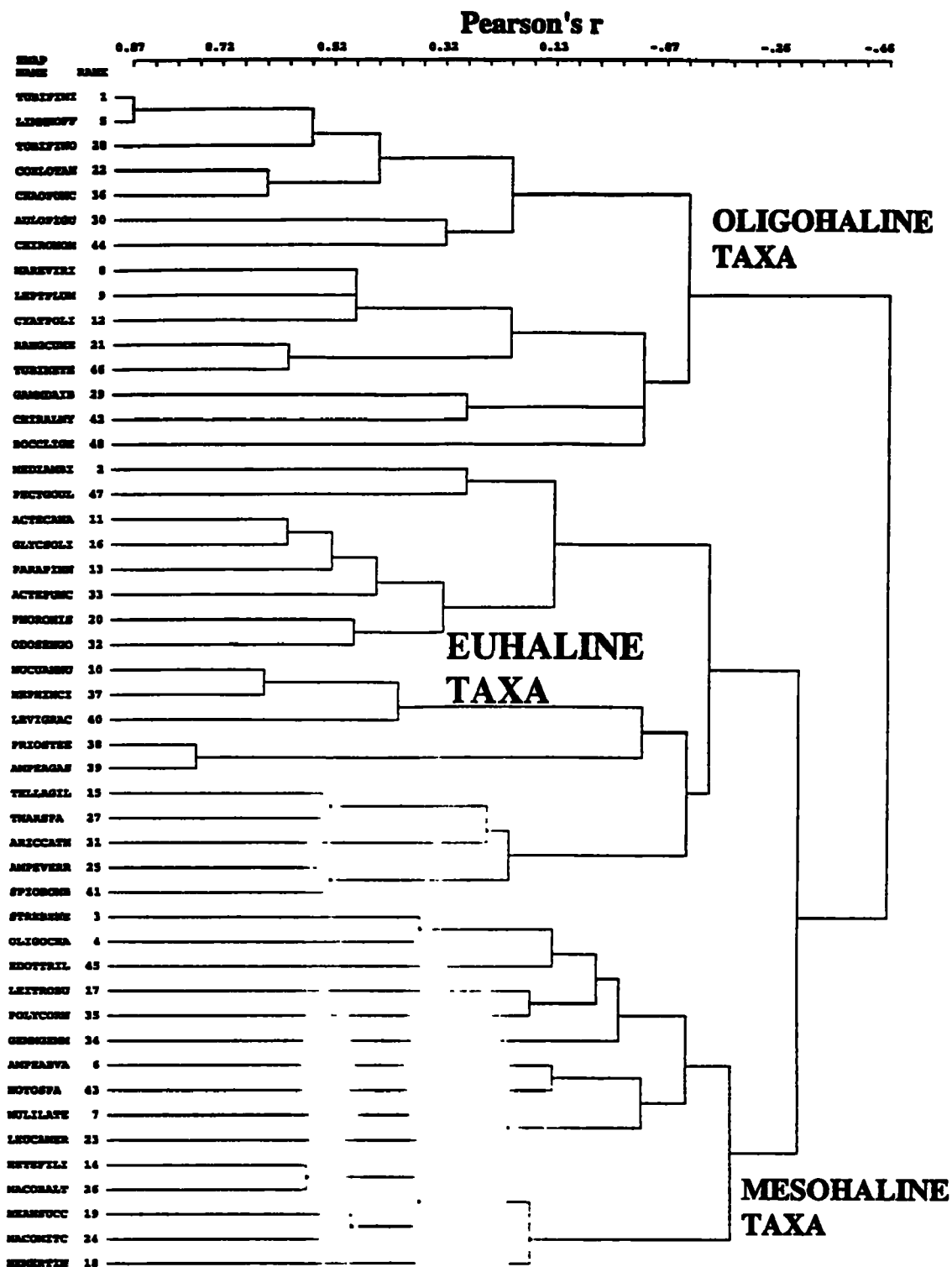
Clustering of species reveals three distinct groupings of species (Figure 14), roughly corresponding to the oligohaline, mesohaline, and euhaline habitats in the Virginian Province. All species that contributed at least 0.5% of the variation in the EMAP-E VP CNESS distances among stations are

shown. Within each of these large salinity-controlled groupings are groups that are characteristic of different grain sizes, biogeographic regions, and depths.

The low salinity species assemblage in Figure 14 consists of two sub groupings. The first subgrouping (TUBIFWI to CHIRONOM) are mainly taxa which could only be found in samples from 0-5 psu salinity, since they involve taxonomic designations not used for samples taken from areas higher than 5 psu salinity. The most important contributor to CNESS distances in the 1990-1993 EMAP-E VP data is the taxon TUBIFTWI, which is the EMAP-E VP code for Tubificidae with capiliform chaetae (see Appendix II for translations for the EMAP-E VP species codes). This group probably does not represent a single species. The fifth most important taxon is LIMNHOFF, *Limnodrilus hoffmeisteri*. TUBIFWO, the 28th most important contributor is another composite taxon; the EMAP-E VP species code stands for Tubificidae without capiliform chaetae.

The oligohaline species group also includes some very important macroinfaunal species. The spionid polychaete *Marenzelleria viridis* (MAREVIRI), formerly called *Scolecopides viridis*, is the eighth most important contributor to CNESS distances in the Virginian Province. It tends to occur with the amphipod *Leptocheirus plumulosus* (LEPTPLUM) and the isopod *Cyathura polita* (CYATPOLI). These oligohaline to low mesohaline taxa tend to be geographically wide-spread in the Virginian Province. These latter three taxa are also abundant throughout the Gulf of Maine region (EMAP-E VP's Arcadian Province).

Figure 14. Cluster analysis of the 48 species that contribute most to CNESS ( $m=25$ ) variation.



The euhaline species assemblage, shown in Figure 14, consists of two subgroupings. The most important species in the first grouping and the second most important taxon contributing to CNESS faunal distances in the entire Virginian Province is the capitellid polychaete *Mediomastus ambiseta* (MEDIAMBI). This head-down subsurface deposit feeder is also the most abundant taxon in the entire Virginian Province.

Included within the second euhaline species assemblage is the *Nucula annulata* (NUCUANNU), *Nephtys incisa* (NEPHINCI) group. These two taxa, tenth and thirty-seventh most important contributors to CNESS distance, are the classic indicator species for both Long Island Sound and Buzzards Bay infaunal communities (Sanders 1956, 1960). Sanders (1956), in his Yale Ph.D. dissertation, described the Long Island Sound benthos using the Petersen-Thorson descriptive designations as a *Nucula proxima* - *Nephtys incisa* community. Buzzards Bay was described as being a *Nucula proxima* - *Yoldia limatula* - *Nephtys incisa* community. *Yoldia limatula* (YOLDLIMA), a larger but less abundant protobranch bivalve, was not among the top forty-eight species contributing the CNESS distances, but is the first taxon to cluster with *Nucula annulata* in the species cluster analysis of all 551 EMAP-E VP taxa (Appendix V). Subsequent to Sanders' surveys of Long Island Sound and Buzzards Bay, Hampson (1971) found that there are two *Nucula* sibling species in the region: *Nucula proxima* dominates in nearshore fine sands and *Nucula annulata* dominates offshore muds. The two species have nearly allopatric distributions, and can be distinguished by the locations of the abductor muscles on the inside of the shells. Both have probably been combined in the EMAP-E VP designation NUCUANNU since the widespread and abundant taxon *Nucula proxima* is not among the EMAP-E VP species.

Within the second euhaline species assemblage are the tellinid bivalve *Tellina agilis* (TELLAGIL), the cirratulid polychaete *Tharyx* sp. A Morris (THARSPA), the paraonid polychaete *Arricidea catherinae* (ARICCATH), the ampeliscid amphipod *Ampelisca verrilli* (AMPEVERR), and the spionid polychaete *Spiophanes bombyx* (SPIOBOMB).

The mesohaline species assemblage, shown in Figure 14, also consists of two sub groupings. The mesohaline taxa include some of the most abundant and wide-spread taxa in the Virginian and Arcadian provinces. All of these taxa can be found in both the shallow subtidal zone (usually in intermediate salinities) and the intertidal zone. The spionid polychaete *Streblospio benedicti* Webster (STREBENE) is a typical numerical dominant in intertidal zones throughout the Virginian and Arcadian Provinces (e.g., 1982, Trueblood *et al.* 1994, Diaz and Schaffner 1990). This spionid is the third most important contributor to the variance in CNESS distances among Virginian province samples. In the subtidal, *S. benedicti* dominates in areas of intermediate salinities ( $\approx 15$ -25 psu). The EMAP-E VP taxon with the highest affinity to this spionid is the class Oligochaeta (OLIGOCHA). This composite EMAP-E VP taxon is only used for samples having salinities greater than 5 psu, at lower salinities the oligochaetes are further divided into species and designations such as *Tubificoides* with capiliform setae (TUBIFTWI, see above). Also associated with this *Streblospio benedicti* - Oligochaete assemblage are other taxa characteristic of the intertidal zone, but which also can be very abundant in shallow subtidal mesohaline environments. These include the spionid polychaete *Polydora cornuta*, formerly called *P. ligni*, (POLYCORN), the orbinid polychaete *Leitoscoloplos robustus* (LEITROBU), the isopod *Edotea triloba* (EDOTTRIL), and the venerid bivalve *Gemma gemma* (GEMMGEMM). Each of these taxa is abundant in intertidal and shallow subtidal mesohaline zones throughout the Virginian and Arcadian provinces.

Included in the first mesohaline species assemblage is the *Ampelisca abdita*-*Ampelisca vadorum* complex (AMPEABVA). This sibling species group is the third most abundant taxon in the Virginian province (1st in the NY/NJ REMAP data) and the sixth most important contributor to the variance in

CNESS distances among stations. *Ampelisca abdita* is the species used in the EMAP-E VP amphipod toxicity assays. *Ampelisca abdita* and *A. vadorum* constitute a sibling species complex (Mills 1967). Since the juveniles cannot be distinguished, the adults of both species are pooled with the juveniles in the EMAP-E VP taxon (AMPEABVA). This sibling species complex co-occurs with the capitellid polychaete *Notomastus* sp. A Ewing (NOTOSPA). The opportunistic mactrid bivalve *Mulinia lateralis* (MULLATE) is the seventh most important contributor to CNESS distances. It is weakly associated with the cumacean *Leucon americanus* (LEUCAMER).

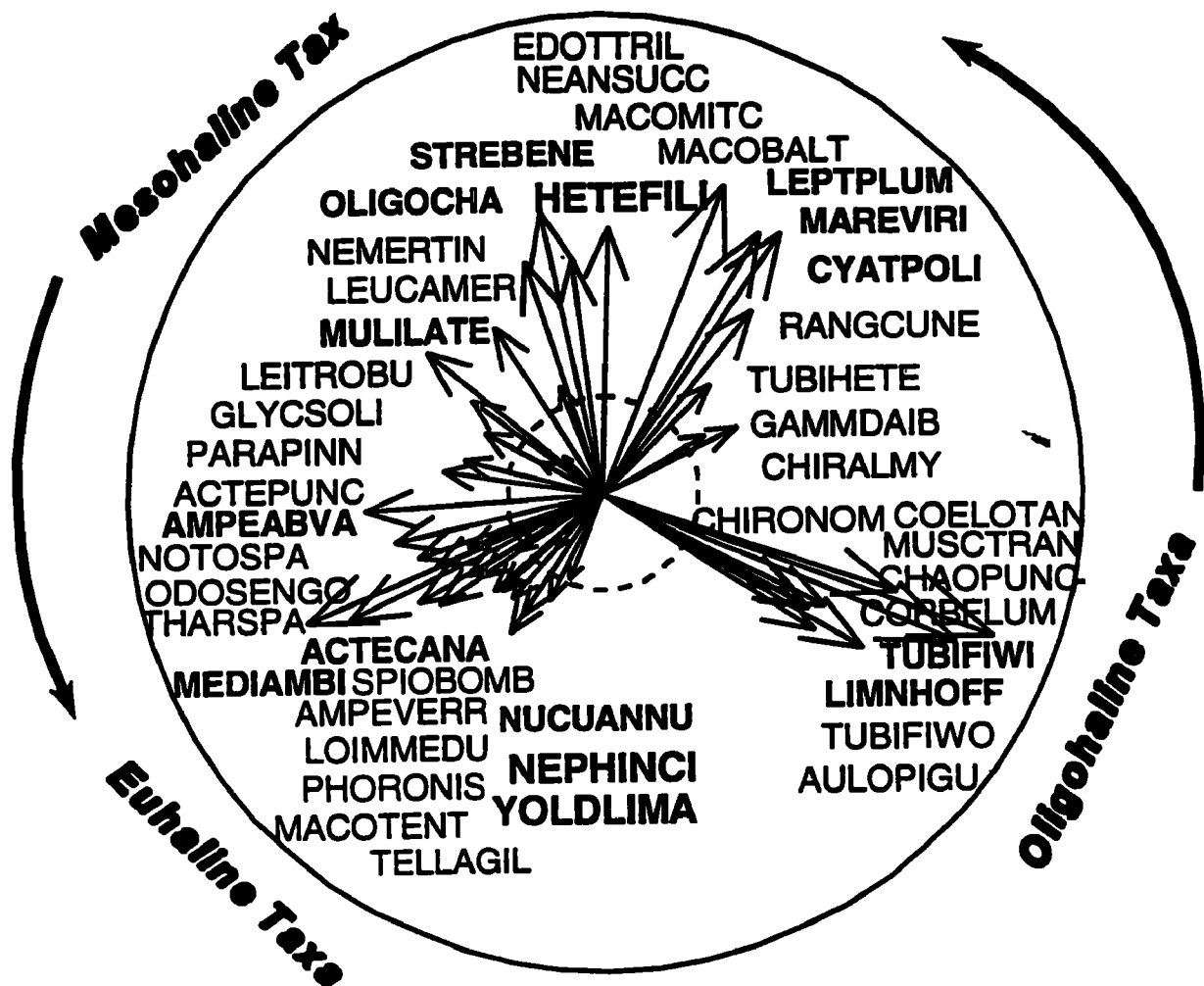
The following mesohaline taxa form a well-defined assemblage, characteristic of slightly lower salinities than the remaining mesohaline taxa: the capitellid polychaete *Heteromastus filiformis* (HETEFILI), the opportunistic tellinid bivalve *Macoma balthica* (MACOBALT), the nereid polychaete *Neanthes succinea* (NEANSUCC), the tellinid bivalve *Macoma mitchelli* (MACMITC), and members of the class Nemertinea (NEMERTIN). Each of these taxa can be found in intertidal zones throughout the Virginian and Arcadian provinces, and thrive in lower mesohaline salinities in the lower subtidal.

Notable for its absence from the species cluster analysis in Figure 14 is the sibling species complex *Capitella*. Figure 14 contains only the most important contributors to CNESS distance, and *Capitella* is a minor component of the Virginian Province communities, being found in only eighty nine samples. As shown in Appendix V, the pollution-indicating *Capitella* sibling species complex appears to be just another relatively rare euhaline taxon. Surprisingly, the species with the highest affinity to *Capitella* in the full species cluster analysis (Appendix V) is the portunid crab *Ovalipes ocellatus* (OVALOCEL). Of the forty eight taxa shown in Figure 14, *Capitella* is associated most closely with the cirratulid polychaete *Tharyx* sp. A Morris (THARSPA).

### PCA-H analysis

The first step in the PCA-H analysis was to determine a random sample size, or NESS<sub>m</sub>, for the CNESS faunal distance index. This random sample size should produce a faunal distance index that is sensitive to the contribution of both rare and abundant species in the community. A NESS<sub>m</sub> of approximately 20-25 produces an index that is highly correlated ( $\tau > 0.8$ ) with both CNESS (NESS<sub>m</sub>=1 or Orloci's chord distance) and CNESS (NESS<sub>m</sub>=100).

Figure 15 shows the Gabriel covariance biplot of species (Gabriel 1971). This is a different way of plotting the species data that were clustered in Figure 14. This figure shows the major species groups in the entire Virginian Province. Only those species that contributed at least 1% to the variation in community structure (measured by CNESS) are plotted. This figure shows the major gradient in species distributions as a function of salinity in the Virginian province. The cluster of species vectors at about 4 o'clock consists of species that were only identified in samples taken from less than 5 psu salinity areas. *Oligochaetes*, *Mulinia lateralis*, and *Streblospio benedicti* are all characteristic of intermediate salinities in the Virginian Province (about 15 psu). The spionid polychaete *Marenzelleria viridis*, the isopod *Cyathura polita*, and the aorid amphipod *Leptocheirus plumulosus* are characteristic of slightly lower salinities (5-10 psu). *Ampelisca abdita* and *A. vadorum* are associated with higher salinities. The key species indicating euhaline conditions in the Virginian province is the capitellid polychaete *Mediomastus ambiseta*. The final three species vectors represent Howard Sanders' classic Long Island Sound and Buzzards Bay *Nucula-Yoldia-Nephtys incisa* community (Sanders 1956 and 1960).

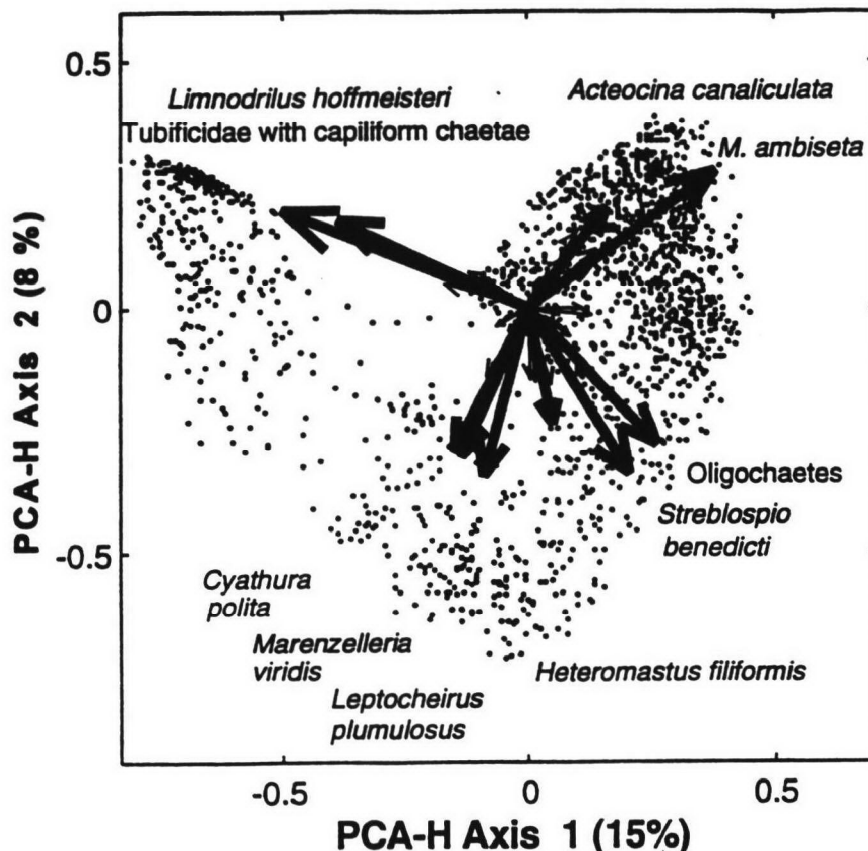


**Figure 15** This is the Gabriel covariance biplot corresponding to the species clusters shown in Figure 14. Each of the 48 most important species is indicated by a vector (arrow), and the cosine of the angle between vectors is a measure of whether species are likely to be found in the same samples. A remarkable feature of this plot is that the major species groupings in different salinity regimes can be read sequentially by moving from 4 o'clock counterclockwise to 7 o'clock. The species codes can be found in Appendix III. Some key species discussed in the text are **bolded**.

Figure 16 shows the Gabriel Euclidean distance biplot for the 1736 samples containing more than 25 individuals (out of 1918 total samples). The most important taxon accounting for CNESS variation among samples is the oligochaete taxon '*Tubificoides* with capiliform chaetae' (TUBIFIWI in Figures 14 and 15). This taxon alone accounts for 5% of the total CNESS variation among samples. The samples in the upper left portion of this plot are all characterized by having high frequencies of *Tubificoides* with capiliform chaetae and *Limnodrilus hoffmeisteri*. The relative frequency of these key species can be determined by projecting each sample onto the species vectors at right angles.

As one moves counterclockwise around Figure 16 from the upper left, the samples are distributed according to salinity. The key species contributing to the position of samples in the first two PCA-H axes are the oligohaline isopod *Cyathura polita* (CYATPOLI in Figures 14-16), the spionid polychaete *Marenzelleria viridis* (MAREVIRI), the aorid amphipod *Leptocheirus plumulosa* (LEPTPLUM), the capitellid polychaete *Heteromastus filiformis* (HETEFILI), the spionid

polychaete *Streblospio benedicti* (STREBENE), and members of the class oligochaeta (OLIGOCHA - an EMAP-E VP designation used only for oligochaetes collected from samples with salinity > 5 psu). The upper right euhaline portion of the biplot is controlled by two euhaline taxa: the capitellid polychaete *Mediomastus ambiseta* (MEDIAMBI), and the gastropod *Acteocina canaliculata* (ACTECANA).

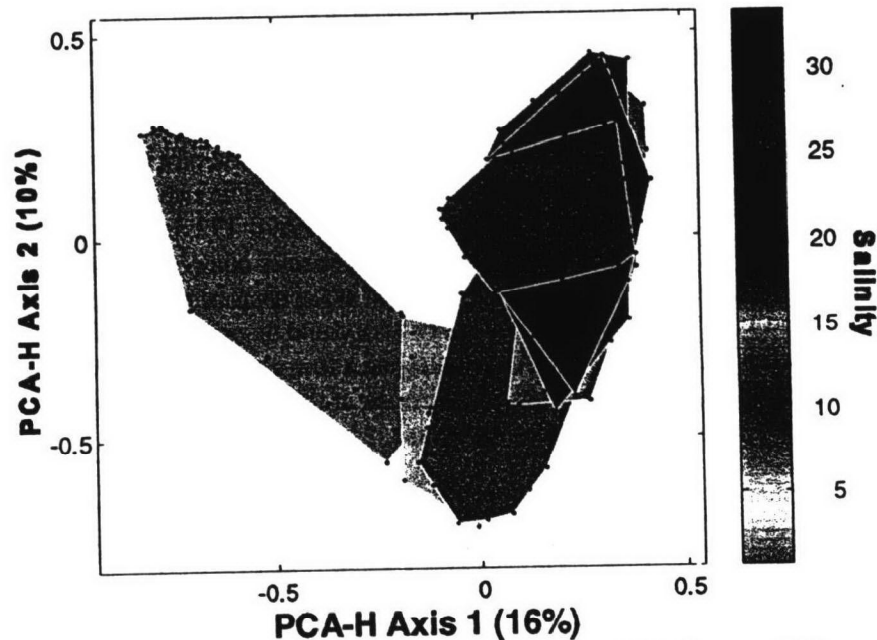


**Figure 16.** A Gabriel Euclidean distance biplot of the full (1918 sample, 551 species) EMAP Virginian Province data at  $m=25$ . All species vectors are plotted; only those accounting for 2% of the variation in the first 2 dimensions are labeled. The ten most important species contributing to CNESS distances are *Tubificoides* with capilliform chaetae (55), *M. ambiseta*, *S. benedicti*, oligochaetes (4%), *Ampelisca abdita-vadorum* complex (3%, not shown), *Mullinia lateralis* (3%, not shown), *Marenzelleria* (formerly *Scolecopelides*) *viridis* (3%), and *Nucula annulata* (2%, not shown). The important species not shown in this plot are important contributors to the third PCA-H axis.

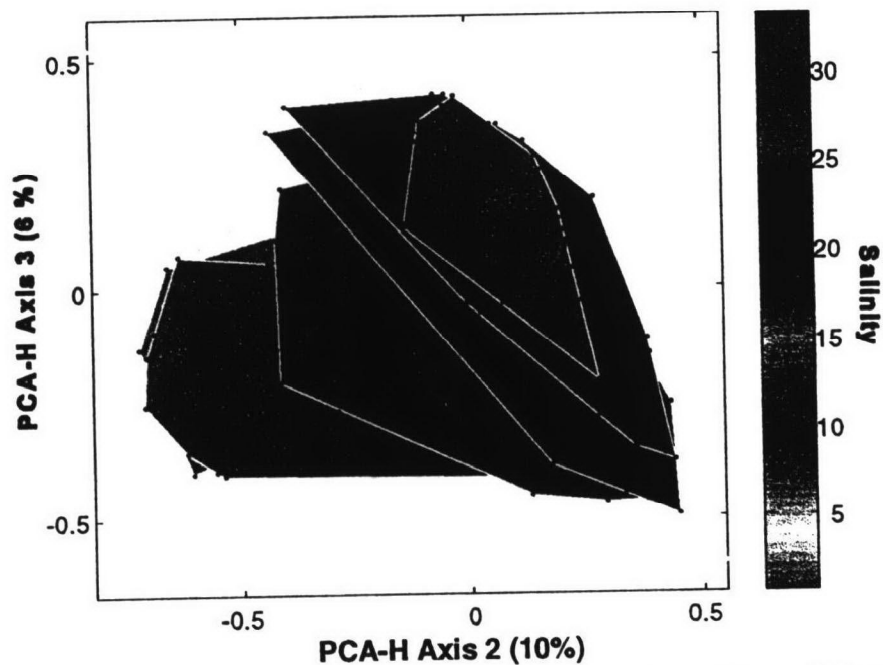
The 1736 samples in Figure 16 were pooled if salinity data existed for the samples and if the CNESS distances among replicates were less than 0.7 (a large CNESS distance, see Methods). The biplot produced for these 320 samples are analyzed in Figures 17-23.

Figure 17 shows the PCA-H ordination of samples, with all samples in 5 psu increments being surrounded with different colored convex hulls. This figure shows clearly that PCA-H axis 1 serves largely to separate samples with salinities less than 5 psu from the remaining samples. Undoubtedly, some of this clear demarcation among samples is due to the use of different taxonomic designations for

EMAP-E VP samples taken from areas with less than 5 psu. It is also clear that there is a second, but less distinct break in community structure between the 5-15 and 15-35 psu samples. In the first two PCA-H axes, the 15-35 psu samples plot on top of each other, but they are separable in the plot of the 2 vs. 3 PCA-H axes, which are shown in Figure 18.



*Figure 17. Convex hulls containing all samples within 5 psu salinity ranges are plotted vs. PCA-H Axes 1 and 2. PCA-H Axis 1 is controlled almost entirely by the contrast between 0-5 and 5-35 psu salinity.*



*Figure 18. Convex hulls are drawn around all samples within each 5 psu salinity range vs. PCA-H Axes 2 and 3. Salinity is still a major determinant of PCA-H scores in the second and higher dimensions.*

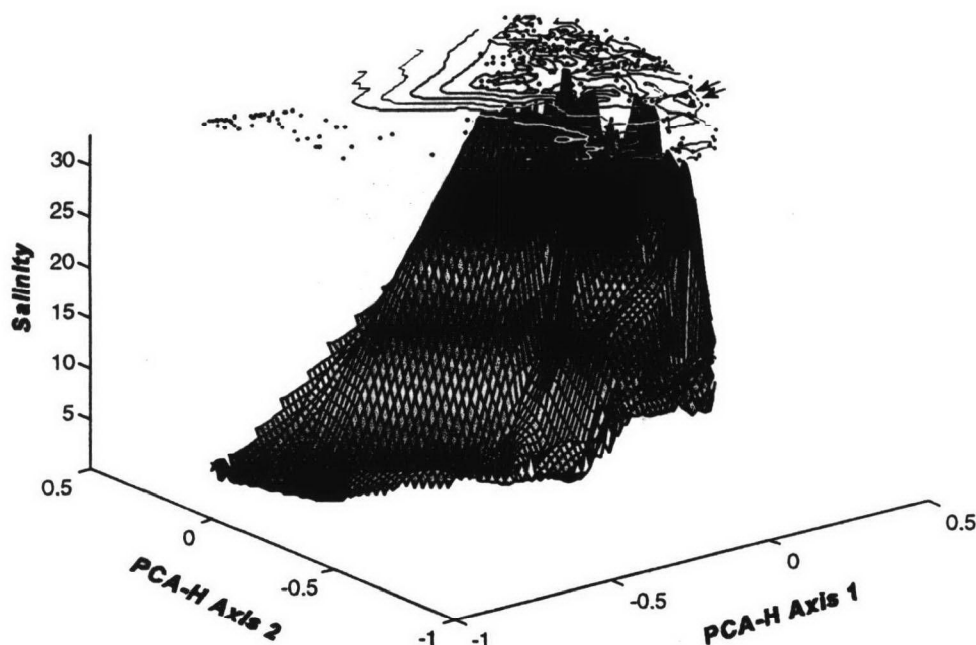


In the two dimensional PCA-H displays in Figure 17, the salinity groupings appear to form a horse-shoe (often called a Kendall's horseshoe) or U shape. This is the expected low-dimensional projection of salinity-controlled coenocline. Salinity continues to control community structure in the 3rd and higher PCA-H dimensions (Fig. 18).

The strong effect of salinity on PCA-H site scores in the first two PCA-H dimensions is graphically shown in Figure 19. The salinity of each sampling event is plotted in the third dimension vs. the first two PCA-H site scores (shown in Figure 17). The samples shown in the contour plot above the figure are distributed in a counter-clockwise fashion from the lower left of the plot to the upper right. The euhaline portion of the estuarine coenocline is shown in the upper right. The two arrows in the mesohaline (10-15 psu) portion of the plot mark two Hudson River samples (VA90-177 and VA90-198), which had measured salinities of 7.35 and 9.55 psu, but which had species compositions characteristic of salinities 3 or 4 psu higher. These two samples produced a 'hole' in the contour plot (marked with the red and green contours for 15 and 10 psu, respectively). This pattern could be produced in a tidal river system when the salinity decreased from 11 to 14 psu to 7 to 10 psu a few weeks before the benthic grab samples were taken. Within the oligohaline and mesohaline portions of the Virginian province, species composition is a very good predictor of salinity (but not vice versa).

The upper right euhaline portion of Figure 19 reveals a rugged mountainous topography. Samples within this region have species compositions characteristic of salinities greater than 15 psu, but there isn't a clear one-to-one correspondence between salinity and community structure.

Figure 20 shows the total number of species per sampling event vs. PCA-H axes 1 and 2. At salinities less than 15 psu, the number of species per sampling event is closely coupled to salinity. At salinities greater than 15 psu, there is a great deal of variation in the total species per sampling event. Undoubtedly some of this variation is due to the effects of disturbance, and some is due to depth, grain-



*Figure 19. Salinity is plotted against PCA-H Axis 1 and 2, showing that salinity is a major factor controlling community structure. The arrows on the right indicate the two Hudson River samples discussed in the text.*

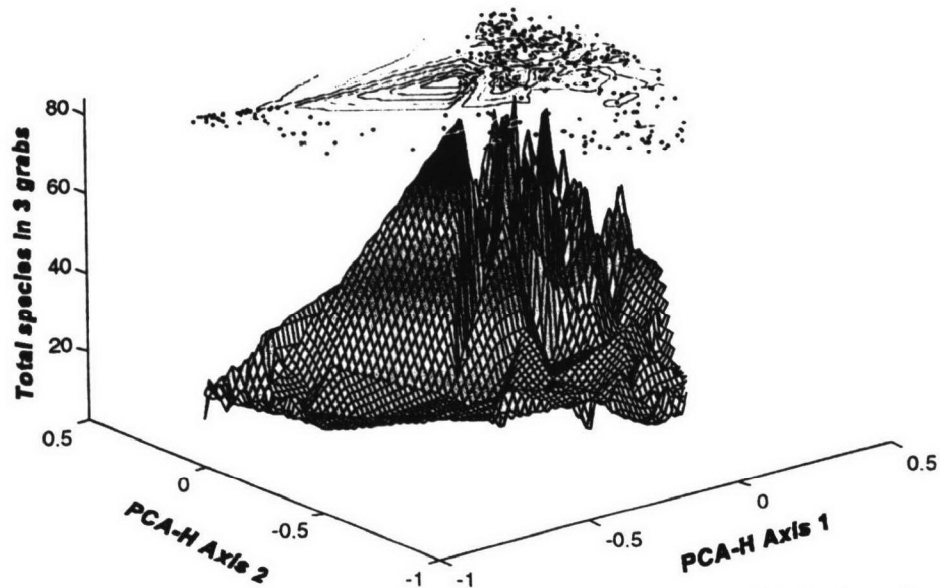


Figure 20. Total number of species per sampling event (3 grabs) is plotted against PCA-H Axes 1 and 2. Total species in 3 grabs in the oligohaline habits (lower left, see Figs. 17 and 19) is uniformly low. Total species in 3 grabs in the euhaline habitats (upper right, see also Figs. 17 & 19) in the Virginian province is much higher, with a much higher variance.

size and biogeographic factors. All of these factors are secondary to the dominant salinity effect.

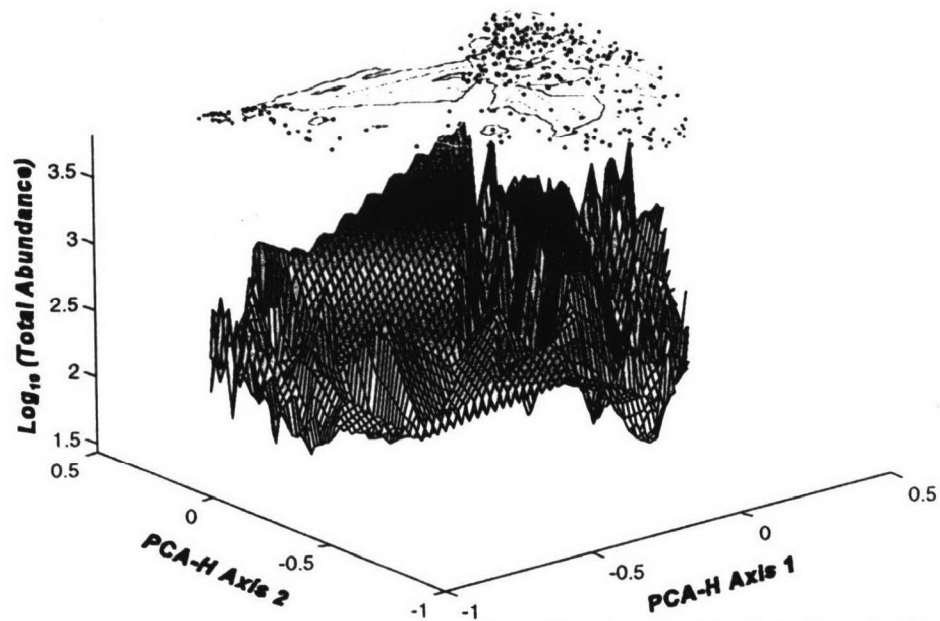


Figure 21.  $\log_{10}$  (Total individuals in 3  $0.044 \text{ m}^2$  grabs) is plotted vs. PCA-H Axes 1 and 2. Infaunal abundances are very low in the oligohaline (<10 psu) portion of the Virginian Province. Abundances are more variable in the euhaline estuarine habitats.

Figure 21 shows that the oligohaline and mesohaline portions of the Virginian province are also associated with relatively low population abundances ( $< 1000$  individuals per  $3 \times 0.044 \text{ m}^2$  grab samples). We plot the  $\log_{10}$  of abundance, because abundance in 3 grabs varies from 25 (the lower cutoff for our analyses) to over three thousand.

Figure 22 shows the plot of the Sanders-Hurlbert  $E(S_{10})$  diversity index vs. PCA-H axes 1 vs. 2. This diversity index exhibits a very high correlation with Shannon's  $H'$  (see Fig. 8 p. 23). Shannon's  $H'$  is far less sensitive to salinity effects than 'Total species per sampling event'. Shannon's  $H'$ , while often used as a species richness index, is very sensitive to species evenness, or the relative distribution of individuals among species. The 'potholes' in Figure 22 indicate samples which have roughly the same salinity-controlled species composition as adjacent samples, but which have very low species evenness. One of the predicted effects of pollution is a drastic reduction in species evenness in a sample. Pollution or disturbance could produce the 'potholes' in Figure 22.

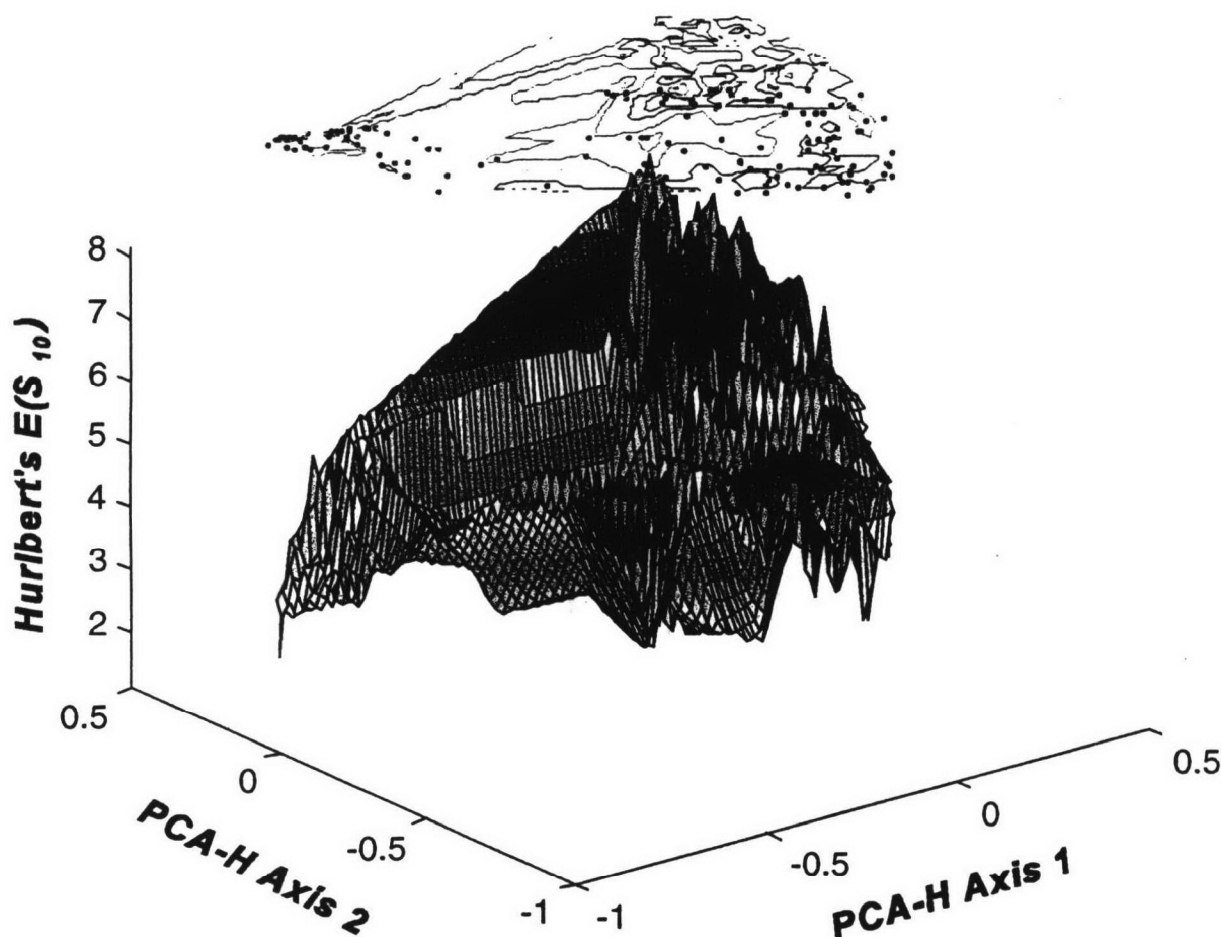


Figure 22.  $E(S_{10})$  is plotted vs. PCA-H Axes 1 and 2.  $E(S_{10})$  is not as sensitive to salinity effects as total species. 'Potholes' in the landscape may pinpoint the degraded areas within each salinity regime.

## CONCLUSIONS

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### On the central role of salinity

It is apparent from our analyses that salinity is the dominant factor controlling EMAP-E VP community structure. Part of this is due to the differences in taxonomy used to sort EMAP-E VP samples from low-salinity regions. More than that, salinity is a major determinant of species richness and community composition. This comes as no surprise. Sanders *et al.* (1965) reached this conclusion in their survey of the Pocasset River in Massachusetts. They concluded that the variance in salinity as well as its absolute value restricts the number of species present. Boesch (1977b) and Diaz and Schaffner (1990) have stressed the central role played by salinity in controlling benthic community structure in Chesapeake Bay. To our knowledge, the analyses in this report provide one of the clearest demonstrations of the role of salinity as the major factor controlling community structure in a broad biogeographic region.

Weisberg *et al.* 's (1993) 1990 EMAP-E VP benthic degradation index (Weisberg *et al.* 1993) explicitly accounted for the effects of salinity on species richness. Salinity effects were not properly assessed in the 1991 and 1992 indices, but Strobel *et al.* (1995) again designed their 1990-1993 index to remove the strong effects of salinity. The sampling properties of Gleason's D diversity are not well worked out. Gleason's D diversity is not among the diversity indices that ecologists use. We would strongly recommend that future analyses use Shannon's  $H'$  or Hurlbert's  $E(S_n)$ . Hurlbert's  $E(S_n)$  has the advantage that it can be made more sensitive to species richness by increasing the sample size. Total species per grab is an acceptable index of diversity. However, as our analyses show, it cannot be used without careful removal of the overriding effects of salinity. Salinity is strongly correlated with the total number of species (Figure 3, p. 13). Without explicitly removing the effects of salinity, a degradation index based on species richness would have a tendency to identify oligohaline and mesohaline habitats as degraded. This tendency would be compounded if the list of opportunistic taxa used in several EMAP-E VP indices included species that are the natural dominants of oligohaline and mesohaline environments.

### Suggestions for improving EMAP-E VP

#### *Sampling*

Two major problems appeared in our preparation of the EMAP-E VP data for community structure analysis. First, many of the replicate grabs from a site were extremely heterogeneous (CNESS > 0.7). Approximately 1/4 of the sampling sites were discarded because the three replicate grab samples were too heterogeneous to be considered true replicates. If the goal of the analysis is to characterize community structure alone, then this heterogeneity is important. However, in comparing sediment chemistry data collected from a different set of grabs than the benthic community structure data, it is essential that the benthic samples exhibit adequate replication. A CNESS distance of 0.7 or above indicates drastic changes in community structure, comparable to sampling sand vs. mud or sampling the same community in early spring and late summer (see Trueblood *et al.* 1994). We suspect that the small-scale heterogeneity was such that different sediment types were sampled with the three replicate biology grabs. If the three benthic grab samples indicate differences in community structure comparable to sampling sand vs. mud, then we felt that we could not trust the corresponding chemical data from the site. Would it correspond to the sandy benthic samples or the muddy ones? The extent

of the inter-replicate within site variance can be obtained by examining the clustering patterns of the sample cluster analysis in Appendix IV.

A second troubling feature of the EMAP-E VP analysis is shown in Appendix IV. In the 1990 sampling, triplicate box cores were taken from a site (STA 099) in New Bedford Harbor on August 15 and September 4, 1990. The differences in community structure at this single site with samples taken three weeks apart is as great as that observed between 'degraded' Chesapeake Bay euhaline samples and 'Clean' Nantucket Sound samples. Additional seasonal sampling should be carried out in the Virginian province to establish the extent of seasonal variability in the benthic communities.

### *Taxonomic issues*

The EMAP-E VP program should have archived taxonomic reference material. The taxonomy of even the most wide-spread taxa in the Virginian province changes on the decadal time scale. Future ecologists will never know what species were really sampled in the EMAP-E VP. This is not the fault of the consulting firm which analyzed the EMAP-E VP data (Cove Associates). Cove Associates uses the latest taxonomic keys and certifies their species identifications with experts. Unfortunately, every year brings new taxonomic revisions. Currently, the status of the most abundant taxon in the EMAP-E VP data is in doubt. *Mediomastus ambiseta* was first described on the East Coast only in the early 1970s by Hobson (1971). Before that time, all *Mediomastus* were probably incorrectly identified as the capitellid *Heteromastus filiformis*, another Virginian province taxon which thrives at much lower salinity.

*Mediomastus* is not just another worm. It is the most abundant taxon in the entire Virginian province. There is a dramatic break in the distribution of *Mediomastus ambiseta* and *M. californiensis* at Cape Cod. Tim Morris at Cove Associates, who identified the capitellids in the EMAP-E VP program, was responsible for correcting a decades-old misclassification of *Mediomastus* in the Gulf of Maine. Throughout the 1960s and 1970s, the dominant *Mediomastus* species in Massachusetts Bay and Cape Cod Bay was misidentified as *Capitella capitata*, *Heteromastus filiformis*, or *Mediomastus ambiseta*. When Cove Associates was hired by the MWRA to process benthic samples in Massachusetts Bay in the mid 1980s, Morris identified the dominant *Mediomastus* species as *Mediomastus californiensis*. Since Morris's revelation, not a single *Mediomastus ambiseta* has been positively identified North of Cape Cod. All *Mediomastus* appear to be *M. californiensis*. *Mediomastus californiensis* was originally described from a California mudflat, and is the numerical dominant at the Los Angeles sewer outfall (Swartz *et al.* 1986), and in many areas of Puget Sound (Llanos, unpublished Puget Sound Ambient Monitoring data). Swartz *et al.* (1986) concluded that *M. californiensis* was an indicator of mild organic enrichment. In 1973, Day published a key to the polychaetes of the North Carolina region, listing *Mediomastus californiensis* as being common off Beaufort North Carolina in 10-20 meters depth. Day (1973) did not list *M. ambiseta*, and his description of *M. californiensis* lists the presence of the key characteristic that separates *M. ambiseta* and *M. californiensis* (abdominal neuropodia with hooks). In 1981, Ewing and Dauer published a key to the Chesapeake Bay capitellids that included both *M. ambiseta* and *M. californiensis*. *Mediomastus californiensis* is the only *Mediomastus* species found in the offshore Minerals Management Survey of the Gulf of Mexico (Ewing 1984).

The only *Mediomastus* species identified in the first three years of the EMAP-E VP program was *Mediomastus ambiseta*. Before the processing of the final year of EMAP-E VP data, the 1993 sampling, Morris (pers. comm.) identified *M. californiensis* for the first time within the Virginian province. This key species was found in only thirteen samples in the 1993 sampling. Cove Associates keeps archive samples of the *Mediomastus* collected from Massachusetts Bay and the Gulf of Maine,

and Morris has been examining the individuals of this key genus. Virtually all of the *Mediomastus* individuals from the first three years of EMAP-E VP sampling were destroyed in order to estimate biomass. This is very unfortunate. Reference material from the EMAP-E VP program would have been very valuable in determining the broad-scale distribution of this key genus. The problem is even more serious because the extensive Minerals Management Service Survey of the Georges Bank region (Neff *et al.* 1989, Battelle & WHOI, 1985) identified a third *Mediomastus* species: *Mediomastus fragilis*. This identification was confirmed by Linda Warren, who has recently revised the genus *Mediomastus* (Warren *et al.* 1994). *Mediomastus fragilis*, first identified in Northern Europe, would key out as *Mediomastus californiensis* using North American polychaete keys.

Many of the other numerically dominant taxa in the EMAP-E VP data set also require taxonomic work. Oligochaetes are the most important group of species in distinguishing oligohaline and mesohaline benthic habitats. The most important taxon controlling CNESS distances among samples is the odd species group 'Tubificidae with capiliform chaetae'. None of the oligochaetes in the EMAP-E program from areas with more than 5 psu salinity were archived for future taxonomic analysis. We will never know how many mesohaline oligochaete species were present in the Virginian Province from 1990-1993. The 1990-1993 benthic index cannot be properly evaluated because we do not know the proportion of oligochaetes that are members of the oligochaete family Tubificidae. The true extent of species turnover along the Virginian Province salinity gradient can never be properly assessed with the EMAP-E VP data because of the lack of taxonomy of the oligochaetes collected in areas having more than 5 psu salinity.

*Nucula proxima* and *Nucula annulata* are among the numerically dominant taxa in the Northern Virginian province. *Nucula annulata* is the tenth most important taxon contributing to CNESS distances in our analysis. Howard Sanders (1956, 1960) described the Long Island Sound and Buzzards Bay communities inhabiting subtidal muds as *Nucula proxima*-*Nephtys incisa* communities. George Hampson (1971) showed that the offshore mud-dwelling species was *Nucula annulata*, while the inshore sand-dwelling species in Buzzards Bay was *Nucula proxima*. *Nucula proxima* and *N. annulata* can be easily confused, but their habitats are very different. *N. proxima* thrives in nearshore fine sands, but *N. annulata* is found in offshore muds. The two species show little overlap in their distributions. In the EMAP-E VP data, *N. annulata* is found in both nearshore sand and offshore mud habitats, and *N. proxima* is not included in the EMAP-E VP species list. We must assume that *N. proxima* was called *N. annulata* in these analyses. If preserved samples were available, it would be a simple matter to obtain samples for nearshore sandy environments to determine whether the dominant protobranch bivalve was *N. proxima* and not *N. annulata*. Dr. Robert Prezant, a malacologist at Indiana University of Pennsylvania, has been sampling the Assateague/Chincoteague area of Virginia for many years. He has sampled many *Nucula* from this shallow sandy area, that the EMAP-E program uses as one of its undegraded reference stations. The EMAP-E program lists only *Nucula annulata* from this shallow sandy area. Dr. Prezant has closely examined the Chincoteague/Assateague *Nucula*. All are *Nucula proxima*, in accordance with Hampson's (1971) description of the distribution of *Nucula* species. In analyzing the EMAP-E data, it is vital to be able to distinguish the dominant species from inshore sandy areas from offshore muds. The fact that *N. proxima* was missed in the four-year EMAP-E VP program is the type of slipup that could have been resolved readily if archive material were available. Unfortunately, all bivalve individuals collected during the EMAP-E VP program were destroyed to determine bivalve biomass for the EMAP-E VP degradation indices.

The cost for archiving benthic samples is high, but most other federal benthic surveys have managed this cost. Archiving samples is not incompatible with measuring biomass. The Minerals Management Service (MMS) insists that biomass be determined, but they also require that all samples be archived.

Only subsets of the individuals need to be analyzed to produce biomass estimates. The remaining material is archived at the Smithsonian. This MMS material is an important resource in the ongoing taxonomic revisions of our nation's marine communities. The EMAP-E VP was designed to serve as a multi-decade monitoring and assessment program. Archiving benthic samples should be a requirement of all such long-term monitoring plans.

### ***Data analysis***

Warwick (1993) asked whether there is an 'absolute' measure of benthic community structure that can determine whether a site was affected by pollution. After assessing indices similar to the EMAP-E VP degradation index, and several other indices of degradation, he answered 'No.' There is no clear-cut index that can determine whether an observed distribution of species in a sample is the result of pollution. Only marine sites that are nearly azoic or dominated by members of the genus *Capitella* can be unambiguously defined as degraded. Warwick (1993) even discounts the use of *Capitella* as a pollution indicator, regarding it more of an indicator of organic enrichment than toxicity. It is equally risky to assign a site with high species richness or abundance as being non-degraded. In the West Falmouth oil spill (Grassle and Grassle 1974, Sanders *et al.* 1980), the Amoco Cadiz oil spill (Cabiocch *et al.* 1982) and even the MERL eutrophication experiments (Smith *et al.* 1979b), species diversity is insensitive to drastic changes in toxic loadings. However, species composition is sensitive to very low changes in pollutant input (*e.g.*, Grassle *et al.* 1981).

### ***Dubious indices and statistics***

In soft-bottom benthic ecology, there has been a plethora of dubious indices proposed to assess community structure. Most of these indices and approaches share a few common features:

- They are less expensive than standard benthic sampling which relies on the identification of all individuals to species.
- They rarely require taxonomic identifications beneath the level of family or competent taxonomists.
- Some require no benthic sampling or a reduced number of replicate samples.

While some of these indices may have merit, all should be viewed with caution, and none should be made the sole basis of a monitoring program. Some indices, such as Jack Word's (1978, 1980 a & b) infaunal trophic index (published only in the SCCWRP biennial reports), can be ruled out almost immediately as being too seriously flawed to merit discussion as a monitoring tool. Word's index forces improper polychaete trophic guild classifications into an improperly constructed mathematical formula to produce an index of pollution effects. Ferraro *et al.* (1989) provide one of the few published uses of Word's infaunal trophic index.

The following is a list of indices that have been proposed to assess marine benthic degradation. We will divide them into two groups. The first group is composed of seriously flawed indices.

#### **Seriously flawed:**

- The nematode/copepod ratio (Raffaelli & Mason 1981, Warwick 1981, Raffaelli 1981, 1982 & 1987, Amjad & Gray 1983, criticized by Lambshead *et al.* 1983 & 1984 Shaw *et al.* 1983).

- **BRAT** the benthic resource assessment technique (Lunz & Kendall 1982). Benthic individuals are ranked by their presence in the guts of important bottom feeding fish species. Benthic habitats composed of "good" fish food are giving a higher BRAT ranking than habitats containing species that are rarely fed on by bottom-feeding fish. This index, as originally proposed had merit. The index was later simplified to matching the size composition of infauna in fish stomachs with the size composition of benthic communities.
- Jack Word's infaunal trophic index (TTI) (Word 1978, 1980 a, b, & c, Ferraro *et al.* 1989)

#### Indices that are worth investigating:

- Organism-sediment index (OSI™) (Rhoads & Germano 1986). This index was applied to the 1990 EMAP-E VP data (see Figure 4, p 14). Difficulty in obtaining samples in coarse sediments greatly reduces the utility of sediment-profile imaging for EMAP-E VP scale monitoring. Grizzle and Pennimen (1991) found a close correspondence between the OSI™ and traditional benthic community structure analysis in the a polluted New Jersey habitat. O'Connor *et al.* (1989) applied the OSI™ to British benthic communities.
- Warwick's species abundance-biomass comparison (the ABC method) (Clarke 1990, Warwick and Clarke 1991, Warwick *et al.* 1987, 1989, 1990, Essink and Beukema 1986, reviewed by Beukema 1988, McManus and Pauly 1990,). Dauer *et al.* (1993) found that the ABC method was a poor predictor of degraded conditions in the Elizabeth River in Chesapeake Bay.
- Caswell's (1976, 1983) neutral model as a pollution or disturbance index. The infinite alleles model of population genetics predicts a logarithmic distribution of species frequencies. When applied to the benthos, Caswell's neutral model is assessing the fit of the log-series to benthic abundance data. Lamshead *et al.* (1983) and Lamshead and Platt (1985) introduced this method for assessing disturbance pollution. Goldman and Lamshead (1989) wrote an improved version of Caswell's program for assessing the effects of disturbance on benthic communities. Warwick *et al.* (1990) applied the neutral model to a pollution study in Bermuda and Warwick (1993) applied the neutral model to a well-characterized pollution gradient in a Norwegian fjord. Both studies found the lack of fit to the neutral model to be a very poor predictor of degradation.
- Departures from the log-normal distribution of individuals among species [Gray & Mirza 1979, Gray 1979a & b, Stenseth 1979, Gray 1980, Mirza & Gray 1981, Gray 1982, 1983, 1989, Gray & Pearson 1982, Gray & Christie 1983, Pearson *et al.* 1983, Bonsdorf and Kovisto 1982, Nelson 1987; poor fit found by Rygg (1986)]
- The variance in species frequencies among replicates at a site. Warwick (1993) argues that polluted sites have a higher variance in faunal similarity than non-degraded communities.

World-wide, no 'degradation index' has yet been found to classify single benthic samples into degraded and non-degraded categories (Warwick 1993). While environmental regulators might need this information desperately (*e.g.*, O'Connor and Dewling 1986), benthic ecologists have been unable to identify a single index that is reliable. No benthic ecologist has developed an index that can be applied for pollution assessment over large geographic areas. Rhoads and Germano's (1986)



organism-sediment index (OSI™) has been one of the most widely used and highly regarded. It is disturbing that the one test of the OSI index vs. the EMAP-E VP index in Weisberg *et al.* (1983) found virtually no statistical association between the two sets of degraded-nondegraded classifications (see Figure 4, p. 14).

The EMAP-E VP analyses of pollution effects has been hindered by not directly incorporating analyses of pollutant concentration, grain size, depth, and salinity in the biotic Integrity indices. Weisberg *et al.* (1993) and Strobel *et al.* (1995) do include salinity normalization of expected species diversity, but far more use could have been made of the extensive physical and chemical data in developing the benthic index. Coats (1995) has recently applied Gallagher's PCA-H method to establish a monitoring baseline for the Massachusetts Water Resource Authority. He produced PCA-H diagrams similar in style to those presented in this report. Coats then determined that grain size was the dominant factor controlling community structure in Massachusetts Bay. He developed a modification of the PCA-H method which he calls detrended PCA-H which removes the dominant grain-size effect from the major patterns in community structure. Coats (1995) then performed a full power analyses of the four years of MWRA Massachusetts Bay data, showing how pollution effects that might result from the MWRA sewage effluent outfall could be detected and assessed.

Coats (1995) DPCA-H method has great potential. However, Coats applied this method to only one small, approximately 100 km<sup>2</sup> region of Massachusetts Bay. This is smaller than many of the estuaries measured in the EMAP-E VP program.

In addition to the PCA-H method, techniques which assess the distribution of individuals among species might be a valuable tool in determining which samples in the EMAP-E program might exhibit patterns indicating disturbance or pollution. John Gray introduced the "log-normal" plotting technique as a indicator of pollution or disturbance. In Gray's method, the distribution of individuals are fit to the log-normal distribution. Recent disturbance or pollution produces a characteristic break in the normally linear plot of the number of species vs. the number of individuals, when plotted on normal probability paper. John Lambshead, at the Natural History Museum in London, has developed another method which is based on Fisher *et al.*'s (1943) log-series. According to Lambshead, undisturbed communities have distributions which are close to the log-series. Lambshead tests his fit to the log series, using Caswell's neutral model, and Goldman and Lambshead (1989) have written a program called CASVAR which tests benthic community structure data to see how closely it conforms to the log series.

The lead author of this report has recently applied a modified form of these methods to the EMAP-E VP data. They seem to work quite well. Samples from the EMAP-E VP reference test data set (listed in Schimmel *et al.* 1994) seem to conform to the log-series expectations. Most of the samples from the "degraded" test data set reveal two types of departure from log-series expectation. Most of the degraded stations exhibit very low evenness, compared to log-series expectations. However, in samples with very low infaunal abundances and very few species, the evenness is much higher than log-series expectations. This failure to recognize departures on either side of the log-series expectation may have produced some of the negative critiques of the log-series method (*e.g.*, Warwick 1993).

Considerable work needs to be done on fitting the log-series to the EMAP-E VP data. Some of the degraded test data sites in Schimmel *et al.* (1994) have distributions of individuals among species which are close to the log-series expectation. For example, the three grabs from the Kill van Kull degraded site (VA91-373, sampled on 8/3/91) have log-series distribution patterns. There is no sign of impact. Analysis of the species composition of this site indicates that two of the three grabs have benthic populations typical of shallow depths and salinities of 28 psu. This site was flagged as

degraded by Schimmel *et al.* (1994) because four sediment contaminants exceeded the 1990 Long and Morgan ER-M concentrations (silver, mercury, nickel, and zinc). However, using the Long *et al.* (1995) revised ER-M values, only mercury and nickel exceed ER-M. The Long *et al.* (1995) ER-M for mercury is 0.71 µg/g, and the Kill van Kull site had 1.76 µg/g. The ER-M for nickel was 51.6 µg/g and the Kill van Kull site had 57.6 µg/g. The organic carbon concentration at this site was 1.8%. It is entirely possible that the relatively high metal and organic pollutant concentrations at this site could be bound to organic carbon or acid-volatile sulfide phases (see Di Toro *et al.* 1990, 1991, 1992), making the mercury unavailable to the biota. The Kill van Kull appears to have a 'reference' benthic community, despite having relatively high sediment contaminant concentrations. Even within the three replicate grab samples from this site, there are some striking differences. Replicate grab three has a distribution of individuals among species that is least similar to the log series. This same grab contains a few species like *Mulinia lateralis* and *Streblospio benedicti* that are usually regarded as opportunistic.

Further work of this sort must be done to assess whether nearly one quarter of the nearshore area in the the Virginian Province is truly degraded (Table 1, p. 16). The EMAP-E VP dataset with its synoptic measurements of benthic community structure, sediment contaminant levels, and abiotic variables will be an invaluable resource in establishing the causal connection between sediment contaminant concentrations and altered patterns in community structure.

## Have the EMAP Goals and Objectives Been Met?

The EMAP-E VP has created a benthic data set that may be unmatched in the world in terms of broad-scale geographic coverage. With the physical and chemical data available for each sampling event, these data should prove to be a rich resource for benthic ecologists for decades to come. The Virginian Province EMAP-E VP program has collected the necessary data to assess the scale and pattern of variability in benthic communities. Understanding this variability, and separating the natural and anthropogenic contributors to it, should be the goal of the Assessment portion of EMAP.

The EPA can be proud that it has created this outstanding database. There is nothing to match it in scale or scope. The EMAP-E VP program has not been successful in developing a benthic degradation index. This is not surprising. Benthic ecologists have been searching for indices that will reliably indicate pollution or disturbance for the past three decades, if not longer. No index has been found to work reliably.

The EMAP-E VP indices are flawed, but the obstacles faced by the EMAP-E investigators were massive. The EMAP-E VP program attempted to find an index that would work across a very large biogeographic province in habitats as diverse as sandy fresh water habitats in the upper Hudson River to marine subtidal muds like Buzzards Bay, Massachusetts. It is not surprising that the indices developed for the EMAP-E VP program have flaws.

We would encourage the EMAP-E VP program to critically evaluate the latest index: Strobel *et al.*'s (1995) 1990-1993 index. It would be very unfortunate if government agencies began using 7000 spionids per m<sup>2</sup> as a regulatory guideline indicating degradation.

The EMAP-E VP data set could become a rich resource for ecologists and regulators alike if it were made more accessible and in a wider variety of formats. It is difficult to access the EMAP-E VP SAS abundance, species name, chemistry and water column data files in order to do most analyses. It doesn't have to be this way. As a model data base management system, EPA should look to NOAA's Coastal Zone Color Scanner data distribution network. CZCS data is distributed in a wide variety of

formats, from the beautiful World-Wide Web graphic displays of chlorophyll *a* concentration throughout the world to the detailed pixel-by-pixel reflectance data needed by investigators interested in perfecting the chlorophyll *a* algorithm. The lead author will provide the community structure data used to produce this report in ASCII or MATLAB™ format to any investigator that might request it.

If future programs like EMAP-E VP are implemented, I would strongly recommend that a subset or perhaps all of the benthic animals identified to species be archived. Many of the species, especially the numerical dominants in the EMAP-E VP program, are taxonomically difficult. These taxa include the *Mediomastus ambiseta-californiensis-fragilis* complex, the *Nucula annulata-proxima-atacellana* complex, oligochaetes, the *Ampelisca abdita-vadorum* complex, and the *Capitella* sibling species complex. Each of these numerically dominant groups has undergone massive taxonomic revision over the last thirty years, the time scale of the planned EMAP-E VP program. Without archival material, future ecologists and regulators will never know what species were really present in the period 1990-1993 in the Virginian Province.

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## APPENDIX I METHODS FOR ANALYZING COMMUNITY STRUCTURE

### Diversity indices

This section will survey the major diversity and similarity (or dissimilarity measures) in use in community ecology today. Magurran (1988) provides a review of the history of diversity measures in community ecology. She ignores the most common method used to assess diversity in marine benthic communities: Sanders-Hurlbert rarefaction.

Sanders (1968) introduced the rarefaction method for assessing species diversity. Single samples are plotted as rarefaction curves representing the number of species observed in the sample and the number of species expected from randomly drawn subsamples of the total sample. Unfortunately, Sanders method for calculating rarefaction curves was wrong. This error was pointed out by Fager (1972), and corrections were published by Hurlbert (1971) and Simberloff (1972). Hurlbert (1971) criticizes the use of diversity indices and introduces a correction to Sanders' (1968) rarefaction method. Simberloff (1972) introduced an identical correction for Sanders' rarefaction method, but Hurlbert (1971) gets priority. Simberloff (1979) introduced a variance estimator for  $E(S_r)$ , but Smith and Grassle (1977) proposed a better measure earlier. This modified rarefaction method is now routinely described as Hurlbert's  $E(S_r)$ . Peet (1974) and Pielou (1969, 1977) review the use of  $H'$  and other measures of diversity.

### Species richness indices

While there are indices specifically designed to assess species evenness or equitability, there are no unbiased estimators of species richness *per se*. An unbiased estimator is a statistic that has an expected value equal to the true value. The EMAP-E VP program used the total number of species per sampling event (usually three replicate samples) as an index of species richness in the 1990, 1991, and 1992 biotic indices. While this is a straightforward measure of species richness, it is also a biased statistic. Bias means that the expected value of the statistic will be a strong function of sample size. Total number of species per event will vary strongly with the number of samples taken. This bias is not alleviated by calculating the mean number of species per grab. Even with samples drawn from the same theoretical distribution, the total number of species will vary strongly with the number of individuals sampled.

The information content measures of diversity, Brillouin's  $H$  and Shannon's  $H'$  are often used as measures of species richness. Shannon's  $H'$  is the older and more widely used:

$$H' = - \sum p_k \log p_k, \quad (6)$$

where,  $p_k$  is the frequency of species  $k$  in the sample, and  $S$  is the number of species. Pielou (1977) recommends Brillouin's information content, abbreviated  $H$ , should be used to calculate the diversity of fully enumerated samples:

$$\text{Brillouin's } H = \frac{1}{N} * \log \left( \frac{N!}{N_1! N_2! \dots N_r!} \right), \quad (7)$$

where,  $N$  is the total number of individuals in a sample, and  $N_i$  is the abundance of species  $i$ . Both  $H$  and  $H'$  can be calculated using Naparien logarithms,  $\log_{10}$  or  $\log_2$ .  $H'$  assumes an infinite population, and if used it should include an estimate of the variance. Both are highly sensitive to differences in species evenness. Pielou (1977) regarded this feature as desirable. Deep-sea benthic ecologists often use the Sanders-Hurlbert rarefaction index  $E(S_n)$  as an index of species richness. While at large  $n$ , the index becomes more sensitive to species richness, it is still very sensitive to differences in species evenness.

Magurran (1988), following May (1975), advocates using the log-series  $\alpha$  as a measure of species richness. A MATLAB m.file, logseries.m, that calculates the log-series  $\alpha$  and its variance estimator is available from the senior author. Magurran (1988, p. 11) describes the Menhinick species richness index, which is simply the number of species divided by  $\sqrt{(\text{number of individuals})}$ . This index is similar to Margalef's species richness index which is  $(\text{Total species}-1)/\sqrt{(\text{number of individuals})}$ .

### *Species evenness indices*

Two samples containing the same number of species can differ in their species diversity. Community ecologists, following Pielou (1977) regard samples with a more equitable distribution of individuals among species as being more diverse. Hurlbert (1971) introduced statistics to measure the evenness component of Brillouin's  $H$ , called  $V$ , and Shannon's  $H'$ , called  $J'$ . An alternate measure of the evenness component for Brillouin's  $H$  is called  $E$ . If the individuals are equally distributed among  $S$  species, the maximum value for  $H'$  is  $\log(S)$ . Both  $V$  and  $J'$  range from 0 to 1. A sample containing just one species has an undefined evenness.

Simpson's diversity, known as Gini diversity in genetics, is often used as a species richness index, but it is very sensitive to species evenness. Simpson's diversity index has both biased and unbiased estimators. Smith and Grassle (1977) showed that the unbiased estimator for Simpson's diversity is one minus the Sanders-Hurlbert expected number of species at  $n=2$  ( $\text{Simpson's diversity} = E(S_2) - 1$ ). At such a low rarefaction sample size, Simpson's diversity and  $E(S_2)$  are influenced strongly by both species richness and evenness. As shown by Peet (1974) and Smith *et al.* (1979a), there is usually a very strong correlation ( $r > 0.95$ ) between Shannon's  $H'$  and  $E(S_{10})$ . This holds for the EMAP-E VP data, but does not hold for species-rich deep-sea communities. Hurlbert's  $E(S_n)$  index can be made less sensitive to species evenness component of diversity by increasing  $n$ , but there is no set rarefaction sample size  $n$  at which point  $E(S_n)$  can be regarded as a species richness index. In some deep-sea benthic samples,  $E(S_{40})$  is strongly correlated with  $J'$ , but not with any of the other indices regarded as species richness indices (*e.g.*,  $H$ ,  $H'$ , total species per sample, and log-series  $\alpha$ ).

It would be nice if there were an expected species evenness for a given community. Departures from this expected evenness might indicate disturbance. Caswell (1976) borrowed the Ewens infinite alleles model from population genetics to establish a 'null model' for the expected  $H'$ , given the number of individuals and species in a sample. The lack of fit to the Caswell neutral model is being used as an index of pollution, especially by Lamshead and co-workers in Great Britain. Goldman and Lamshead (1989) describe a program CASVAR.FOR which they use to fit Caswell's neutral model to benthic data. The Ewens infinite alleles model fits data to a log series, and the results of the neutral model tests are similar to that obtained by fitting the log-series to community structure data. May (1975) was the first to show that rarefaction curves generated from shallow-water data seem to conform to the expectations produced by the log-series (Fisher *et al.* 1943). An unfortunate consequence of applying the neutral model and fitting the log-series to benthic data is that highly impacted, species-poor, benthic communities often depart from the log-series and neutral model expectations in having too equitable a distribution of individuals among species. Warwick (1993)

tested the neutral model using data from a known pollution gradient and concluded that it was a poor predictor of benthic degradation. John Gray proposed that both undisturbed and highly impacted benthic communities should conform to the log-normal distribution. Gray and Mirza (1979) proposed that departures from the log-normal distribution of individuals among species could be used to assess transitions from one 'stable state' to another. Stenseth (1979) provided a mathematical model for Gray's empirical result. Lamshead *et al.* (1983) analyzed the distributions of individuals among species in a number of published benthic data sets, finding that they conformed neither to the log-normal (canonical or otherwise) or log-series. Hughes (1984, 1986) provides analyses and a model showing that the expected number of individuals among species in shallow-water benthic communities is even more inequitable than log-series expectations.

### ***Jackknifed diversity indices***

All diversity indices are biased to some extent. Bias corrections exist for  $H'$  (Peet 1974). This jackknife method can be applied to any diversity index. Smith and Grassle (1977) showed that  $E(S_n)$  is a minimum variance unbiased estimator of diversity, but only if the underlying populations are independently Poisson distributed. Heltshe and Forester (1985) present the jackknife bias correction and variance estimator for the Brillouin and  $H'$  diversity estimators. The lead author has adapted this jackknife bias correction for  $E(S_n)$  and programmed the algorithm in MATLAB. Organic enrichment often dramatically increases the number of benthic individuals in a sample. Using a strongly biased species richness index, such as 'Total species per event', greatly weakens the utility of diversity as an indicator of pollution effects.

### **Rarefaction, CNESS and Principal Components Analysis of Hypergeometric probabilities (PCA-H)**

The clear and concise description of benthic community structure is fundamental to the analysis of both basic and applied benthic ecological problems. We define community structure as "the variation and covariation of species abundances in time and space."

Sanders' (1968) rarefied species diversity, modified by Hurlbert as  $E(S_n)$ , and Grassle & Smith's (1976) faunal similarity index NESS are both based on the sample  $\times$  spp. matrix of hypergeometric probabilities ( $H$ ). These hypergeometric probabilities are simply the probability of sampling species  $k$  in sample  $i$  with a random draw of  $m$  individuals:

$$\begin{aligned}
 H_{ikm} &= 1 - \frac{\binom{Total_{i.} - x_{ik}}{m}}{\binom{Total_{i.}}{m}} \\
 &= 1 - \left[ \frac{\frac{(Total_{i.} - x_{ik})!}{m! * (TOTAL_{i.} - x_{ij} - m)!}}{\frac{Total_{i.}!}{m! * (TOTAL_{i.} - m)!}} \right] \quad (8)
 \end{aligned}$$

$Total_{i.}$  = the sample total.

$x_{ik}$  = the abundance of species  $k$  in sample  $i$ .

$m=NESSm$ =Number of individuals to be drawn at random.

!= a factorial.

Any sample by species matrix of counts can be converted quickly to a hypergeometric probability matrix  $H$ . In the original calculation of NESS and Hurlbert's  $E(S_n)$ , fractional abundances, that might arise from calculating the mean species abundances in replicate samples, were rounded to integers prior to the calculation of hypergeometric probabilities using factorials. However, this rounding is not a good idea. In all of The lead author's programs for calculating  $E(S_n)$ , NESS, NNESS, and CNESS, factorials are calculated using the natural log of the  $\Gamma$  (gamma) distribution since  $\Gamma(n+1)=n!$ . The  $\Gamma$  distribution is continuous, and since it does not require integer values,  $E(S_n)$ , NNESS, and CNESS can be calculated using non-integer data. The senior author provides FORTRAN and Matlab programs (with documentation) for calculating hypergeometric probabilities, Hurlbert's  $E(S_n)$ , NESS, and CNESS.

$E(S_n)$ , or the rarefied species diversity for sample  $i$  with a random draw of  $n$  individual is simply the row sum of the  $H$  matrix. It is defined as:

$$E(S_n) = \sum_{k=1}^S 1 - \frac{\binom{N-N_k}{n}}{\binom{N}{n}}.$$

where,  $n$  = random sample size.

$\binom{N}{n}$  = binomial coefficient.

(9)

= No. of ways to sample  $N$  objects,  $n$  at a time.

=  $\frac{N!}{(N-n)! * n!}$

$N$  = Total individuals in sample.

$N_k$  = Individuals of species  $k$ .

$S$  = Number of species.



Smith and Grassle (1977) determined that  $E(S_p)$  was a minimum variance unbiased estimator (MVUE) of diversity and presented equations to estimate the variance of  $E(S_p)$ .

### **NESS, NNESS, and CNESS**

The NESS faunal similarity index was described by Grassle and Smith (1976). Trueblood *et al.* (1994) correct a flaw in the original index, calling this new version NNESS. They also proposed a metric version of NNESS, called CNESS. The equations for NNESS and CNESS are shown below:

$$\begin{aligned} NNESS_{ijm} &= \frac{ESS_{ijm}}{\frac{1}{2} * (ESS_{iim} + ESS_{jjm})} \\ CNESS_{ijm} &= \sqrt{2 * \left( 1 - \frac{ESS_{ijm}}{\sqrt{ESS_{iim} * ESS_{jjm}}} \right)} \end{aligned} \quad (10)$$

NESS and CNESS are families of similarity and dissimilarity indices. NNESS at its upper and lower sample sizes converges to the Sorensen binary and Morisita similarity indices. NNESS at its upper and lower sample sizes converges to Sorensen's index and the Morisita-Horn similarity index. At a sample size of 1, CNESS is Orloci's (1978) chord distance. Kenkel and Orloci (1986) showed that the chord distance analyzed with non-metric multidimensional scaling (NMDS) was the best of eight procedures tested for recovering the patterns in complex simulated ecological data. No one has apparently described a binary similarity index corresponding to CNESS at  $m=\infty$ .

### **Principal Components Analysis of Hypergeometric Probabilities (PCA-H)**

There is a major advantage of CNESS over NNESS. While both indices have a straightforward geometric interpretation, CNESS is a metric but NNESS is only a semimetric. CNESS is the Pythagorean distance between the intersection of sample vectors, with positions determined by the  $H$  matrix, and the unit hypersphere. These intersection points with the unit hypersphere are calculated through a row normalization of the  $H$  (*i.e.*, the sum of squared elements in each row is 1). Because these distances are chords on the hypersphere, they are called chord distances. CNESS is the chord distance between sample vectors at a distance of one unit from the origin. These Pythagorean distances are calculated in  $S$ -dimensional ordination space, where  $S$  is the number of species. For samples containing more than 3 species, the human mind cannot perceive the distribution of samples in ordination space. We can perceive the distances among samples only in 2- or 3-dimensional displays.

Principal component analysis projects the major sources of variation in a complex swarm of points in  $S$ -dimensional space in fewer dimensions, often only 2 or 3. The first step in a principal components analysis of hypergeometric probabilities, called PCA-H here, is to row-normalize the  $H$  matrix so that the sum of the squared elements on each row is 1. This is the mathematical equivalent of projecting sample points onto the unit hypersphere. CNESS is the Pythagorean distance among sample points projected onto the hypersphere. Geometrically, these distances are the lengths of chords between points on the hypersphere, hence the name chord distance (reserved for  $CNESS_{ijm=1}$ ). This row-normalized  $H$  matrix is then centered by column, so that the mean of each column is 0. This new matrix, called  $XR$ , contains all of the information necessary to calculate CNESS, which is simply the

Pythagorean distance among samples with coordinates specified by the rows of **XR**. Principal components analysis identifies which linear combination of species is most important in determining the CNESS distances among samples. PCA creates a low-dimension projection of **XR** by transforming the original **S** axes to new axes, now called principal components, that are linear functions of the old. The number of principal components is the minimum of the number of samples or species in the original data. Pythagorean distances between samples plotted with respect to these new axes will be the same as those calculated with the original axes in **XR**. However, these new axes or principal components are derived so that the first axis represents the largest source of variation in CNESS distances among samples. The second and higher principal components reflect less important sources of variation in CNESS distances among samples, and are orthogonal to all previous ordination axes. These principal components are also normed so that the sum of the squared elements of each principal component equals 1. If **V** is the matrix of principal components, with the number of rows equal to number of species and the number of columns equal to the number of components, the first principal component is represented by the first column of the matrix,  $V(:,1)$ . Orthogonal and normal principal components (=orthonormal) implies that  $V(:,j)' * V(:,i) = 0 \forall i \neq j$  and  $V * V' = I$ , where **I** is the identity matrix. The positions of each sample in this new multidimensional space, defined by the principal components, are contained in the sample x principal component score matrix **Y**, which can be calculated by:  $Y = XR * V$ . The **Y** matrix of principal component scores is identical to that obtained by a principal coordinates analysis of the original CNESS matrix.

The relative amounts of variation explained by each principal component are provided by the sum of the squared principal component scores for each axis, divided by the sum of the squared coordinates for all samples in the original **XR** matrix. If an Eigenanalysis is used to calculate principal components, the percentage of variation explained by each component is the eigenvalue corresponding to that component divided by the sum of the eigenvalues for all components.

There are at least a dozen different algorithms to calculate the principal components of a given data set. These will be summarized in a later section on the matrix algebra of PCA-H. These algorithms can differ greatly in the amount of computer memory required, processing speed and numerical accuracy. The large size of the EMAP-E data set required using some non-standard, but still highly accurate, methods to calculate principal components.

PCA-H retains the information on species frequencies. A simple metric scaling or Principal Coordinates analysis or a Non-metric multidimensional scaling of CNESS distances does not retain the information on which species control contribute to differences in faunal composition among samples. Gabriel's (1971) graphical biplot can retrieve this species frequency data and show the relative importance of each species to the CNESS distances among samples. The biplot reveals those species that account for the major sources of variation in CNESS distances among samples. A graphical biplot of PCA-H results shows the relative CNESS distances among samples and the species that account for the distances. In the biplot, species are represented by vectors (arrows). The terminus for the arrows are the elements of **V**, which may be called the species loadings. Since the square of these coordinates for each axis sum to 1, the relative lengths of arrows in a 2-dimensional biplot shows the relative importance of each species in controlling the CNESS distances among samples. The sample positions in the first 2 principal components can be calculated using  $Y(:,1:2) = XR * V(:,1:2)$ . The longer a species' arrow, the more important that species is in controlling the position of samples in a two-dimensional display. The length and direction of the arrow away from the origin are important. The cosine of the angle with each axis is directly related to the principal component loading for that species on that axis. The relative species composition of a sample can be determined by projecting the sample points at right angles onto the longest species vectors. Digby and Kempton (1987) provide a clear description of the use of Gabriel (1971) graphical biplot. Note that the asymmetric display used

by Digby and Kempton, and in this report, is different from and preferable to that originally described by Gabriel.

Ter Braak (1983) came very close to describing the PCA-H method. In his discussion of the geometric relationship between faunal similarity and diversity, he stated that samples might be plotted according to their hypergeometric probabilities. The distances between samples  $i$  and  $j$  in his proposed ordination would be  $\sqrt{(ESS_i + ESS_j - 2ESS_{ij})}$ . This distance measure would have the unfortunate consequence of having no set upper limit and would be heavily dependent on the diversity of samples.

The full set of MATLAB programs needed to perform all PCA-H analyses in Trueblood *et al.* (1994) are now on the lead author's web page.

### ***Choosing the appropriate sample size, $m$***

The lead author developed a non-parametric procedure using Kendall's non-parametric rank order correlation coefficient ( $\tau$ =tau) to find a value for  $m$  that yielded a distance index that was highly correlated with both the  $CNESS_{m=1}$  and  $CNESS_{m=\text{large } n}$  matrices. This procedure is described in Trueblood *et al.* (1994), and the program that performs it (findcnm.m) is provided on the lead author's web page.

The largest sample size  $m$  for which NNESS or CNESS can be calculated is set by the minimum sample total in the data set. The original NESS algorithm was even more restrictive, with the largest  $m$  being half the minimum sample total. One can extend the range of  $m$  by transforming the  $H$  matrix to 1's and zeros (*i.e.*, the Boolean transform option in COMPAH) and then calculating the chord distance among samples. This procedure is equivalent to calculating CNESS at  $m=\infty$ .

The  $m$  size that is sensitive to both the rare and abundant species varies depending upon the distribution of individuals among species. For most soft-bottom benthic data,  $m=10-20$  is an appropriate sample size. Trueblood *et al.* (1994) found that  $m=15$  was appropriate for an intertidal benthic community. If the species distributions are heavily dominated by one or a few species, then  $m$  should be increased above 10. A NNESS value of 20-25 appears optimal for the EMAP-E data.

### ***Interpreting the graphical displays:***

#### **Graphical biplots**

The biplot produced by PCA-H is the asymmetrical Euclidean distances biplot. The plot presents a low-dimensional projection of the samples, representing the best least-squares fit of the original CNESS distances. For this reason, samples will always be less than  $\sqrt{2}$  units apart.

Species are plotted as vectors. The relative frequencies of a species in a sample can be estimated by projecting the sample orthogonally onto the appropriate species vector. Only one tail of the species vector is shown, but each species vector projects in the opposite direction as well. The origin represents the mean frequencies of a species in the normalized  $H$  matrix. The length of the species vectors indicates the importance of that species in that 2-dimensional projection.

Digby and Kempton (1987) provide a particularly clear explanation of how the Euclidean distance biplot method can be used to recover the basic structure of the original data matrix.

This biplot method is different from the dual display biplot in correspondence analysis (see Greenacre 1984). That biplot is a symmetric biplot in which both samples and species are plotted in scaled coordinates. In that display, the angles between samples and species vectors determine the association between a given species and sample.

The asymmetric Gabriel Euclidean distance biplot display should not be used to examine the statistical association among species (*i.e.*, the R-mode ordination). To analyze the association of species among samples, the species should be plotted in scaled coordinates such that the sum of the squared species coordinates in each dimension equals the eigenvalue for that dimension (Legendre and Legendre 1983). This scaling, called the covariance biplot, is performed using the MATLAB m.file *rmode.m*. Non-significant species vectors are not labeled. The data can also be clustered using the same similarity measure, the angle between species vectors. COMPAH can perform this clustering using the following steps:

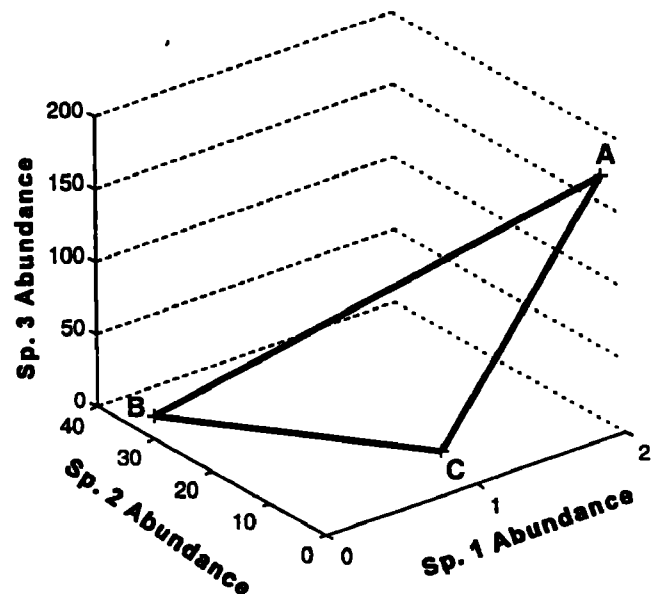
- 1) Calculate the hypergeometric probability matrix, **H**
- 2) Standardize the **H** matrix by station (the sum of squared **H** elements for each station will sum to 1)
- 3) Cluster using Pearson's *r* (the equivalent of clustering based on the angular cosines among species vectors in the r-mode plot)

Some applications of the Gabriel biplot method rescale the species vectors uniformly to aid in the projection of samples onto species vectors. As noted by Gower (1987), this is not a good idea. The endpoint of a species vector indicates the maximum value for a species. If a sample point is plotted at a greater distance than the tip of a species vector, then its position is determined by a combination of species.

### *The Geometry of Sanders-Hurlbert $E(S_n)$ and CNESS*

A simple 3-species, 3-sample data set is used to demonstrate the geometric interpretation of the Sanders-Hurlbert  $E(S_n)$  diversity index and CNESS. Both are related to distances among samples and the origin when sample points are plotted using the hypergeometric probability matrix **H**.

Figure 22 shows the position of three sample points, A-C, in a 3-dimensional space determined by the abundances of Species 1-3. The Euclidean distances among sample points in this species space is a very poor indicator of faunal similarity. One of the more troubling aspects of straight Euclidean distance is the 'double-zero' problem. Samples sharing no species will appear similar because they both have sample coordinates near the origin.



**Figure 23.** Three samples are plotted in species space. The Pythagorean distance among samples is a poor, unbounded, distance measure of faunal similarity. Note the greatly compressed vertical scale.

Plotting samples by the relative frequencies of species in samples (Figure 24) is an excellent basis for ordination. Using such a plot, ter Braak (1983) describes the geometric interpretation of faunal similarity and Gini-Simpson diversity index. Unfortunately, Euclidean distances among sample points determined solely by species frequencies are often very insensitive to the rarer species in a community.

Figure 25 shows the Sanders-Hurlbert rarefaction curves for the three samples. Sample C has the same three species as sample A but has greater evenness. Sample A is as species-rich as sample C, but the equitability among species frequencies is low.

There is a straightforward geometric interpretation of the rarefaction curves shown in Figure 25. The Sanders-Hurlbert  $E(S_n)$  is the City-Block distance (=Manhattan metric) from the origin to the sample point plotted using hypergeometric probabilities. This city block distance is shown in Figure 26.

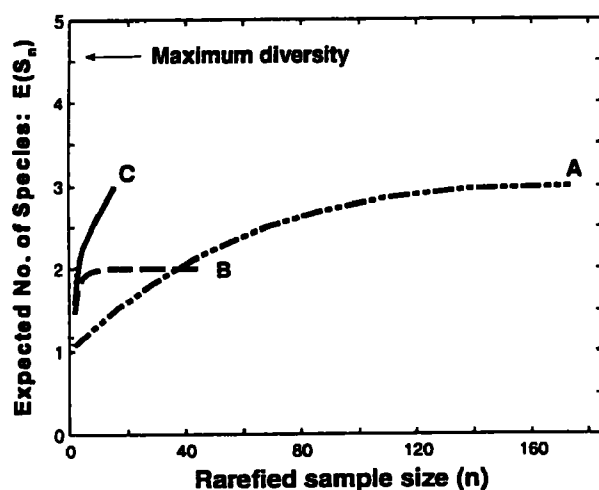


Figure 25. The Sanders-Hurlbert rarefaction curves for the three samples shown in the previous figures. While A and C have the same species richness (all 3 species), sample C has the greater evenness.

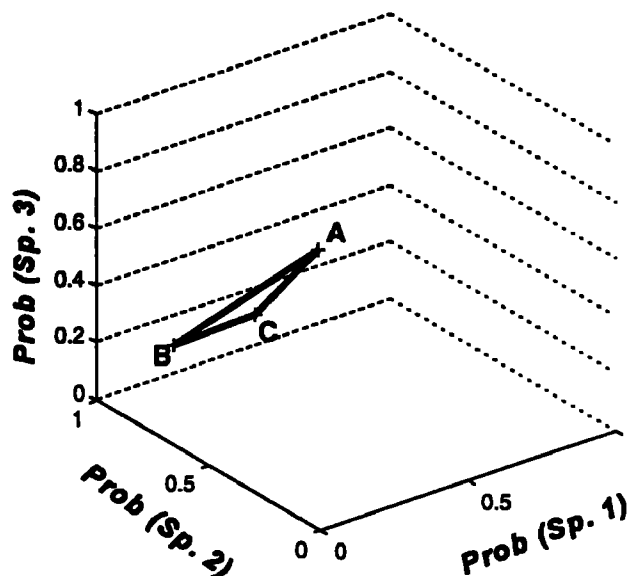


Figure 24. The same three stations can be plotted using the probability that they will be sampled with a random draw of 1, 2, or  $m$  individuals (the hypergeometric probabilities). The  $H(m=1)$  sample coordinates are shown.

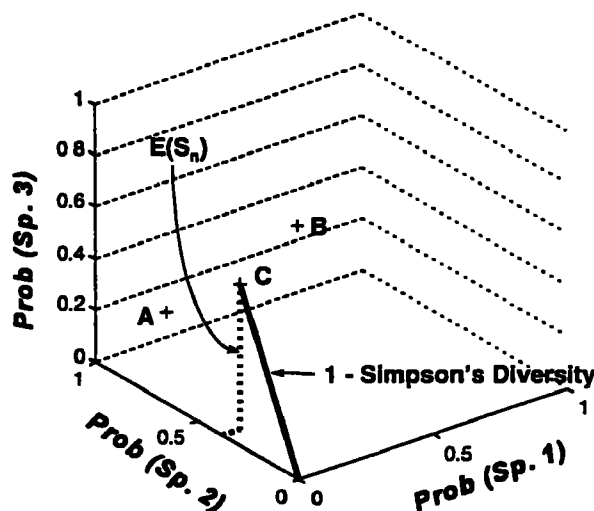


Figure 26. The Sanders-Hurlbert diversity from the previous picture is the city-block distance between the origin and the sample point, with points plotted using hypergeometric probabilities. The Euclidean distance to the origin is  $\sqrt{ESS_n}$ . At  $m=1$ , the distance between a sample point and the origin is Simpson's diversity; the closer to the origin, the higher the diversity (ter Braak 1983).

Figure 27 shows the position of sample points plotted using hypergeometric probabilities at  $\text{NESS}_m$  values from 1 to 40. Both the Pythagorean distance and city-block distance between the origin and sample points increases monotonically. The city block distance is  $E(S_n)$ , and it is this distance that is plotted in rarefaction curves (e.g., Figure 25). With increasing  $\text{NESS}_m$ , the probability of sampling at least one individual of the abundant taxa approaches 1.0. That is why both CNESS and NNESS become relatively insensitive to changes in the abundance of dominant species at large random sample sizes.

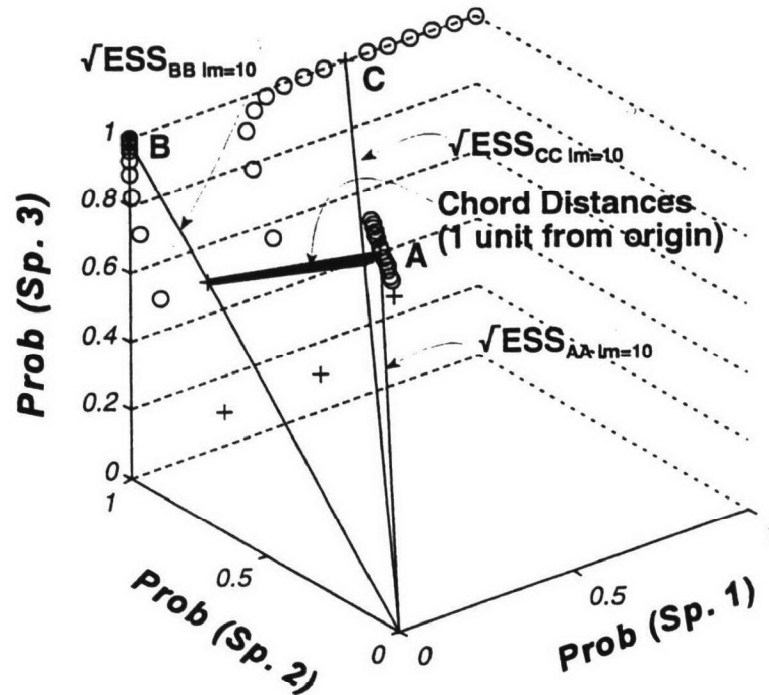


Figure 27.  $\text{CNESS}_{m=10}$  is the Euclidean distance between sample points 1 unit from the origin on the vectors connecting the origin and sample positions set with  $H_{m=10}$ . The original species frequencies are plotted as '+'s.

Figure 27 shows the chord distances among sample vectors at a distance one unit from the origin. These coordinates are from the row-normalized  $H$  matrix. The distances among these points are the CNESS faunal distances. These distances also serve as chords along the unit hypersphere and are also known as chord distances.

Figure 28 shows the same configuration of points as in Figure 27 after subtracting the mean value for each species (centering). Centering the normalized H matrix leaves the distances among points unaltered but rigidly translates the data points so that the centroid is at the origin. If the data are not centered prior to PCA, then the distances among stations are reflected in the second and higher PCA axes. The first PCA axis serves only to center the data.

Figure 29 shows the results of the metric scaling of the three sample points using  $NESS_m=1$  (identical to performing a Principal coordinates analysis of Orloci's chord distance or a PCA-H with  $NESS_m=1$ ) and  $NESS_m=10$ . A Procrustes rotation (Digby and Kempton 1987) was used to rigidly rotate the PCA-H ( $NESS_m=1$ ) ordination to fit the PCA-H ( $NESS_m=10$ ) ordination.

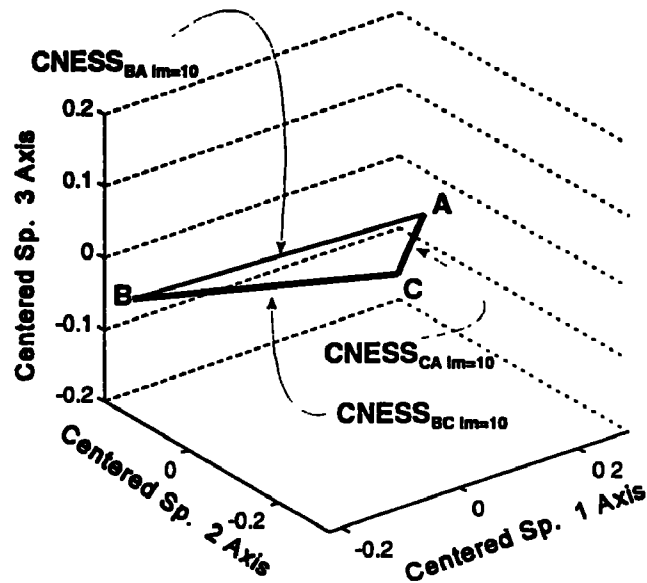


Figure 28. After centering the normalized data by species, the CNESS distances from the previous plot can be seen more clearly. Principal components analysis will show the planar projection of this 3-d configuration.

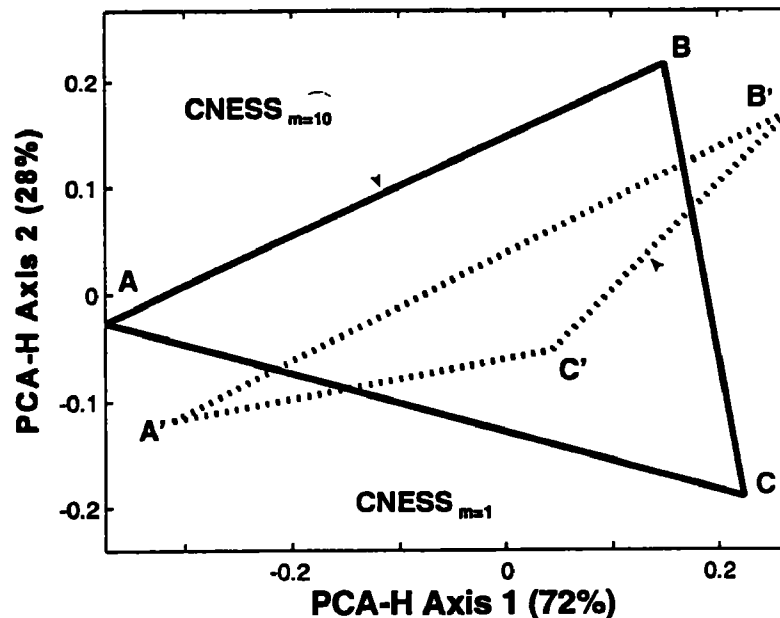
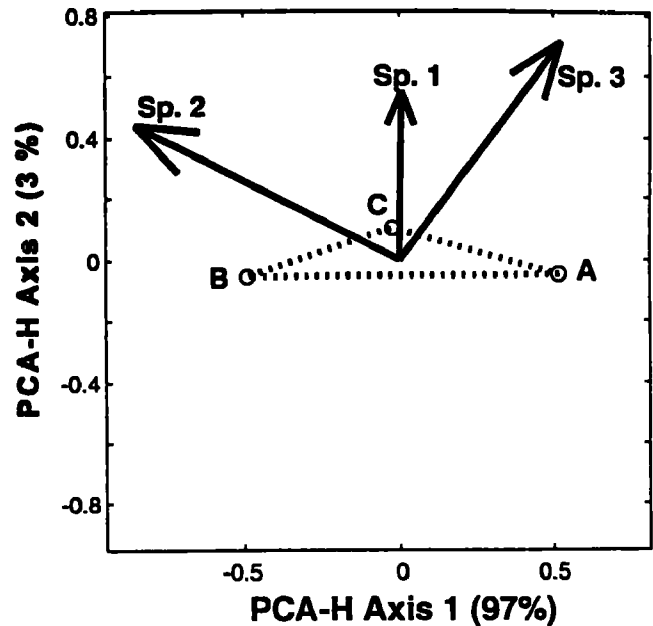


Figure 29. The CNESS distances among sample points at  $NESS_m=1$  (Orloci's chord distance) [dotted lines] and CNESS ( $NESS_m=10$ ) [solid lines]. These plots are identical to those produced using principal coordinates analysis of Orloci's chord distance (=PCA-H with  $NESS_m=1$ ).

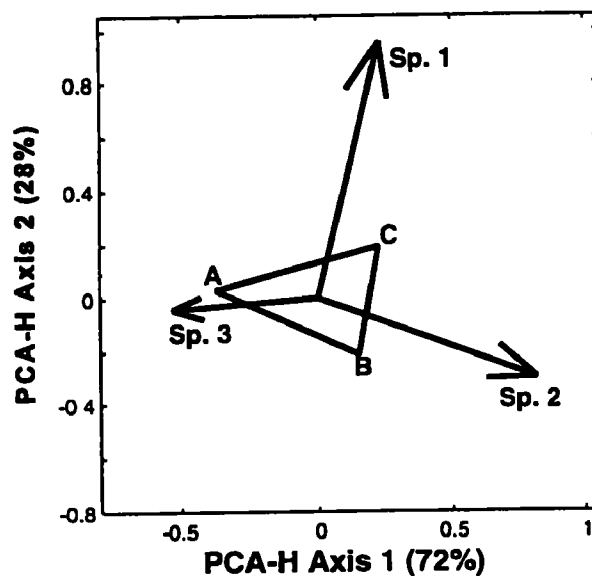
The Gabriel Euclidean distance biplots for the two metric scalings shown in Figure 29 are shown in Figures 30 and 31. Species 1, the rarest of the three species in the data contributes virtually nothing to the CNESS distances among samples (note that only 3% of the CNESS variation is expressed on the 2nd PCA-H axis).

With  $NESS_m=10$ , Species 1 becomes an important contributor to CNESS distances (Figure 31)

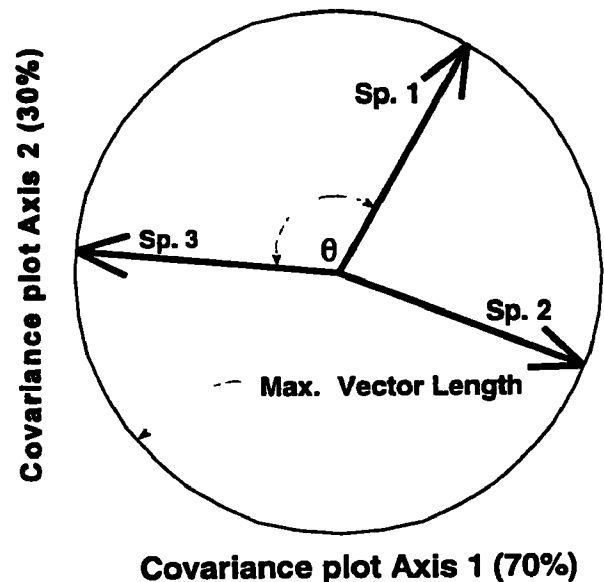
Figure 32 shows the Gabriel covariance plot of species vectors. The R-mode clustering of the normalized  $H$  matrix using Pearson's  $r$  is mathematically equivalent to clustering species using the cosine of the angles among species vectors in the covariance biplot.



**Figure 30.** The Gabriel Euclidean distance biplot showing the species contribution to CNESS distance at  $NESS_m=1$ . Species 1 contributes little to CNESS distance). Only 3% of the variation is on Axis 2.



**Figure 31.** The Gabriel Euclidean distance biplot for CNESS ( $m=10$ ). Species 1, the rarest species, now contributes much more to CNESS distances among samples and PCA-H axis 2 explains 28% of the variance in CNESS.



**Figure 32.** The covariance plot showing the inverse relationship between the frequencies of Species 2 and 3. The cosine of angles among species vectors can be clustered for an R-mode analysis (see Trueblood et al. 1994.)



## APPENDIX II TERMS AND DEFINITIONS

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**Arch Effect** (=Kendall's horseshoe) The horse-shoe like shape produced when coenocline data are analyzed using Q-mode ordination. The arch can be observed in most forms of PCA and non-metric multidimensional scaling. The arch has at least two and perhaps three causes and no clear-cut solutions other than plotting using the appropriate full dimensionality:

- (1) In principal coordinate analysis and non-metric multidimensional scaling, the similarity or dissimilarity values may "bottom out" so that samples sharing no species cannot be ranked. Williamson's step-across procedure has been proposed as a solution to this problem.
- (2) non-linearity in the data. Most Eigenanalysis procedures fit a linear, additive model to the data. If species abundances are not linearly related to each other, the arch phenomenon occurs.
- (3) Inherently, high-dimension data. For example, when the frequency of heterozygotes, homozygous recessive, and homozygous genotypes is analyzed by CA, a 2-dimensional arched structure is produced.

**Centered data** Data presented as deviations from their mean value.

**Centered SSCP matrix** In standard PCA, data are usually (but not always standardized by the mean (*i.e.*, centered). For Q-mode analysis, the mean of each species is usually subtracted from each species' cell. The centered SSCP matrix is the sum of squares and cross products matrix formed by multiplying the data matrix by its transpose.

**Correlation** A standardized form of covariance obtained by dividing the covariance of two variables by the product of the standard deviations of x and y.

**Covariance** a measure of association between 2 variables; covariance is the mean of the cross products of the centered data; expected value of the sum of cross products between 2 variables expressed as deviations from their respective mean. The covariance between z-transformed variables is also known as correlation.

**DPCA-H** Coats' (1995) term for detrended Principal components analysis of hypergeometric probabilities.

**Eigenanalysis** The process of finding the eigenvalue-eigenvector pairs of a square matrix **A**. The eigenvalues are the elements of the diagonal matrix **L** and the eigenvectors are the columns of **U** where  $A=U'LU$ .

**eigenvalues** (=characteristic values, latent values) a set of real or even imaginary scalars which can be used with their associated eigenvectors as an alternate description of a square matrix **A**. An  $N \times N$  matrix **A** is said to have an eigenvector **u** and corresponding eigenvalue  $\lambda$  if

$$A u = \lambda u.$$

Every square, full-rank matrix **A** can be decomposed into a product of the diagonal eigenvalue matrix **L** and eigenvector matrix **U** such that:  $A=U'LU$ , where **U'** is the transpose of the **U** matrix.

**eigenvectors** a column vector associated with its respective eigenvalue; Normalized eigenvectors of unit length (sum of squares of elements equal 1.0) are the principal components. **Right eigenvectors**  $u_R$  satisfy:

$$A u_R = \lambda u_R \quad (12)$$

where,  $\lambda$  is the eigenvalue associated with the eigenvector  $u$ , and  $A$  is a square matrix. **Left eigenvectors**  $u_L$  satisfy:

$$u_L A = \lambda u_L \quad (13)$$

Every left eigenvector is the transpose of a right eigenvector of the transpose of  $A$ . The left and right eigenvalues are identical.

**Graphical biplot** Legendre and Legendre (1983) review this technique, introduced by Gabriel (1971). Greenacre addresses the graphical biplot, or joint display in Correspondence analysis. There are 3 types of graphical biplots. In the first, the variable loadings for the R-mode PCA are normalized so that the sum of squares of loadings equal the eigenvalue for the axis. The site scores are normalized so that the sum of squared PCA scores on each is one. This is a **covariance biplot**. In this scaling, the angle between arrows of each pair of species, plotted as vectors provides an approximation of their pair-wise correlation, *i.e.*,  $r = \cos\theta$ . The orthogonal projection of sites onto species vectors indicates the rank order of sites with respect to that species.

In the second form of graphical biplot called the **Euclidean distance plot**, the eigenvectors (species loadings) are standardized to unit sums of squares and the site scores are standardized so that the sums of squares equals the eigenvalue of each axis (a normalized eigenvector times the vector of observations will produce site scores with a sum of squares =  $\lambda$ ). This plot is intended to preserve the Euclidean distances between sites and is called a **Euclidean distance plot**.

Greenacre (1984) calls both of these plots asymmetric, since the sites and variables are scaled differently. The third type of graphical biplot is the symmetric biplot where sites and variable vectors are scaled so that the sum of squared elements equals the eigenvalue.

**Loadings** The elements of the eigenvectors are also the weights or **loadings** of the various original descriptors. If the eigenvectors have been normalized to unit length (*i.e.*, the sum of the squared loadings for a variable across factors equals 1.0), then the elements of the eigenvector matrix (the loadings) are direction cosines of the angles between the original descriptors and the principal axes. So that if the element of the  $U$  vector (the loading for a variable) is .8944, the angle is  $\cos^{-1}(.8944) = \arccos(.8944) = 26^\circ$  (Legendre and Legendre 1983).

**normalization** A term often misused by environmental scientists. Normalization refers to the standardization of an  $n$ -dimensional vector to unit length (*i.e.*, a projection of a data point onto the unit hypersphere). The etymology of normalization is from *norm*, the length of a vector. There are an infinite number of eigenvectors associated with each eigenvalue. PCA and FA normalize these eigenvectors to either the unit length or the square of the eigenvalue.

**Ordination**     **Direct ordination** The process of arranging sites (or species) in relation to one or more environmental (or successional) gradients or to abstract axes representing such gradients.

**Indirect ordination** a collective term for continuous multivariate techniques which arrange objects (*e.g.*, sites or species) along axes, regardless of the interpretation of the axes.

Pielou (1984): Ordination is a procedure for adapting a multidimensional swarm of data points in such a way that when it is projected onto a two-space (*e.g.*, a sheet of paper) any intrinsic pattern the swarm may possess becomes apparent.

**orthogonal factors**     factors that are not correlated with each other.

**Orthogonal matrix**     A square matrix that when used as a transformation matrix, causes a rigid rotation of the data swarm without any change of scale. The product of an orthogonal matrix and its transpose is the identity matrix (Pielou, 1984, p. 253):  $A'A=AA'=I$ , where  $I$  is the identity matrix.

**PCA-H**     Principal component analysis of hypergeometric probabilities (Gallagher *et al.* 1992, Trueblood *et al.* 1994).

**principal component method**     Developed by Hotelling. PCA is simply the rotation of the original system of axes in the multidimensional space. The principal axes are orthogonal and the eigenvalues measure the amount of variance associated with each principal axis. PCA is used to summarize in a few important dimensions the greatest part of the variability of a dispersion matrix of a large number of descriptors (R mode) or cases (Q-mode).

**principal component scores**     the value of a principal component for individual points, hence the new coordinates of data points measured along axes created by the principal component method. A principal component score can be regarded as an additional variable for each case, this variable is a linear function of the original variables.

**principal coordinates analysis**     An ordination based on a metric similarity or dissimilarity matrix.

**Q-mode, R-mode**     Legendre & Legendre (1983, p. 172). The measurement of dependence between two descriptors (variables) is achieved by means of coefficients like Pearson's product-moment correlation,  $r$ . This type of study of the data matrix is therefore called an **R analysis**. In contrast, a study of an ecological data matrix based upon the relationship between objects is called **Q analysis**. Many authors (*e.g.*, Pielou 1984) reverse this conventional usage.

**SSCP**     the sum-of-squares-and-cross-products matrix. the matrix formed by multiplying a matrix times its transpose. The  $(i,i)$ th element is the sum of squares of the  $i$ th variable. The  $(h,i)$ th element is the sum of cross-products of the  $h$ 'th and  $i$ th variables.

**standardization-** an algebraic operation (e.g.,  $x_i/(\text{standard deviation of } x_i)$ ) performed on a variable or site vector to achieve a desired property (e.g., non-dimensionality, common variance). Standardization requires calculation of the row or column sums of a data matrix. Data measured on different scales must be standardized prior to analysis. Norm standardization is dividing each element by  $\sqrt{\sum (x_i)^2}$ . If the data have been previously centered, then dividing the centered variables by the norm is equivalent to dividing the original variable by the standard deviation.

**transformation** A transformation can be performed without knowledge of the row or column sums of a data matrix. A standardization requires such knowledge.

**variance** a measure of the dispersion of a variable; defined as the sum of squared deviations from the mean divided by the number of cases or entities.

## APPENDIX III FULL EMAP-E VIRGINIAN PROVINCE MODIFIED FAUNAL LIST

This appendix shows the full EMAP-E VP faunal list. It also shows which EMAP-E VP faunal groupings must be dropped and those that must be pooled to replicate the community structure analyses in this report.

EMAP-E VP SPECIES CODES					
VALID TAXA					
NO	CODE	GENUS SPP.	PHYLUM	CLASS	FAMILY
1	AMPHARCT	<i>Ampharete arctica</i>	Annelida	Polychaeta	Ampharetidae
2	ANOBGRAC	<i>Anobothrus gracilis</i>	Annelida	Polychaeta	Ampharetidae
3	ASABOCUL	<i>Asabellides oculata</i>	Annelida	Polychaeta	Ampharetidae
4	HOBFLOR	<i>Hobsonia florida</i>	Annelida	Polychaeta	Ampharetidae
5	MELIMACU	<i>Melinna maculata</i>	Annelida	Polychaeta	Ampharetidae
6	PSEUPAUC	<i>Pseudeurythoe paucibranchiata</i>	Annelida	Polychaeta	Amphinomidae
7	ARABSPEA	<i>Arabellidae sp. A Morris</i>	Annelida	Polychaeta	Arabellidae
8	DRILLONG	<i>Drilonereis longa</i>	Annelida	Polychaeta	Arabellidae
9	DRILSPEB	<i>Drilonereis sp. B Gardiner</i>	Annelida	Polychaeta	Arabellidae
10	NOTOSPIN	<i>Notocirrus spiniferus</i>	Annelida	Polychaeta	Arabellidae
11	AMASCAPE	<i>Amastigos caperatus</i>	Annelida	Polychaeta	Capitellidae
12	HETEFILI	<i>Heteromastus filiformis</i>	Annelida	Polychaeta	Capitellidae
13	MEDIAMBI	<i>Mediomastus ambiseta</i>	Annelida	Polychaeta	Capitellidae
14	MEDICALI	<i>Mediomastus californiensis</i>	Annelida	Polychaeta	Capitellidae
15	NOTOLOBA	<i>Notomastus lobatus</i>	Annelida	Polychaeta	Capitellidae
16	NOTOLURI	<i>Notomastus luridus</i>	Annelida	Polychaeta	Capitellidae
17	NOTOSPA	<i>Notomastus sp. A Ewing</i>	Annelida	Polychaeta	Capitellidae
18	CHAEVARI	<i>Chaetopterus varopedatus</i>	Annelida	Polychaeta	Chaetopteridae
19	SPIOCOST	<i>Spiochaetopterus costarum</i>	Annelida	Polychaeta	Chaetopteridae
20	BHAWHETE	<i>Bhawania heteroseta</i>	Annelida	Polychaeta	Chrysopetalidae
21	CAULBIOC	<i>Caulleriella cf. bioculata</i>	Annelida	Polychaeta	Cirratulidae
22	CAULSPEB	<i>Caulleriella sp. B Blake</i>	Annelida	Polychaeta	Cirratulidae
23	CIRRGRAN	<i>Cirriformia grandis</i>	Annelida	Polychaeta	Cirratulidae
24	THARACUT	<i>Tharyx acutus</i>	Annelida	Polychaeta	Cirratulidae
25	THARSPA	<i>Tharyx sp. A Morris</i>	Annelida	Polychaeta	Cirratulidae
26	COSSSOYE	<i>Cossura longocirrata</i>	Annelida	Polychaeta	Cossuridae
27	DORVRUDO	<i>Dorvillea rudolphi</i>	Annelida	Polychaeta	Dorvilleidae
28	DORVSPEA	<i>Dorvilleidae sp. A Hilbig</i>	Annelida	Polychaeta	Dorvilleidae
29	MEIOSPEA	<i>Meiodorvillea sp. A Morris</i>	Annelida	Polychaeta	Dorvilleidae
30	PAROCAEC	<i>Parougia caeca</i>	Annelida	Polychaeta	Dorvilleidae
31	PROTKEFE	<i>Protodorvillea kefersteini</i>	Annelida	Polychaeta	Dorvilleidae
32	MARPBELL	<i>Marphysa belli</i>	Annelida	Polychaeta	Eunicidae
33	MARPSANG	<i>Marphysa sanguinea</i>	Annelida	Polychaeta	Eunicidae
34	BRADVILL	<i>Brada villosa</i>	Annelida	Polychaeta	Flabelligeridae

NO	CODE	GENUS SPP.	PHYLUM	CLASS	FAMILY
35	PERAFFI	<i>Pherusa affinis</i>	Annelida	Polychaeta	Flabelligendae
36	GLYCAME	<i>Glycera americana</i>	Annelida	Polychaeta	Glyceridae
37	GLYCDIBR	<i>Glycera dibranchiata</i>	Annelida	Polychaeta	Glyceridae
38	GLYCROBU	<i>Glycera robusta</i>	Annelida	Polychaeta	Glyceridae
39	HEMIROSE	<i>Hemipodus roseus</i>	Annelida	Polychaeta	Glyceridae
40	GLYCSOLI	<i>Glycinde solitaria</i>	Annelida	Polychaeta	Goniadidae
41	GONIGRAC	<i>Goniadella gracilis</i>	Annelida	Polychaeta	Goniadidae
42	OPHIGIGA	<i>Ophioglycera gigantea</i>	Annelida	Polychaeta	Goniadidae
43	GYPTVITT	<i>Gyptis crypta</i>	Annelida	Polychaeta	Hesionidae
44	MICRABER	<i>Microphthalmus aberrans</i>	Annelida	Polychaeta	Hesionidae
45	MICRFRAG	<i>Microphthalmus fragilis</i>	Annelida	Polychaeta	Hesionidae
46	MICRSCZE	<i>Microphthalmus sczelkowi</i>	Annelida	Polychaeta	Hesionidae
47	MICRSIMI	<i>Microphthalmus similis</i>	Annelida	Polychaeta	Hesionidae
48	PARALUTE	<i>Parahesionia luteola</i>	Annelida	Polychaeta	Hesionidae
49	PODAOBSC	<i>Podarke obscura</i>	Annelida	Polychaeta	Hesionidae
50	PODALEVI	<i>Podarkeopsis levifuscina</i>	Annelida	Polychaeta	Hesionidae
51	NINONIGR	<i>Ninoe nigripes</i>	Annelida	Polychaeta	Lumbrineridae
52	LUMBACIC	<i>Scoletoma acicularum</i>	Annelida	Polychaeta	Lumbrineridae
53	SCOLHEBE	<i>Scoletoma hebes</i>	Annelida	Polychaeta	Lumbrineridae
54	LUMBTENI	<i>Scoletoma tenuis</i>	Annelida	Polychaeta	Lumbrineridae
55	CLYMTORQ	<i>Clymenella torquata</i>	Annelida	Polychaeta	Maldanidae
56	MACRZONA	<i>Macroclymene zonalis</i>	Annelida	Polychaeta	Maldanidae
57	SABAELO	<i>Sabaco elongatus</i>	Annelida	Polychaeta	Maldanidae
58	AGLACIRC	<i>Aglaophamus circinata</i>	Annelida	Polychaeta	Nephtyidae
59	AGLAVERR	<i>Aglaophamus verrilli</i>	Annelida	Polychaeta	Nephtyidae
60	NEPHBUCE	<i>Nephtys buce</i>	Annelida	Polychaeta	Nephtyidae
61	NEPHCRYP	<i>Nephtys cryptomma</i>	Annelida	Polychaeta	Nephtyidae
62	NEPHINCI	<i>Nephtys incisa</i>	Annelida	Polychaeta	Nephtyidae
63	NEPHPICT	<i>Nephtys picta</i>	Annelida	Polychaeta	Nephtyidae
64	CERAIIRI	<i>Ceratonereis irritabilis</i>	Annelida	Polychaeta	Nereididae
65	LAEOCULV	<i>Laeonereis culveri</i>	Annelida	Polychaeta	Nereididae
66	NEANAREN	<i>Neanthes arenaceodentata</i>	Annelida	Polychaeta	Nereididae
67	NEANSUCC	<i>Neanthes succinea</i>	Annelida	Polychaeta	Nereididae
68	NEANVIRE	<i>Neanthes virens</i>	Annelida	Polychaeta	Nereididae
69	NEREGRAY	<i>Nereis gravi</i>	Annelida	Polychaeta	Nereididae
70	PLATDUME	<i>Platynereis dumerilii</i>	Annelida	Polychaeta	Nereididae
71	DIOPCUPR	<i>Diopatra cuprea</i>	Annelida	Polychaeta	Onuphidae
72	ONUUPERM	<i>Onuphis eremita</i>	Annelida	Polychaeta	Onuphidae
73	OPHEBICO	<i>Ophelia bicornis</i>	Annelida	Polychaeta	Opheliidae
74	OPHEACUM	<i>Ophelia acuminata</i>	Annelida	Polychaeta	Opheliidae
75	TRAVSPEA	<i>Travisia sp. A Morris</i>	Annelida	Polychaeta	Opheliidae
76	TRAVSPEB	<i>Travisia sp. B Morris</i>	Annelida	Polychaeta	Opheliidae
77	LEITFRAG	<i>Leitoscoloplos fragilis</i>	Annelida	Polychaeta	Orbinidae
78	LEITROBU	<i>Leitoscoloplos robustus</i>	Annelida	Polychaeta	Orbinidae
79	ORBIRISE	<i>Orbinia riseri</i>	Annelida	Polychaeta	Orbinidae
80	ORBISWAN	<i>Orbinia swani</i>	Annelida	Polychaeta	Orbinidae
81	SCOLCAPE	<i>Scoloplos capensis</i>	Annelida	Polychaeta	Orbinidae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
82	SCOLRUBR	<i>Scoloplos rubra</i>	Annelida	Polychaeta	Orbiniidae
83	MYRIOCUL	<i>Galathowenia oculata</i>	Annelida	Polychaeta	Oweniidae
84	OWENFUSI	<i>Owenia fusiformis</i>	Annelida	Polychaeta	Oweniidae
85	ARICCATH	<i>Aricidea catherinae</i>	Annelida	Polychaeta	Paraonidae
86	ARICCERU	<i>Aricidea cerruti</i>	Annelida	Polychaeta	Paraonidae
87	ARICFRAG	<i>Aricidea fragilis</i>	Annelida	Polychaeta	Paraonidae
88	ARICWASS	<i>Aricidea wassi</i>	Annelida	Polychaeta	Paraonidae
89	CIRRSPEA	<i>Cirrophorus sp. A Morris</i>	Annelida	Polychaeta	Paraonidae
90	CIRROSPB	<i>Cirrophorus sp. B Morris</i>	Annelida	Polychaeta	Paraonidae
91	LEVIGRAC	<i>Levinsenia gracilis</i>	Annelida	Polychaeta	Paraonidae
92	LEVISPEA	<i>Levinsenia sp. A Morris</i>	Annelida	Polychaeta	Paraonidae
93	PARADSPB	<i>Paradonets sp. B Morris</i>	Annelida	Polychaeta	Paraonidae
94	PARAFULG	<i>Paraonis fulgens</i>	Annelida	Polychaeta	Paraonidae
95	PARAPYGO	<i>Paraonis pygoentomatica</i>	Annelida	Polychaeta	Paraonidae
96	PECTGOUL	<i>Pectinaria gouldii</i>	Annelida	Polychaeta	Pectinariidae
97	EUMISANG	<i>Eumida sanguinea</i>	Annelida	Polychaeta	Phyllodocidae
98	HESIELON	<i>Hesionura elongata</i>	Annelida	Polychaeta	Phyllodocidae
99	ETEOFOLI	<i>Hypereteone foliosa</i>	Annelida	Polychaeta	Phyllodocidae
100	ETEOHETE	<i>Hypereteone heteropoda</i>	Annelida	Polychaeta	Phyllodocidae
101	HYPELONG	<i>Hypereteone longa</i>	Annelida	Polychaeta	Phyllodocidae
102	PARASPEC	<i>Paranaitis speciosa</i>	Annelida	Polychaeta	Phyllodocidae
103	PHYLAREN	<i>Phyllodoce arenae</i>	Annelida	Polychaeta	Phyllodocidae
104	PHYLMACU	<i>Phyllodoce maculata</i>	Annelida	Polychaeta	Phyllodocidae
105	PHYLMUCO	<i>Phyllodoce mucosa</i>	Annelida	Polychaeta	Phyllodocidae
106	ANCIHART	<i>Ancistrosyllis hartmanae</i>	Annelida	Polychaeta	Pilargidae
107	ANCIJONE	<i>Ancistrosyllis jonesi</i>	Annelida	Polychaeta	Pilargidae
108	CABIINCE	<i>Cabira incerta</i>	Annelida	Polychaeta	Pilargidae
109	SIGABASS	<i>Sigambra bassi</i>	Annelida	Polychaeta	Pilargidae
110	SIGATENT	<i>Sigambra tentaculata</i>	Annelida	Polychaeta	Pilargidae
111	PISIREMO	<i>Pisone remota</i>	Annelida	Polychaeta	Pisionidae
112	HARMEXTE	<i>Harmothoe extenuata</i>	Annelida	Polychaeta	Polynoidae
113	HARMIMBR	<i>Harmothoe imbricata</i>	Annelida	Polychaeta	Polynoidae
114	HARMMACG	<i>Harmothoe macginitiei</i>	Annelida	Polychaeta	Polynoidae
115	HARTMOOR	<i>Hartmania moorei</i>	Annelida	Polychaeta	Polynoidae
116	LEPICOMM	<i>Lepidametria commensalis</i>	Annelida	Polychaeta	Polynoidae
117	LEPISQUA	<i>Lepidonotus squamatus</i>	Annelida	Polychaeta	Polynoidae
118	LEPISUBL	<i>Lepidonotus sublevis</i>	Annelida	Polychaeta	Polynoidae
119	LEPIVARI	<i>Lepidonotus variabilis</i>	Annelida	Polychaeta	Polynoidae
120	MALMSPA	<i>Malmgreniella sp. A Weston</i>	Annelida	Polychaeta	Polynoidae
121	MALMSPEB	<i>Malmgreniella sp. B Weston</i>	Annelida	Polychaeta	Polynoidae
122	PROTCHAE	<i>Protodriloides chaetifer</i>	Annelida	Polychaeta	Protodrilidae
123	SABEVULG	<i>Sabellaria vulgaris</i>	Annelida	Polychaeta	Sabellariidae
124	CHONINFU	<i>Chone infundibuliformis</i>	Annelida	Polychaeta	Sabellidae
125	DEMOMICR	<i>Demonax microphthalmus</i>	Annelida	Polychaeta	Sabellidae
126	EUCHELEG	<i>Euchone elegans</i>	Annelida	Polychaeta	Sabellidae
127	EUCHINCO	<i>Euchone incolor</i>	Annelida	Polychaeta	Sabellidae

NO	CODE	GENUS SPP.	PHYLUM	CLASS	FAMILY
128	LAONKROY	<i>Laonome kroeyeri</i>	Annelida	Polychaeta	Sabellidae
129	MANAAEST	<i>Manayunkia aestuarina</i>	Annelida	Polychaeta	Sabellidae
130	MYXIINFU	<i>Myxicola infundibulum</i>	Annelida	Polychaeta	Sabellidae
131	PSEURENI	<i>Pseudopotamilla reniformis</i>	Annelida	Polychaeta	Sabellidae
132	SCALINFL	<i>Scalibregma inflatum</i>	Annelida	Polychaeta	Scalibregmatidae
133	PHOLMINU	<i>Pholoe minuta</i>	Annelida	Polychaeta	Sigalionidae
134	SIGAAREN	<i>Sigalion arenicola</i>	Annelida	Polychaeta	Sigalionidae
135	STENBOA	<i>Sthenelais boa</i>	Annelida	Polychaeta	Sigalionidae
136	STHELIMI	<i>Sthenelais limicola</i>	Annelida	Polychaeta	Sigalionidae
137	AOPPYGM	<i>Aopronospio pygmaea</i>	Annelida	Polychaeta	Spionidae
138	BOCLHAMA	<i>Boccardiella hamata</i>	Annelida	Polychaeta	Spionidae
139	BOCCLIGE	<i>Boccardiella ligerica</i>	Annelida	Polychaeta	Spionidae
140	CARAHOB	<i>Carazziella hobsonae</i>	Annelida	Polychaeta	Spionidae
141	DISPUNCI	<i>Dispio uncinata</i>	Annelida	Polychaeta	Spionidae
142	MAREVIRI	<i>Marenzelleria viridis</i>	Annelida	Polychaeta	Spionidae
143	PARAPINN	<i>Paraprionospio pinnata</i>	Annelida	Polychaeta	Spionidae
144	POLYAGGR	<i>Polydora aggregata</i>	Annelida	Polychaeta	Spionidae
145	POLYCAUL	<i>Polydora caulleryi</i>	Annelida	Polychaeta	Spionidae
146	POLYCORN	<i>Polydora cornuta</i>	Annelida	Polychaeta	Spionidae
147	POLYGIAR	<i>Polydora giardi</i>	Annelida	Polychaeta	Spionidae
148	POLYQUAD	<i>Polydora quadrilobata</i>	Annelida	Polychaeta	Spionidae
149	POLYSOCI	<i>Polydora socialis</i>	Annelida	Polychaeta	Spionidae
150	POLYWEBS	<i>Polydora websteri</i>	Annelida	Polychaeta	Spionidae
151	PRIOHETE	<i>Prionospio heterobranchia</i>	Annelida	Polychaeta	Spionidae
152	PRIOPERK	<i>Prionospio perkinsi</i>	Annelida	Polychaeta	Spionidae
153	PRIOSTEE	<i>Prionospio steenstrupi</i>	Annelida	Polychaeta	Spionidae
154	PYGOELEG	<i>Pygospio elegans</i>	Annelida	Polychaeta	Spionidae
155	SCOLBOUS	<i>Scolecopsis bousfieldi</i>	Annelida	Polychaeta	Spionidae
156	SCOLQUAD	<i>Scolecopsis quadrilobata</i>	Annelida	Polychaeta	Spionidae
157	SCOLSQUA	<i>Scolecopsis squamata</i>	Annelida	Polychaeta	Spionidae
158	SCOLTEXA	<i>Scolecopsis texana</i>	Annelida	Polychaeta	Spionidae
159	SPIOFILI	<i>Spio filicornis</i>	Annelida	Polychaeta	Spionidae
160	SPIOLIMI	<i>Spio limicola</i>	Annelida	Polychaeta	Spionidae
161	SPIOSETO	<i>Spio setosa</i>	Annelida	Polychaeta	Spionidae
162	SPIOBOMB	<i>Spiophanes bombyx</i>	Annelida	Polychaeta	Spionidae
163	STREBENE	<i>Streblospio benedicti</i>	Annelida	Polychaeta	Spionidae
164	STERSCUT	<i>Sternaspis scutatus</i>	Annelida	Polychaeta	Sternaspididae
165	AUTOSPEA	<i>Autolytus sp. A Glasby</i>	Annelida	Polychaeta	Syllidae
166	BRANWELL	<i>Brania wellfleetensis</i>	Annelida	Polychaeta	Syllidae
167	EXOGLISP	<i>Exogone dispar</i>	Annelida	Polychaeta	Syllidae
168	EXOGHEBE	<i>Exogone hebes</i>	Annelida	Polychaeta	Syllidae
169	EXOGSPEA	<i>Exogone sp. A Glasby</i>	Annelida	Polychaeta	Syllidae
170	EXOGVERU	<i>Exogone verugera</i>	Annelida	Polychaeta	Syllidae
171	ODONFULG	<i>Odontosyllis fulgurans</i>	Annelida	Polychaeta	Syllidae
172	PARALONG	<i>Parapionosyllis longicirrata</i>	Annelida	Polychaeta	Syllidae
173	PIONSPEA	<i>Pionosyllis sp. A Glasby</i>	Annelida	Polychaeta	Syllidae
174	PIONSPEB	<i>Pionosyllis sp. B Glasby</i>	Annelida	Polychaeta	Syllidae



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175	PROCCORN	<i>Proceraea cornuta</i>	Annelida	Polychaeta	Syllidae
176	SPHAACIC	<i>Sphaerosyllis aciculata</i>	Annelida	Polychaeta	Syllidae
177	SPHATAYL	<i>Sphaerosyllis taylori</i>	Annelida	Polychaeta	Syllidae
178	STREAREN	<i>Streptosyllis arenae</i>	Annelida	Polychaeta	Syllidae
179	STREPETT	<i>Streptosyllis pettiboneae</i>	Annelida	Polychaeta	Syllidae
180	STREVARI	<i>Streptosyllis varians</i>	Annelida	Polychaeta	Syllidae
181	SYLLCONV	<i>Syllides convoluta</i>	Annelida	Polychaeta	Syllidae
182	SYLLVERR	<i>Syllides verrilli</i>	Annelida	Polychaeta	Syllidae
183	AMPHORNA	<i>Amphitrite ornata</i>	Annelida	Polychaeta	Terebellidae
184	ENOPSANG	<i>Enoplobranchus sanguineus</i>	Annelida	Polychaeta	Terebellidae
185	LOIMMEDU	<i>Loimia medusa</i>	Annelida	Polychaeta	Terebellidae
186	NICOZOST	<i>Nicolea zostericola</i>	Annelida	Polychaeta	Terebellidae
187	PISTCRIS	<i>Pista cristata</i>	Annelida	Polychaeta	Terebellidae
188	PISTPALM	<i>Pista palmata</i>	Annelida	Polychaeta	Terebellidae
189	POLYHAEM	<i>Polycirrus cf. haematodes</i>	Annelida	Polychaeta	Terebellidae
190	POLYEXIM	<i>Polycirrus eximius</i>	Annelida	Polychaeta	Terebellidae
191	POLYMEDU	<i>Polycirrus medusa</i>	Annelida	Polychaeta	Terebellidae
192	TERESTRO	<i>Terebellides stroemi</i>	Annelida	Polychaeta	Trichobranchidae
193	TROCMULT	<i>Trochochaeta multisetosa</i>	Annelida	Polychaeta	Trochochaetidae
194	POLYSPEA	<i>Polychaeta sp. A Arcuri</i>	Annelida	Polychaeta	Unidentified
195	POLYSPEB	<i>Polychaeta sp. B Arcuri</i>	Annelida	Polychaeta	Unidentified
196	AMPEAGAS	<i>Ampelisca agassizi</i>	Arthropoda	Amphipoda	Ampeliscidae
197	AMPEVERR	<i>Ampelisca verrilli</i>	Arthropoda	Amphipoda	Ampeliscidae
198	BYBLSERR	<i>Byblis serrata</i>	Arthropoda	Amphipoda	Ampeliscidae
199	AMPILONG	<i>Amphithoe longimana</i>	Arthropoda	Amphipoda	Ampithoidae
200	AMPIVALI	<i>Amphithoe valida</i>	Arthropoda	Amphipoda	Ampithoidae
201	CYMACOMP	<i>Cymadusa compta</i>	Arthropoda	Amphipoda	Ampithoidae
202	LEMBSMIT	<i>Lembos smithi</i>	Arthropoda	Amphipoda	Aoridae
203	LEMBWEBS	<i>Lembos websteri</i>	Arthropoda	Amphipoda	Aoridae
204	LEPTPING	<i>Leptocheirus pinguis</i>	Arthropoda	Amphipoda	Aoridae
205	LEPTPLUM	<i>Leptocheirus plumulosus</i>	Arthropoda	Amphipoda	Aoridae
206	MICRANOM	<i>Microdeutopus anomalus</i>	Arthropoda	Amphipoda	Aoridae
207	MICRGRYL	<i>Microdeutopus gryllotalpa</i>	Arthropoda	Amphipoda	Aoridae
208	PSEUOBLI	<i>Pseudunciola obliqua</i>	Arthropoda	Amphipoda	Aoridae
209	RUDINAGL	<i>Rudilemboides naglei</i>	Arthropoda	Amphipoda	Aoridae
210	UNCIDISS	<i>Unciola dissimilis</i>	Arthropoda	Amphipoda	Aoridae
211	UNCIINER	<i>Unciola inermis</i>	Arthropoda	Amphipoda	Aoridae
212	UNCIRRO	<i>Unciola irrorata</i>	Arthropoda	Amphipoda	Aoridae
213	UNCISERR	<i>Unciola serrata</i>	Arthropoda	Amphipoda	Aoridae
214	ARIGHAMA	<i>Argissa hamatipes</i>	Arthropoda	Amphipoda	Argissidae
215	BATECATH	<i>Batea catharinensis</i>	Arthropoda	Amphipoda	Bateridae
216	CALLLAEV	<i>Calliopius laevisculus</i>	Arthropoda	Amphipoda	Calliopidae
217	COROACHE	<i>Corophium acherusicum</i>	Arthropoda	Amphipoda	Corophiidae
218	COROACUT	<i>Corophium acutum</i>	Arthropoda	Amphipoda	Corophiidae
219	COROBONN	<i>Corophium bonellii</i>	Arthropoda	Amphipoda	Corophiidae
220	COROCRAS	<i>Corophium crassicorne</i>	Arthropoda	Amphipoda	Corophiidae
221	COROINSI	<i>Corophium insidiosum</i>	Arthropoda	Amphipoda	Corophiidae

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222	COROLACU	<i>Corophium lacustre</i>	Arthropoda	Amphipoda	Corophiidae
223	COROSEXT	<i>Corophium sextoni</i>	Arthropoda	Amphipoda	Corophiidae
224	COROSIMI	<i>Corophium simile</i>	Arthropoda	Amphipoda	Corophiidae
225	COROTUBE	<i>Corophium tuberculatum</i>	Arthropoda	Amphipoda	Corophiidae
226	DEXATHEC	<i>Dexamine thea</i>	Arthropoda	Amphipoda	Dexaminidae
227	GAMMANNU	<i>Gammarus annulatus</i>	Arthropoda	Amphipoda	Gammaridae
228	GAMMDAIB	<i>Gammarus daiberi</i>	Arthropoda	Amphipoda	Gammaridae
229	GAMMFASC	<i>Gammarus fasciatus</i>	Arthropoda	Amphipoda	Gammaridae
230	GAMMOCEA	<i>Gammarus oceanicus</i>	Arthropoda	Amphipoda	Gammaridae
231	MUCRMUCR	<i>Mucrogammarus mucronatus</i>	Arthropoda	Amphipoda	Gammaridae
232	ACANMILL	<i>Acanthohaustorius millsi</i>	Arthropoda	Amphipoda	Haustoriidae
233	ACANSIMI	<i>Acanthohaustorius similis</i>	Arthropoda	Amphipoda	Haustoriidae
234	BATHPARK	<i>Bathyporeia parkeri</i>	Arthropoda	Amphipoda	Haustoriidae
235	LEPIDYTI	<i>Lepidactylus dytiscus</i>	Arthropoda	Amphipoda	Haustoriidae
236	PARAATTE	<i>Parahaustorius attenuatus</i>	Arthropoda	Amphipoda	Haustoriidae
237	PARAHOLM	<i>Parahaustorius holmesi</i>	Arthropoda	Amphipoda	Haustoriidae
238	PARALNGI	<i>Parahaustorius longimerus</i>	Arthropoda	Amphipoda	Haustoriidae
239	PROTDEIC	<i>Protohaustorius cf deichmannae</i>	Arthropoda	Amphipoda	Haustoriidae
240	PROTWIGL	<i>Protohaustorius wigleyi</i>	Arthropoda	Amphipoda	Haustoriidae
241	PSEUBORE	<i>Pseudohaustorius borealis</i>	Arthropoda	Amphipoda	Haustoriidae
242	PSEUCARO	<i>Pseudohaustorius caroliniensis</i>	Arthropoda	Amphipoda	Haustoriidae
243	GAMMSUTH	<i>Gammaropsis sutherlandi</i>	Arthropoda	Amphipoda	Isacidae
244	MICRRANE	<i>Microtopotus ranevi</i>	Arthropoda	Amphipoda	Isacidae
245	PHOTDENT	<i>Photis dentata</i>	Arthropoda	Amphipoda	Isacidae
246	PHOTPOLL	<i>Photis pollex</i>	Arthropoda	Amphipoda	Isacidae
247	PHOTPUGN	<i>Photis pugnator</i>	Arthropoda	Amphipoda	Isacidae
248	CERATUBU	<i>Cerapus tubularis</i>	Arthropoda	Amphipoda	Ischyroceridae
249	ERICBRAS	<i>Erichthonius brasiliensis</i>	Arthropoda	Amphipoda	Ischyroceridae
250	ERICFASC	<i>Erichthonius fasciatus</i>	Arthropoda	Amphipoda	Ischyroceridae
251	ISCHANGU	<i>Ischyrocerus anguipes</i>	Arthropoda	Amphipoda	Ischyroceridae
252	JASSMARM	<i>Jassa marmorata</i>	Arthropoda	Amphipoda	Ischyroceridae
253	LISTBARN	<i>Listriella barnardi</i>	Arthropoda	Amphipoda	Liljeborgiidae
254	LISTCLYM	<i>Listriella clymenellae</i>	Arthropoda	Amphipoda	Liljeborgiidae
255	LISTSMIT	<i>Listriella smithi</i>	Arthropoda	Amphipoda	Liljeborgiidae
256	ANONLILJ	<i>Anonyx liljeborgi</i>	Arthropoda	Amphipoda	Lysianassidae
257	HIPPSERR	<i>Hippomedon serratus</i>	Arthropoda	Amphipoda	Lysianassidae
258	LYSIALBA	<i>Lysianopsis alba</i>	Arthropoda	Amphipoda	Lysianassidae
259	ORCHMINU	<i>Orchomenella minuta</i>	Arthropoda	Amphipoda	Lysianassidae
260	DULIAPPE	<i>Dulichella appendiculata</i>	Arthropoda	Amphipoda	Melitidae
261	ELASLAEV	<i>Elasmopus laevis</i>	Arthropoda	Amphipoda	Melitidae
262	MELINTTI	<i>Melita nitida</i>	Arthropoda	Amphipoda	Melitidae
263	MONOSPEI	<i>Monoculodes sp. 1</i> <i>Waiting</i>	Arthropoda	Amphipoda	Oedicerotidae

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264	SYNCAMER	<i>Synchelidium americanum</i>	Arthropoda	Amphipoda	Oedicerotidae
265	EOBRSPIN	<i>Eobrolgus spinosus</i>	Arthropoda	Amphipoda	Phoxocephalidae
266	HARPPROP	<i>Harpinia propinqua</i>	Arthropoda	Amphipoda	Phoxocephalidae
267	PHOXHOLB	<i>Phoxocephalus holbolli</i>	Arthropoda	Amphipoda	Phoxocephalidae
268	RHEPEPIS	<i>Rhepoxynius epistomus</i>	Arthropoda	Amphipoda	Phoxocephalidae
269	RHEPHUDS	<i>Rhepoxynius hudsoni</i>	Arthropoda	Amphipoda	Phoxocephalidae
270	PARAAEST	<i>Parapleustes aestuarius</i>	Arthropoda	Amphipoda	Pleustidae
271	PLEUGLAB	<i>Pleusymtes glaber</i>	Arthropoda	Amphipoda	Pleustidae
272	STENGRAC	<i>Stenopleustes gracilis</i>	Arthropoda	Amphipoda	Pleustidae
273	STENNER	<i>Stenopleustes inermis</i>	Arthropoda	Amphipoda	Pleustidae
274	DYOPMONA	<i>Dyopedos monacanthus</i>	Arthropoda	Amphipoda	Podoceridae
275	PARACYPR	<i>Parametopella cypris</i>	Arthropoda	Amphipoda	Stenothoidae
276	STENMINU	<i>Stenothoe minuta</i>	Arthropoda	Amphipoda	Stenothoidae
277	STENVALI	<i>Stenothoe valida</i>	Arthropoda	Amphipoda	Stenothoidae
278	HUTCMACR	<i>Hutchinsoniella macracantha</i>	Arthropoda	Cephalocarida	Hutchinsoniellida
279	ABLAPARA	<i>Ablabesmyia parajania</i>	Arthropoda	Chironomidae	Tanypodinae
280	PROCSUBL	<i>Procladius sublettei</i>	Arthropoda	Chironomidae	Tanypodinae
281	BODOSPEA	<i>Bodotria</i> sp. A Morris	Arthropoda	Cumacea	Bodotridae
282	CYCLVARI	<i>Cyclaspis varians</i>	Arthropoda	Cumacea	Bodotridae
283	MANCSTEL	<i>Mancocuma stellifera</i>	Arthropoda	Cumacea	Bodotridae
284	BODOTRII	<i>Pseudoleptocuma minor</i>	Arthropoda	Cumacea	Bodotridae
285	PSEUMINO	<i>Pseudoleptocuma minor</i>	Arthropoda	Cumacea	Bodotridae
286	DIASQUAD	<i>Diastylis quadrispinosa</i>	Arthropoda	Cumacea	Diastylidae
287	DIASSCUL	<i>Diastylis sculpta</i>	Arthropoda	Cumacea	Diastylidae
288	OXYUSMIT	<i>Oxyurostylis smithi</i>	Arthropoda	Cumacea	Diastylidae
289	EUDOPUSI	<i>Eudorella pusilla</i>	Arthropoda	Cumacea	Leuconidae
290	LEUCAMER	<i>Leucon americanus</i>	Arthropoda	Cumacea	Leuconidae
291	ALMYPROX	<i>Almyracuma proximoculi</i>	Arthropoda	Cumacea	Nannastacidae
292	ALPHHETE	<i>Alpheus heterochaelis</i>	Arthropoda	Decapoda	Alpheidae
293	AUTOMSPA	<i>Automate</i> sp. A Williams	Arthropoda	Decapoda	Alpheidae
294	CALLSETI	<i>Callianassa setimanus</i>	Arthropoda	Decapoda	Callianassidae
295	CRANSEPT	<i>Crangon septemspinosa</i>	Arthropoda	Decapoda	Crangonidae
296	LIBIEMAR	<i>Libinia emarginata</i>	Arthropoda	Decapoda	Majidae
297	OGYRALPH	<i>Ogyrides alphaerostris</i>	Arthropoda	Decapoda	Ogyrididae
298	PAGUACAD	<i>Pagurus acadianus</i>	Arthropoda	Decapoda	Paguridae
299	PAGUANNU	<i>Pagurus annulipes</i>	Arthropoda	Decapoda	Paguridae
300	PAGULONG	<i>Pagurus longicarpus</i>	Arthropoda	Decapoda	Paguridae
301	PAGUPOLL	<i>Pagurus pollicaris</i>	Arthropoda	Decapoda	Paguridae
302	EUCEPRAE	<i>Euceramus praelongus</i>	Arthropoda	Decapoda	Porcellanidae
303	POLYGIBB	<i>Polyonyx gibbesi</i>	Arthropoda	Decapoda	Porcellanidae
304	OVALOCEL	<i>Ovalipes ocellatus</i>	Arthropoda	Decapoda	Portunidae
305	PROCVICI	<i>Processa vicina</i>	Arthropoda	Decapoda	Processidae
306	UPOGAFFI	<i>Upogebia affinis</i>	Arthropoda	Decapoda	Upogebiidae
307	NEOPSA YI	<i>Dyspanopeus sayi</i>	Arthropoda	Decapoda	Xanthidae
308	HEXAANGU	<i>Hexapanopeus angustifrons</i>	Arthropoda	Decapoda	Xanthidae
309	PANOHERB	<i>Panopeus herbstii</i>	Arthropoda	Decapoda	Xanthidae
310	RHITHARR	<i>Rhithronpanopeus harrisi</i>	Arthropoda	Decapoda	Xanthidae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
311	APANMAGN	<i>Amakusanthura magnifica</i>	Arthropoda	Isopoda	Anthuridae
312	CYATBURB	<i>Cyathura burbancki</i>	Arthropoda	Isopoda	Anthuridae
313	CYATPOLI	<i>Cyathura polita</i>	Arthropoda	Isopoda	Anthuridae
314	PTILTENU	<i>Ptilanthura tenuis</i>	Arthropoda	Isopoda	Anthuridae
315	POLIPOLI	<i>Politolana polita</i>	Arthropoda	Isopoda	Cirolanidae
316	CHIRALMY	<i>Chiridotea almyra</i>	Arthropoda	Isopoda	Idoteidae
317	CHIRCOEC	<i>Chiridotea coeca</i>	Arthropoda	Isopoda	Idoteidae
318	EDOTTRIL	<i>Edotea triloba</i>	Arthropoda	Isopoda	Idoteidae
319	ERICATTE	<i>Erichsonella attenuata</i>	Arthropoda	Isopoda	Idoteidae
320	ERICFILI	<i>Erichsonella filiformis</i>	Arthropoda	Isopoda	Idoteidae
321	IDOTBALT	<i>Idotea balthica</i>	Arthropoda	Isopoda	Idoteidae
322	IDOTPHOS	<i>Idotea phosphorea</i>	Arthropoda	Isopoda	Idoteidae
323	JAERMARI	<i>Jaera marina</i>	Arthropoda	Isopoda	Janiridae
324	PLEUINER	<i>Pleurogonium inerme</i>	Arthropoda	Isopoda	Munnidae
325	PLEUSPIN	<i>Pleurogonium spinosissimum</i>	Arthropoda	Isopoda	Munnidae
326	ANCIDEPR	<i>Ancinus depressus</i>	Arthropoda	Isopoda	Sphaeromatidae
327	CASSOVAL	<i>Cassidinidea ovalis</i>	Arthropoda	Isopoda	Sphaeromatidae
328	PARACAUD	<i>Paracerceis caudata</i>	Arthropoda	Isopoda	Sphaeromatidae
329	SPHAQUAD	<i>Sphaeroma quadridentatum</i>	Arthropoda	Isopoda	Sphaeromatidae
330	CALLBREV	<i>Callipallene brevirostris</i>	Arthropoda	Pycnogonida	Callipallenidae
331	ANOPPETI	<i>Anoplodactylus petiolatus</i>	Arthropoda	Pycnogonida	Phoxichilidiidae
332	TANYORBI	<i>Tanystylum orbiculare</i>	Arthropoda	Pycnogonida	Tanystylidae
333	NANNGRAY	<i>Nannosquilla gravi</i>	Arthropoda	Stomatopoda	Nannosquillidae
334	SQUIEMPU	<i>Squilla empusa</i>	Arthropoda	Stomatopoda	Squillidae
335	LEPTDUBI	<i>Leptochelia dubia</i>	Arthropoda	Tanaidacea	Nototanaridae
336	TANAPSAM	<i>Tanaissus psammophilus</i>	Arthropoda	Tanaidacea	Nototanaridae
337	HARGRAPA	<i>Hargeria rapax</i>	Arthropoda	Tanaidacea	Paratanaridae
338	TANASPEA	<i>Tanaidacea sp. A Williams</i>	Arthropoda	Tanaidacea	Tanaidacea
339	CYRNFRAT	<i>Cynellus fraternus</i>	Arthropoda	Trichoptera	Polycentropodidae
340	CERIAMER	<i>Ceriantheopsis americanus</i>	Cnidaria	Anthozoa	Cerianthidae
341	CAUDAREN	<i>Caudina arenata</i>	Echinodermata	Holothuroidea	Caudinidae
342	STERUNIS	<i>Stereoderma unisemita</i>	Echinodermata	Holothuroidea	Cucumariidae
343	HAVESCAB	<i>Havelockia scabra</i>	Echinodermata	Holothuroidea	Phyllophoridae
344	PENTPULC	<i>Pentamera pulcherrima</i>	Echinodermata	Holothuroidea	Phyllophoridae
345	LEPTTENU	<i>Leptosynapta tenuis</i>	Echinodermata	Holothuroidea	Synaptidae
346	SACCKOWA	<i>Saccoglossus kowalevskii</i>	Hemichordata	Hemichordata	Harrmannidae
347	STERCAND	<i>Stereobalanus candensis</i>	Hemichordata	Hemichordata	Harrmannidae
348	ANADOVAL	<i>Anadara ovalis</i>	Mollusca	Bivalvia	Arcidae
349	ANADTRAN	<i>Anadara transversa</i>	Mollusca	Bivalvia	Arcidae
350	ARCTISLA	<i>Arctica islandica</i>	Mollusca	Bivalvia	Arcticidae
351	ASTACAST	<i>Astarte castanea</i>	Mollusca	Bivalvia	Astartidae
352	ASTACREN	<i>Astarte crenata</i>	Mollusca	Bivalvia	Astartidae
353	ASTASPEA	<i>Astarte sp. A Mountford</i>	Mollusca	Bivalvia	Astartidae
354	ASTAUNDA	<i>Astarte undata</i>	Mollusca	Bivalvia	Astartidae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
355	CERAPINN	<i>Cerastoderma pinnulatum</i>	Mollusca	Bivalvia	Cardiidae
356	LAEVMORT	<i>Laevicardium mortoni</i>	Mollusca	Bivalvia	Cardiidae
357	CYCLBORE	<i>Cyclocardia borealis</i>	Mollusca	Bivalvia	Carditidae
358	CORBFLUM	<i>Corbicula fluminea</i>	Mollusca	Bivalvia	Corbiculidae
359	CORBCONT	<i>Corbula contracta</i>	Mollusca	Bivalvia	Corbulidae
360	DONAVARI	<i>Donax variabilis</i>	Mollusca	Bivalvia	Donacidae
361	ALIGELEV	<i>Aligena elevata</i>	Mollusca	Bivalvia	Kelliidae
362	PARVMULT	<i>Parvilucina multilineata</i>	Mollusca	Bivalvia	Lucinidae
363	LYONAREN	<i>Lyonsia arenosa</i>	Mollusca	Bivalvia	Lyonsiidae
364	LYONHYAL	<i>Lyonsia hyalina</i>	Mollusca	Bivalvia	Lyonsiidae
365	MULILATE	<i>Mulinia lateralis</i>	Mollusca	Bivalvia	Mactridae
366	RANGCUNE	<i>Rangia cuneata</i>	Mollusca	Bivalvia	Mactridae
367	SPISSOLI	<i>Spisula solidissima</i>	Mollusca	Bivalvia	Mactridae
368	MYAAREN	<i>Mya arenaria</i>	Mollusca	Bivalvia	Myidae
369	YOLDLIMA	<i>Yoldia limatula</i>	Mollusca	Bivalvia	Nuculanidae
370	NUCUANNU	<i>Nucula annulata</i>	Mollusca	Bivalvia	Nuculidae
371	NUCUDELP	<i>Nucula delphinodonta</i>	Mollusca	Bivalvia	Nuculidae
372	CRASVIRG	<i>Crassostrea virginica</i>	Mollusca	Bivalvia	Ostreidae
373	PANDGOUL	<i>Pandora gouldiana</i>	Mollusca	Bivalvia	Pandoridae
374	AEQUIRRA	<i>Argopecten irradians</i>	Mollusca	Bivalvia	Pectinidae
375	PERIMARG	<i>Periploma margaritacea</i>	Mollusca	Bivalvia	Periplomataceae
376	PETRPOL	<i>Petricola pholadiformis</i>	Mollusca	Bivalvia	Petricolidae
377	TAGEDIVI	<i>Tagelus divisus</i>	Mollusca	Bivalvia	Solecurtidae
378	TAGEPLEB	<i>Tagelus plebeius</i>	Mollusca	Bivalvia	Solecurtidae
379	SILICOST	<i>Siliqua costata</i>	Mollusca	Bivalvia	Solemyidae
380	SOLEVELU	<i>Solemya velum</i>	Mollusca	Bivalvia	Solemyidae
381	ENSIDIRE	<i>Ensis directus</i>	Mollusca	Bivalvia	Solenidae
382	MUSCTRAN	<i>Musculium transversum</i>	Mollusca	Bivalvia	Sphaeriidae
383	MACOBALT	<i>Macoma balthica</i>	Mollusca	Bivalvia	Tellinidae
384	MACOMITC	<i>Macoma mitchelli</i>	Mollusca	Bivalvia	Tellinidae
385	MACOTENT	<i>Macoma tenta</i>	Mollusca	Bivalvia	Tellinidae
386	TELLAGIL	<i>Tellina agilis</i>	Mollusca	Bivalvia	Tellinidae
387	ASTHHEMP	<i>Asthenothaerus hemphilli</i>	Mollusca	Bivalvia	Thracidae
388	BUSHELEG	<i>Bushia elegans</i>	Mollusca	Bivalvia	Thracidae
389	BIVASPEA	<i>Bivalvia sp. A Mountford</i>	Mollusca	Bivalvia	Unidentified
390	ELLICOMP	<i>Elliptio complanta</i>	Mollusca	Bivalvia	Unionidae
391	GEMMGEMM	<i>Gemma gemma</i>	Mollusca	Bivalvia	Veneridae
392	MERCMERC	<i>Mercenaria mercenaria</i>	Mollusca	Bivalvia	Veneridae
393	PITAMORR	<i>Pitar morrhuanus</i>	Mollusca	Bivalvia	Veneridae
394	ACTEPUNC	<i>Rictaxis punctostriatus</i>	Mollusca	Gastropoda	Acteonidae
395	LAEVFUSC	<i>Laevapex fuscus</i>	Mollusca	Gastropoda	Ancylidae
396	BITHTENT	<i>Bithynia tentaculata</i>	Mollusca	Gastropoda	Bithyniidae
397	CAECJOHN	<i>Caecum johnsoni</i>	Mollusca	Gastropoda	Caecidae
398	CAECREGU	<i>Caecum regulare</i>	Mollusca	Gastropoda	Caecidae
399	CAECSPEA	<i>Caecum sp. A Mountford</i>	Mollusca	Gastropoda	Caecidae
400	CAECSPEB	<i>Caecum sp. B Mountford</i>	Mollusca	Gastropoda	Caecidae
401	CALYPSPA	<i>Calyptraetidae sp. A Mountford</i>	Mollusca	Gastropoda	Calyptraetidae
402	BITTALTE	<i>Butium alternatum</i>	Mollusca	Gastropoda	Certhiidae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
403	SEILADAM	<i>Seila adamsi</i>	Mollusca	Gastropoda	Cerithiopsidae
404	ANACLAFR	<i>Anachis lafresnayi</i>	Mollusca	Gastropoda	Columbellidae
405	ANACOBES	<i>Anachis obesa</i>	Mollusca	Gastropoda	Columbellidae
406	ASTYLUNA	<i>Astryis lunata</i>	Mollusca	Gastropoda	Columbellidae
407	DORIOBSC	<i>Doridella obscura</i>	Mollusca	Gastropoda	Corambiidae
408	CYLIBIDE	<i>Cylichnella bidentata</i>	Mollusca	Gastropoda	Cylichnidae
409	EPITGREE	<i>Epitonium greenlandicum</i>	Mollusca	Gastropoda	Epitonidae
410	EPITHUMP	<i>Epitonium humphreysi</i>	Mollusca	Gastropoda	Epitonidae
411	EPITRUPI	<i>Epitonium rupicola</i>	Mollusca	Gastropoda	Epitonidae
412	CRATPILA	<i>Cratena pilata</i>	Mollusca	Gastropoda	Facelinidae
413	GASTSPEA	<i>Gastropoda sp. A Mountford</i>	Mollusca	Gastropoda	Gastropoda
414	HAMISOLI	<i>Haminoea solitaria</i>	Mollusca	Gastropoda	Haminoeidae
415	AMNILIMO	<i>Amnicola limosa</i>	Mollusca	Gastropoda	Hydrobiidae
416	CINCWINK	<i>Cincinnatia winkleyi</i>	Mollusca	Gastropoda	Hydrobiidae
417	HYDRTRUN	<i>Hydrobia truncata</i>	Mollusca	Gastropoda	Hydrobiidae
418	LITTENU	<i>Littoridinops tenuipes</i>	Mollusca	Gastropoda	Hydrobiidae
419	LACUVINC	<i>Lacuna vincia</i>	Mollusca	Gastropoda	Lacunidae
420	EUPLCAUD	<i>Eupleura caudata</i>	Mollusca	Gastropoda	Muncidae
421	UROSCINE	<i>Urosalpinx cinerea</i>	Mollusca	Gastropoda	Muncidae
422	ILYAOSBO	<i>Ilyanassa obsoleta</i>	Mollusca	Gastropoda	Nassariidae
423	NASSTRIV	<i>Nassarius trivittatus</i>	Mollusca	Gastropoda	Nassariidae
424	NASSVIBE	<i>Nassarius vibex</i>	Mollusca	Gastropoda	Nassariidae
425	NATIPUSI	<i>Natica pusilla</i>	Mollusca	Gastropoda	Naticidae
426	POLIHRO	<i>Polinices heros</i>	Mollusca	Gastropoda	Naticidae
427	GONIVIRG	<i>Goniobasis virginica</i>	Mollusca	Gastropoda	Pleuroceridae
428	BOONBISU	<i>Boonea bisuturalis</i>	Mollusca	Gastropoda	Pyramidellidae
429	BOONIMPR	<i>Boonea impressa</i>	Mollusca	Gastropoda	Pyramidellidae
430	BOONSEMI	<i>Boonea seminuda</i>	Mollusca	Gastropoda	Pyramidellidae
431	ODOSSULC	<i>cf. Odostomia sulcosa</i>	Mollusca	Gastropoda	Pyramidellidae
432	FARGBART	<i>Fargoa bartschi</i>	Mollusca	Gastropoda	Pyramidellidae
433	FARGBUSH	<i>Fargoa bushiana</i>	Mollusca	Gastropoda	Pyramidellidae
434	FARGGIBB	<i>Fargoa gibbosa</i>	Mollusca	Gastropoda	Pyramidellidae
435	ODOSENGO	<i>Odostomia engonia</i>	Mollusca	Gastropoda	Pyramidellidae
436	ODOSSPEA	<i>Odostomia sp. A Mountford</i>	Mollusca	Gastropoda	Pyramidellidae
437	SAYECHES	<i>Savella chesapeakea</i>	Mollusca	Gastropoda	Pyramidellidae
438	TURBINTE	<i>Turbonilla interrupta</i>	Mollusca	Gastropoda	Pyramidellidae
439	TURBSPEB	<i>Turbonilla sp. B Mountford</i>	Mollusca	Gastropoda	Pyramidellidae
440	TURB?AEQ	<i>Turbonilla ?aequalis</i>	Mollusca	Gastropoda	Pyramidellidae
441	ACTECANA	<i>Acteocina canaliculata</i>	Mollusca	Gastropoda	Scaphandridae
442	ACTEORYZ	<i>Acteocina oryza</i>	Mollusca	Gastropoda	Scaphandridae
443	KURTATRO	<i>Kurtziella atrostyla</i>	Mollusca	Gastropoda	Turridae
444	TURRSPEA	<i>Turridae sp. A Mountford</i>	Mollusca	Gastropoda	Turridae
445	VALVSINC	<i>Valvata sincera</i>	Mollusca	Gastropoda	Valvatidae
446	VALVTRIC	<i>Valvata tricarinata</i>	Mollusca	Gastropoda	Valvatidae
447	VITRFLOR	<i>Vitrinella floridana</i>	Mollusca	Gastropoda	Vitrinellidae

NO	CODE	GENUS SPP.	PHYLUM	CLASS	FAMILY
<b>Higher-Level Valid Taxa</b>					
448	OLIGOCHA	<i>Oligochaeta</i>	Annelida	Oligochaeta	Unidentified
449	ACROCFAM	<i>Acrocirridae</i>	Annelida	Polychaeta	Acrocirridae
450	ARABIRMU	<i>Arabella</i> <i>incolor-multidentata</i> <i>complex</i>	Annelida	Polychaeta	Arabellidae
451	CAPITELL	<i>Capitella spp.</i>	Annelida	Polychaeta	Capitellidae
452	APHELOCH	<i>Aphelochaeta spp.</i>	Annelida	Polychaeta	Cirratulidae
453	DODECACE	<i>Dodecaceria spp</i>	Annelida	Polychaeta	Cirratulidae
454	MONTBPDS	<i>Monticellina</i> <i>baptisteae-dorsobranchia</i> <i>lis</i>	Annelida	Polychaeta	Cirratulidae
455	OPHRYOTR	<i>Ophryotrocha spp.</i>	Annelida	Polychaeta	Dorvilleidae
456	MAGELONA	<i>Magelona spp</i>	Annelida	Polychaeta	Magelonidae
457	POLYGORD	<i>Polygordius spp</i>	Annelida	Polychaeta	Polygordiidae
458	PROTODRI	<i>Protodrilus spp</i>	Annelida	Polychaeta	Protodrilidae
459	SPHAEROD	<i>Sphaerodoropsis spp.</i>	Annelida	Polychaeta	Sphaerodoridae
460	LAONICE	<i>Laonice spp</i>	Annelida	Polychaeta	Spionidae
461	BRANCLSW	<i>Brania</i> <i>clavata-swedmarki</i> <i>complex</i>	Annelida	Polychaeta	Syllidae
462	TYPOAL_1	<i>Typosyllis alternata-sp 1</i> <i>complex</i>	Annelida	Polychaeta	Syllidae
463	AMPEABVA	<i>Ampelisca</i> <i>abditia-vadorum complex</i>	Arthropoda	Amphipoda	Ampeliscidae
464	GITANOPS	<i>Gitanopsis spp</i>	Arthropoda	Amphipoda	Amphilocheidae
465	THALASSI	<i>Thalassinidea</i>	Arthropoda	Crustacea	Thalassinidea
466	TRICORYT	<i>Tricorythodes spp</i>	Arthropoda	Ephemeroptera	Tricorythidae
467	OPHIUROI	<i>Ophiuroidea</i>	Echinodermata	Ophiuroidea	Unidentified
468	RAETACF	<i>cf. Raeta spp.</i>	Mollusca	Bivalvia	Macluridae
469	PISIDIUM	<i>Pisidium spp</i>	Mollusca	Bivalvia	Pisidiidae
470	ANODONTA	<i>Anodonta spp.</i>	Mollusca	Bivalvia	Unionidae
471	FERRISSI	<i>Ferrissia spp</i>	Mollusca	Gastropoda	Acroloxidae
472	COLUMBEL	<i>Columbella spp</i>	Mollusca	Gastropoda	Columbellidae
473	MELANELL	<i>Melanella spp</i>	Mollusca	Gastropoda	Elmidae
474	LYOGYRUS	<i>Lyogyrus spp</i>	Mollusca	Gastropoda	Hydrobidae
475	BUSYCON	<i>Busycon spp.</i>	Mollusca	Gastropoda	Melongenidae
476	PHYSELLA	<i>Physella spp.</i>	Mollusca	Gastropoda	Physidae
477	PROMENET	<i>Promenetus spp</i>	Mollusca	Gastropoda	Planorbidae
478	PLEUROCE	<i>Pleurocera spp</i>	Mollusca	Gastropoda	Pleuroceridae
479	NEMERTIN	<i>Nemertinea</i>	Nemertinea	Nemertinea	Unidentified
480	PHORONIS	<i>Phoronis spp.</i>	Phoronida	Phoronida	Phoronidae
481	SIPUNCUL	<i>Sipuncula</i>	Sipuncula	Sipuncula	Unidentified

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
<b>FRESHWATER TAXA</b>					
482	ENCHYTRA	<i>Enchytraeidae</i>	Annelida	Oligochaeta	Enchytraeidae
483	LUMBRICU	<i>Lumbriculidae</i>	Annelida	Oligochaeta	Lumbriculidae
484	ARCTLOMO	<i>Arcteonais lomondi</i>	Annelida	Oligochaeta	Naididae
485	BRATUNID	<i>Bratislavia unidentata</i>	Annelida	Oligochaeta	Naididae
486	CHAETOGA	<i>Chaetogaster spp.</i>	Annelida	Oligochaeta	Naididae
487	DERODIGI	<i>Dero diguata</i>	Annelida	Oligochaeta	Naididae
488	NAISPARD	<i>Nais pardalis</i>	Annelida	Oligochaeta	Naididae
489	NAISPSEU	<i>Nais pseudobtusa</i>	Annelida	Oligochaeta	Naididae
490	PIGUMICH	<i>Piguetella michiganensis</i>	Annelida	Oligochaeta	Naididae
491	SLAVAPPE	<i>Slavina appendiculata</i>	Annelida	Oligochaeta	Naididae
492	SPECJOSI	<i>Specaria josinae</i>	Annelida	Oligochaeta	Naididae
493	STEPTAND	<i>Stephensoniana tandvi</i>	Annelida	Oligochaeta	Naididae
494	STEPTRIV	<i>Stephensoniana trivandana</i>	Annelida	Oligochaeta	Naididae
495	STYLLACU	<i>Syllaria lacustris</i>	Annelida	Oligochaeta	Naididae
496	AULOLIMN	<i>Aulodrilus limnobius</i>	Annelida	Oligochaeta	Tubificidae
497	AULOPAUC	<i>Aulodrilus paucichaeta</i>	Annelida	Oligochaeta	Tubificidae
498	AULOPIGU	<i>Aulodrilus pigueti</i>	Annelida	Oligochaeta	Tubificidae
499	AULOPLUR	<i>Aulodrilus pluriseta</i>	Annelida	Oligochaeta	Tubificidae
500	BRANSOWE	<i>Branchiura sowerbyi</i>	Annelida	Oligochaeta	Tubificidae
501	HABESPEC	<i>Haber cf. speciosus</i>	Annelida	Oligochaeta	Tubificidae
502	ILYOTEMP	<i>Ilyodrilus templetoni</i>	Annelida	Oligochaeta	Tubificidae
503	ISOCFREY	<i>Isochaetides freyi</i>	Annelida	Oligochaeta	Tubificidae
504	LIMNCERV	<i>Limnodrilus cervix</i>	Annelida	Oligochaeta	Tubificidae
505	LIMNCLAP	<i>Limnodrilus clapedianus</i>	Annelida	Oligochaeta	Tubificidae
506	LIMNHOFF	<i>Limnodrilus hoffmeisteri</i>	Annelida	Oligochaeta	Tubificidae
507	LIMNUDEK	<i>Limnodrilus udekemianus</i>	Annelida	Oligochaeta	Tubificidae
508	QUISMULT	<i>Quistadrilus multisetosus</i>	Annelida	Oligochaeta	Tubificidae
509	TELMVEJD	<i>Telmatodrilus vej dovskii</i>	Annelida	Oligochaeta	Tubificidae
510	TUBIFIWI	<i>Tubificidae with capilliform chaetae</i>	Annelida	Oligochaeta	Tubificidae
511	TUBIFTWO	<i>Tubificidae without capilliform chaetae</i>	Annelida	Oligochaeta	Tubificidae
512	TUBIBROW	<i>Tubificoides brownae</i>	Annelida	Oligochaeta	Tubificidae
513	TUBIHETE	<i>Tubificoides heterochaetus</i>	Annelida	Oligochaeta	Tubificidae
514	AXARUS	<i>Axarus spp.</i>	Arthropoda	Chironomidae	Chironomini
515	CHIRONOM	<i>Chironomus spp</i>	Arthropoda	Chironomidae	Chironomini
516	CLADOPLE	<i>Cladoplema spp</i>	Arthropoda	Chironomidae	Chironomini
517	CRYPFULV	<i>Cryptochironomus fulvus</i>	Arthropoda	Chironomidae	Chironomini
518	CRYPTOTE	<i>Cryptotendipes spp</i>	Arthropoda	Chironomidae	Chironomini
519	DEMICRYP	<i>Demicroptochironomus spp.</i>	Arthropoda	Chironomidae	Chironomini
520	DICRNERV	<i>Dicrotendipes nervosus</i>	Arthropoda	Chironomidae	Chironomini
521	DICROTEN	<i>Dicrotendipes spp</i>	Arthropoda	Chironomidae	Chironomini
522	ENDOCHIR	<i>Endochironomus spp</i>	Arthropoda	Chironomidae	Chironomini
523	GLYPTOTE	<i>Glyptotendipes spp</i>	Arthropoda	Chironomidae	Chironomini
524	HARNISCH	<i>Harnischia spp</i>	Arthropoda	Chironomidae	Chironomini



NO	CODE	GENUS SPP.	PHYLUM	CLASS	FAMILY
525	MICROCHI	<i>Microchironomus spp.</i>	Arthropoda	Chironomidae	Chironomini
526	PARACLAD	<i>Paracladopelma spp.</i>	Arthropoda	Chironomidae	Chironomini
527	PARALAUT	<i>Paralauterborniella spp.</i>	Arthropoda	Chironomidae	Chironomini
528	POLYTRIP	<i>Polypedilum tripodura</i>	Arthropoda	Chironomidae	Chironomini
529	PSEUDUCH	<i>Pseudochironomus spp.</i>	Arthropoda	Chironomidae	Chironomini
530	STICTOCH	<i>Stictochironomus spp.</i>	Arthropoda	Chironomidae	Chironomini
531	NANOCLAD	<i>Nanocladius spp.</i>	Arthropoda	Chironomidae	Orthocladinae
532	COELOTAN	<i>Coelotanytus spp.</i>	Arthropoda	Chironomidae	Tanypodinae
533	PROCHOLO	<i>Procladius (Holotanytus) spp.</i>	Arthropoda	Chironomidae	Tanypodinae
534	TANYPUS	<i>Tanytus spp.</i>	Arthropoda	Chironomidae	Tanypodinae
535	CLADOTAN	<i>Cladotanytus spp.</i>	Arthropoda	Chironomidae	Tanytarsini
536	RHEOTANY	<i>Rheotanytus spp.</i>	Arthropoda	Chironomidae	Tanytarsini
537	TANYTARS	<i>Tanytarsus spp.</i>	Arthropoda	Chironomidae	Tanytarsini
538	DUBIRAPH	<i>Dubiraphia spp.</i>	Arthropoda	Coleoptera	Elmidae
539	STENELMI	<i>Stenelmis spp.</i>	Arthropoda	Coleoptera	Elmidae
540	BEZZIA	<i>Bezzia spp.</i>	Arthropoda	Diptera	Ceratopogonidae
541	PALPOMYI	<i>Palpomyia spp.</i>	Arthropoda	Diptera	Ceratopogonidae
542	PROBEZZI	<i>Probezzia spp.</i>	Arthropoda	Diptera	Ceratopogonidae
543	SPHAEROM	<i>Sphaeromus spp.</i>	Arthropoda	Diptera	Ceratopogonidae
544	CHAOPUNC	<i>Chaoborus punctipennis</i>	Arthropoda	Diptera	Chaoboridae
545	DOLICHOP	<i>Dolichopodidae</i>	Arthropoda	Diptera	Dolichopodidae
546	BRACHYCE	<i>Brachycercus spp.</i>	Arthropoda	Ephemeroptera	Caenidae
547	CAENIS	<i>Caenis spp.</i>	Arthropoda	Ephemeroptera	Caenidae
548	HEXALIMB	<i>Hexagenia limbata</i>	Arthropoda	Ephemeroptera	Ephemerae
549	HEXAGENI	<i>Hexagenia spp.</i>	Arthropoda	Ephemeroptera	Ephemerae
550	HYDROPTI	<i>Hydropsyche spp.</i>	Arthropoda	Trichoptera	Hydropsychidae
551	OECETIS	<i>Oecetis spp.</i>	Arthropoda	Trichoptera	Leptoceridae

### EMAP TAXA POOLED WITH OTHER TAXA

552	ASYCHIS				
553	AMPEABDI	<i>Ampelisca abdita</i>	Arthropoda	Amphipoda	Ampeliscidae
554	AMPEVADO	<i>Ampelisca vadorum</i>	Arthropoda	Amphipoda	Ampeliscidae
555	ORCHOMEN	<i>Orchomenella spp.</i>	Arthropoda	Amphipoda	Lysianassidae
556	YOLDIA	<i>Yoldia spp.</i>	Mollusca	Bivalvia	Nuculanidae
557	PANDORA	<i>Pandora spp.</i>	Mollusca	Bivalvia	Pandoridae
558	PANDORID	<i>Pandoridae</i>	Mollusca	Bivalvia	Pandoridae
559	SOLEMYA	<i>Solemya spp.</i>	Mollusca	Bivalvia	Solemyidae
560	SOLEMYID	<i>Solemyidae</i>	Mollusca	Bivalvia	Solemyidae
561	MUSCULIU	<i>Musculium spp.</i>	Mollusca	Bivalvia	Sphaeridae
562	TELLINA	<i>Tellina spp.</i>	Mollusca	Bivalvia	Tellinidae
563	EUDORELL	<i>Eudorella spp.</i>	Arthropoda	Cumacea	Leuconidae
564	MICRATRA	<i>Microphiopholis atra</i>	Echinodermata	Ophiuroidea	Amphiuridae
565	MELINNA	<i>Melinna spp.</i>	Annelida	Polychaeta	Ampharetidae
566	APHESPEA	<i>Aphelochaeta sp. A Blake</i>	Annelida	Polychaeta	Cirratulidae
567	MONTBAPT	<i>Monticellina baptistae</i>	Annelida	Polychaeta	Cirratulidae
568	MONTDORS	<i>Monticellina dorsobranchialis</i>	Annelida	Polychaeta	Cirratulidae
569	PHERUSA	<i>Pherusa spp.</i>	Annelida	Polychaeta	Flabelligeridae
570	LUMBHEBE	<i>Scoletoma hebes</i>	Annelida	Polychaeta	Lumbrineridae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
571	ASYCELO	<i>Sabaco elongatus</i>	Annelida	Polychaeta	Maldanidae
572	LEITOSCO	<i>Leitoscoloplos</i> spp.	Annelida	Polychaeta	Orbinidae
573	OWENIA	<i>Owenia</i> spp.	Annelida	Polychaeta	Oweniidae
574	PECTINAR	<i>Pectinaria</i> spp.	Annelida	Polychaeta	Pectinariidae
575	BRANCLAV	<i>Brania clavata</i>	Annelida	Polychaeta	Syllidae
576	BRANSWED	<i>Brania swedmarki</i>	Annelida	Polychaeta	Syllidae
577	TYPOALTE	<i>Typosyllis alternata</i>	Annelida	Polychaeta	Syllidae
578	TYPOSPEI	<i>Typosyllis</i> sp. 1 NMFS	Annelida	Polychaeta	Syllidae
579	AMPHITRI	<i>Amphitritinae</i>	Annelida	Polychaeta	Terebellidae
<b>Dropped EMAP-E Taxa (See Text)</b>					
580	NEVEDUPL				
757	ERPODFAM	Erpodeiidae	Annelida	Hirudinea	Erpodeiidae
758	HIRUDINE	Hirudinea	Annelida	Hirudinea	Unidentified
779	DERO	<i>Dero</i> spp.	Annelida	Oligochaeta	Naididae
780	NAIDIDAE	Naididae	Annelida	Oligochaeta	Naididae
781	STEPHENS	<i>Stephensoniana</i> spp.	Annelida	Oligochaeta	Naididae
782	TUBIFICO	<i>Tubificoides</i> spp.	Annelida	Oligochaeta	Tubificidae
784	AMPHARTD	Ampharetidae	Annelida	Polychaeta	Ampharetidae
785	ARABELLA	<i>Arabella</i> spp	Annelida	Polychaeta	Arabellidae
786	ARABELLI	Arabellidae	Annelida	Polychaeta	Arabellidae
787	CAPITELD	Capitellidae	Annelida	Polychaeta	Capitellidae
788	NOTOMAST	<i>Notomastus</i> spp	Annelida	Polychaeta	Capitellidae
789	CIRRATUL	Cirratulidae	Annelida	Polychaeta	Cirratulidae
790	EUNICIDA	Eunicidae	Annelida	Polychaeta	Eunicidae
791	FLABELLI	Flabelligeridae	Annelida	Polychaeta	Flabelligeridae
792	GLYCERA	<i>Glyceria</i> spp	Annelida	Polychaeta	Glyceridae
793	GLYCERID	Glyceridae	Annelida	Polychaeta	Glyceridae
794	GONIADID	Goniadidae	Annelida	Polychaeta	Goniadidae
795	GYPTIS	<i>Gyptis</i> spp	Annelida	Polychaeta	Hesionidae
796	HESIONID	Hesionidae	Annelida	Polychaeta	Hesionidae
797	MICROPH	<i>Microphthalmus</i> spp	Annelida	Polychaeta	Hesionidae
798	LUMBRIND	Lumbrineridae	Annelida	Polychaeta	Lumbrineridae
799	LUMBRINE	<i>Scoletoma</i> spp	Annelida	Polychaeta	Lumbrineridae
800	MALDANID	Maldanidae	Annelida	Polychaeta	Maldanidae
801	NEPTYIID	Nephtyidae	Annelida	Polychaeta	Nephtyidae
802	NEPTYYS	<i>Nephtys</i> spp	Annelida	Polychaeta	Nephtyidae
803	NEREIDAE	Nereididae	Annelida	Polychaeta	Nereididae
804	ONUPHIDA	Onuphidae	Annelida	Polychaeta	Onuphidae
805	OPHELID	Opheliidae	Annelida	Polychaeta	Opheliidae
806	TRAVISIA	<i>Travisia</i> spp	Annelida	Polychaeta	Opheliidae
807	ORBINA	<i>Orbinia</i> spp.	Annelida	Polychaeta	Orbiniidae
808	ORBINIID	Orbiniidae	Annelida	Polychaeta	Orbiniidae
809	SCOLOPLO	<i>Scoloplos</i> spp	Annelida	Polychaeta	Orbiniidae
810	OWENIIDA	Oweniidae	Annelida	Polychaeta	Oweniidae
811	ARICIDEA	<i>Aricidea</i> spp	Annelida	Polychaeta	Paraonidae
812	PARAONID	Paraonidae	Annelida	Polychaeta	Paraonidae
813	ETEONE	<i>Hypereteone</i> spp	Annelida	Polychaeta	Phyllodocidae
814	PHYLLODO	<i>Phyllodoce</i> spp	Annelida	Polychaeta	Phyllodocidae
815	PHYLLDCDE	Phyllodocidae	Annelida	Polychaeta	Phyllodocidae

NO	CODE	GENUS SPP.	PHYLUM	CLASS	FAMILY
816	PILARGID	Pilargidae	Annelida	Polychaeta	Pilargidae
817	SIGAMBRA	Sigambra spp.	Annelida	Polychaeta	Pilargidae
818	HARMOTHO	Harmothoe spp.	Annelida	Polychaeta	Polynoidae
819	LEPIDONO	Lepidonotus spp.	Annelida	Polychaeta	Polynoidae
820	POLYNOID	Polynoidae	Annelida	Polychaeta	Polynoidae
821	SABELLAR	Sabellariidae	Annelida	Polychaeta	Sabellariidae
822	EUCHONE	Euchone spp.	Annelida	Polychaeta	Sabellidae
823	FABRICIN	Fabricinae	Annelida	Polychaeta	Sabellidae
824	SABELLID	Sabellidae	Annelida	Polychaeta	Sabellidae
825	SCALIBRE	Scalibregmatidae	Annelida	Polychaeta	Scalibregmatidae
826	FILOGRAN	Filograninae sp. A Morris	Annelida	Polychaeta	Serpulidae
827	HYDRDIAN	Hydroides dianthus	Annelida	Polychaeta	Serpulidae
828	HYDRPROT	Hydroides protulicola	Annelida	Polychaeta	Serpulidae
829	HYDROIDE	Hydroides spp.	Annelida	Polychaeta	Serpulidae
830	SERPULID	Serpulidae	Annelida	Polychaeta	Serpulidae
831	SIGALION	Sigalionidae	Annelida	Polychaeta	Sigalionidae
832	STENELAI	Sthenelais spp.	Annelida	Polychaeta	Sigalionidae
833	POLYDORA	Polydora spp.	Annelida	Polychaeta	Spionidae
834	PRIONOSP	Prionospio spp.	Annelida	Polychaeta	Spionidae
835	SCOLELEP	Scolecopsis spp.	Annelida	Polychaeta	Spionidae
836	SPIO	Spio spp.	Annelida	Polychaeta	Spionidae
837	SPIONIDA	Spionidae	Annelida	Polychaeta	Spionidae
838	SPIRORBD	Spirorbidae	Annelida	Polychaeta	Spirorbidae
839	SPIRORBI	Spirorbis spp.	Annelida	Polychaeta	Spirorbidae
840	AUTOLYNI	Autolyninae	Annelida	Polychaeta	Syllidae
841	AUTOLYTU	Autolytus spp.	Annelida	Polychaeta	Syllidae
842	BRANIA	Brania spp.	Annelida	Polychaeta	Syllidae
843	EXOGONE	Exogone spp.	Annelida	Polychaeta	Syllidae
844	PIONOSYL	Pionosyllis spp.	Annelida	Polychaeta	Syllidae
845	SPHAEROS	Sphaerosyllis spp.	Annelida	Polychaeta	Syllidae
846	STREPTOS	Streptosyllis spp.	Annelida	Polychaeta	Syllidae
847	SYLLIDAE	Syllidae	Annelida	Polychaeta	Syllidae
848	SYLLIDES	Syllides spp.	Annelida	Polychaeta	Syllidae
849	TYPOSYLL	Typosyllis spp.	Annelida	Polychaeta	Syllidae
850	PISTA	Pista spp.	Annelida	Polychaeta	Terebellidae
851	POLYCIRN	Polycirrinae Unidentified	Annelida	Polychaeta	Terebellidae
852	POLYCIRR	Polycirrus spp.	Annelida	Polychaeta	Terebellidae
853	TEREBELL	Terebellidae	Annelida	Polychaeta	Terebellidae
854	POLYCSUB	Polychaeta: Other - Deep Deposit Feeders	Annelida	Polychaeta	Unidentified
855	POLYCCAR	Polychaeta: Other - Omnivores & Carnivore	Annelida	Polychaeta	Unidentified
856	POLYCSUR	Polychaeta: Other - Surface Feeders	Annelida	Polychaeta	Unidentified
857	POLYCHAE	Polychaeta: Other - Unidentified & fragments	Annelida	Polychaeta	Unidentified
581	AMPELISC	Ampelisca spp.	Arthropoda	Amphipoda	Ampeliscidae
582	AMPITHOE	Ampithoe spp.	Arthropoda	Amphipoda	Ampithoidae
583	AMPITHOI	Ampithoidae	Arthropoda	Amphipoda	Ampithoidae
584	AORIDAE	Aoridae	Arthropoda	Amphipoda	Aoridae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
585	LEMBOS	<i>Lembos</i> spp.	Arthropoda	Amphipoda	Aoridae
586	LEPTOCHE	<i>Leptocheirus</i> spp.	Arthropoda	Amphipoda	Aoridae
587	MICRODEU	<i>Microdeutopus</i> spp.	Arthropoda	Amphipoda	Aoridae
588	UNCIOLA	<i>Unciola</i> spp.	Arthropoda	Amphipoda	Aoridae
589	AEGILONG	<i>Aeginina longicornis</i>	Arthropoda	Amphipoda	Caprellidae
590	CAPRANDR	<i>Caprella andreae</i>	Arthropoda	Amphipoda	Caprellidae
591	CAPRPENA	<i>Caprella penantis</i>	Arthropoda	Amphipoda	Caprellidae
592	CAPRELLA	<i>Caprella</i> spp.	Arthropoda	Amphipoda	Caprellidae
593	CAPRELLI	Caprellidae	Arthropoda	Amphipoda	Caprellidae
594	LUCOINCE	<i>Luconacia incerta</i>	Arthropoda	Amphipoda	Caprellidae
595	PARATENU	<i>Paracaprella tenuis</i>	Arthropoda	Amphipoda	Caprellidae
596	COROPHIU	<i>Corophium</i> spp.	Arthropoda	Amphipoda	Corophiidae
597	GAMMARID	Gammaridae	Arthropoda	Amphipoda	Gammaridae
598	GAMMARUS	<i>Gammarus</i> spp.	Arthropoda	Amphipoda	Gammaridae
599	ACANTHOH	<i>Acanthohaustorius</i> spp.	Arthropoda	Amphipoda	Haustoriidae
600	HAUSTIDA	Haustoriidae	Arthropoda	Amphipoda	Haustoriidae
601	PARAHAUS	<i>Parahaustorius</i> spp.	Arthropoda	Amphipoda	Haustoriidae
602	PROTOHAU	<i>Protohaustorius</i> spp.	Arthropoda	Amphipoda	Haustoriidae
603	PHOTIS	<i>Photis</i> spp.	Arthropoda	Amphipoda	Isaeidae
604	ERICTHON	<i>Erichthonius</i> spp.	Arthropoda	Amphipoda	Ischyrocerae
605	LILJEBOR	Liljeborgiidae	Arthropoda	Amphipoda	Liljeborgiidae
606	LISTRIEL	<i>Listriella</i> spp.	Arthropoda	Amphipoda	Liljeborgiidae
607	LYSIADAE	Lysianassidae	Arthropoda	Amphipoda	Lysianassidae
608	MELITIDA	Melitidae	Arthropoda	Amphipoda	Melitidae
609	MONOCULO	<i>Monoculodes</i> spp.	Arthropoda	Amphipoda	Oedicerotidae
610	PHOXOCEP	Phoxocephalidae	Arthropoda	Amphipoda	Phoxocephalidae
611	RHEPOXYN	<i>Rhepoxynius</i> spp.	Arthropoda	Amphipoda	Phoxocephalidae
612	PODOCERI	Podoceridae	Arthropoda	Amphipoda	Podoceridae
613	STENOTHO	<i>Stenothoe</i> spp.	Arthropoda	Amphipoda	Stenothoidae
614	AMPHIPOD	Amphipoda: Other	Arthropoda	Amphipoda	Unidentified
625	HOMAAMER	<i>Homarus americanus</i>	Arthropoda	Astacidea	Nephropsidae
674	CHRNMDAE	Chironomidae	Arthropoda	Chironomidae	Chironomidae
675	CHIRONIM	Chironomina	Arthropoda	Chironomidae	Chironomina
676	CRYPTOCH	<i>Cryptochironomus</i> spp.	Arthropoda	Chironomidae	Chironomina
677	POLYPEDI	<i>Polypedium</i> spp.	Arthropoda	Chironomidae	Chironomina
678	PROCLADI	<i>Procladius</i> spp.	Arthropoda	Chironomidae	Tanypodinae
679	TANYTTRB	Tanytarsini	Arthropoda	Chironomidae	Tanytarsini
680	BALABALA	<i>Balanus balanoides</i>	Arthropoda	Cirripedia	Balanidae
681	BALACREN	<i>Balanus crenatus</i>	Arthropoda	Cirripedia	Balanidae
682	BALAIMPR	<i>Balanus improvisus</i>	Arthropoda	Cirripedia	Balanidae
683	BALANUS	<i>Balanus</i> spp.	Arthropoda	Cirripedia	Balanidae
684	BALA VENU	<i>Balanus venustus</i>	Arthropoda	Cirripedia	Balanidae
685	CLADOCER	Cladocera	Arthropoda	Cladocera	Unidentified
686	COLLEMBO	Collembola	Arthropoda	Collembola	Unidentified
687	CALANOID	Calanoida	Arthropoda	Copepoda	Calanoida
688	CALIGOID	Caligoida	Arthropoda	Copepoda	Caligoida
689	HARPACTI	Harpacticoida	Arthropoda	Copepoda	Harpacticoida
690	BODOTRIN	Bodotriidae	Arthropoda	Cumacea	Bodotriidae
691	CUMACEA	Cumacea	Arthropoda	Cumacea	Unidentified

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
692	BRACHYUR	Brachyura	Arthropoda	Decapoda	Brachyura
693	CANCIRRO	Cancer irroratus	Arthropoda	Decapoda	Cancridae
694	CANCER	Cancer spp.	Arthropoda	Decapoda	Cancridae
695	CARIDEA	Caridea	Arthropoda	Decapoda	Caridea
696	HIPPOLYT	Hippolytidae	Arthropoda	Decapoda	Hippolytidae
697	LIBINIA	Libinia spp.	Arthropoda	Decapoda	Majidae
698	MAJIDAE	Majidae	Arthropoda	Decapoda	Majidae
699	PAGURIDA	Paguridae	Arthropoda	Decapoda	Paguridae
700	PAGURUS	Pagurus spp.	Arthropoda	Decapoda	Paguridae
865	PALAPUGI	Palaemonetes pugio	Arthropoda	Decapoda	Palaemonidae
701	PENAEIDA	Penaeidae	Arthropoda	Decapoda	Penaeidae
702	TRACCONS	Trachypenaeus constrictus	Arthropoda	Decapoda	Penaeidae
703	DISSMELL	Dissodactylus mellitae	Arthropoda	Decapoda	Pinnotheridae
704	PINNCHAE	Pinnixa chaetoptera	Arthropoda	Decapoda	Pinnotheridae
705	PINNRETI	Pinnixa retiens	Arthropoda	Decapoda	Pinnotheridae
706	PINNSAYA	Pinnixa sayana	Arthropoda	Decapoda	Pinnotheridae
707	PINNIXA	Pinnixa spp.	Arthropoda	Decapoda	Pinnotheridae
708	PINNOTHR	Pinnotheres spp	Arthropoda	Decapoda	Pinnotheridae
709	PINNOTHE	Pinnotheridae	Arthropoda	Decapoda	Pinnotheridae
710	CALLSAPI	Callinectes sapidus	Arthropoda	Decapoda	Portunidae
711	CALLINEC	Callinectes spp.	Arthropoda	Decapoda	Portunidae
712	CARCMAEN	Carcinus maenas	Arthropoda	Decapoda	Portunidae
713	OVALIPES	Ovalipes spp.	Arthropoda	Decapoda	Portunidae
714	PORTUNID	Portunidae	Arthropoda	Decapoda	Portunidae
715	DECAPODA	Decapoda	Arthropoda	Decapoda	Unidentified
716	XANTHIDA	Xanthidae	Arthropoda	Decapoda	Xanthidae
717	CERATFAM	Ceratopogonidae	Arthropoda	Diptera	Ceratopogonidae
718	DIPTERA	Diptera	Arthropoda	Diptera	Unidentified
724	EPHEMFAM	Ephemerae	Arthropoda	Ephemeroptera	Ephemerae
760	HYDRACAR	Hydracarina	Arthropoda	Hydracarina	Unidentified
761	INSECTA	Insecta	Arthropoda	Insecta	Unidentified
762	ANTHURID	Anthuridae	Arthropoda	Isopoda	Anthuridae
763	CYATHURA	Cyathura spp.	Arthropoda	Isopoda	Anthuridae
764	CHIRIDOT	Chiridotea spp.	Arthropoda	Isopoda	Idoteidae
765	ERICHSON	Erichsonella spp	Arthropoda	Isopoda	Idoteidae
766	IDOTEA	Idotea spp.	Arthropoda	Isopoda	Idoteidae
767	IDOTEIDA	Idoteidae	Arthropoda	Isopoda	Idoteidae
768	ISOPODA	Isopoda: Other	Arthropoda	Isopoda	Unidentified
769	LIMUPOLY	Limulus polyphemus	Arthropoda	Merostomata	Limulidae
772	HETEFORM	Heteromysis formosa	Arthropoda	Mysidacea	Mysidae
773	MYSIDAE	Mysidae	Arthropoda	Mysidacea	Mysidae
774	MYSIALMY	Mysidopsis almyra	Arthropoda	Mysidacea	Mysidae
775	MYSIBIGE	Mysidopsis bigelowi	Arthropoda	Mysidacea	Mysidae
776	MYSIDOPS	Mysidopsis spp.	Arthropoda	Mysidacea	Mysidae
777	NEOMAMER	Neomysis americana	Arthropoda	Mysidacea	Mysidae
783	OSTRACOD	Ostracoda	Arthropoda	Ostracoda	Unidentified
861	PYCNOGON	Pycnogonida	Arthropoda	Pycnogonida	Unidentified
862	TANAIDAC	Tanaidacea	Arthropoda	Tanaidacea	Unidentified
863	HYDROFAM	Hydroptilidae	Arthropoda	Trichoptera	Hydroptilidae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
665	ALCYONID	Alcyonidium spp.	Bryozoa	Bryozoa	Alcyonidiidae
666	CALLCRAT	Callopora craticula	Bryozoa	Bryozoa	Calloporidae
667	TURBDICH	Turbicellopora dichotoma	Bryozoa	Bryozoa	Celleporinidae
668	MEMBTENU	Membranipora tenuis	Bryozoa	Bryozoa	Membraniporidae
669	ANGUPALM	Anguinella palmata	Bryozoa	Bryozoa	Nolellidae
670	SCHIUNIC	Schizoporella unicomis	Bryozoa	Bryozoa	Schizoporellidae
671	AMATVIDO	Amathua vidovici	Bryozoa	Bryozoa	Vesiculariidae
617	BOSTPILU	Bostrichobranchus pilularis	Chordata	Ascidacea	Molgulidae
618	MOLGAREN	Molgula arenata	Chordata	Ascidacea	Molgulidae
619	MOLGMANH	Molgula manhattensis	Chordata	Ascidacea	Molgulidae
620	PEROVIRI	Perophora viridis	Chordata	Ascidacea	Perophoridae
621	AMARSTEL	Amaroucium stellatum	Chordata	Ascidacea	Polyclinidae
622	BOTRSCHL	Botryllus schlosseri	Chordata	Ascidacea	Styelidae
623	CNEMMOLL	Cnemidocarpa mollis	Chordata	Ascidacea	Styelidae
624	ASCIDIAC	Ascidacea	Chordata	Ascidacea	Unidentified
673	BRANCARI	Branchiostoma caribaeum	Chordata	Cephalochordata	Branchiostomidae
672	BRANVIRG	Branchiostoma caribaeum	Chordata	Cephalochordata	Branchiostomidae
615	PARARAPI	Paranthus rapiformis	Cnidaria	Anthozoa	Actinostolidae
616	ANTHOZOA	Anthozoa	Cnidaria	Anthozoa	Unidentified
626	ASTERIAS	Asterias spp.	Echinodermata	Asteroidea	Asteridae
627	ASTEROID	Asteroidea	Echinodermata	Asteroidea	Unidentified
719	ECHINODE	Echinodermata	Echinodermata	Echinodermata	Unidentified
720	ARBAPUNC	Arbacia punctulata	Echinodermata	Echinoidea	Arbaciidae
721	ECHIPARM	Echinarachnius parma	Echinodermata	Echinoidea	Echinarachnidae
722	MELLQUIN	Mellita quinquesperforata	Echinodermata	Echinoidea	Mellitidae
723	ECHINOID	Echinoidea	Echinodermata	Echinoidea	Unidentified
759	HOLOTHUR	Holothuroidea	Echinodermata	Holothuroidea	Unidentified
756	HEMICHOR	Hemichordata	Hemichordata	Hemichordata	Unidentified
770	MISCELLA	Miscellanea	Miscellanea	Miscellanea	Unidentified
771	NOORGPRS	No Organisms Present	Miscellanea	Miscellanea	Unidentified
628	ANOMSIMP	Anomia simplex	Mollusca	Bivalvia	Anomiidae
629	ANOMIA	Anomia spp.	Mollusca	Bivalvia	Anomiidae
630	ANOMSQUA	Anomia squamula	Mollusca	Bivalvia	Anomiidae
631	ARCIDFAM	Arcidae	Mollusca	Bivalvia	Arcidae
632	ASTARTE	Astarte spp.	Mollusca	Bivalvia	Astartidae
633	ASTARTID	Astartidae	Mollusca	Bivalvia	Astartidae
634	MYTILEUC	Mytilopsis leucophaeta	Mollusca	Bivalvia	Dreissenidae
635	GALEOMMA	Galeommatacea	Mollusca	Bivalvia	Galeommatacea
636	LYONSIA	Lyonsia spp.	Mollusca	Bivalvia	Lyonsiidae
637	MACTRFAM	Mactridae	Mollusca	Bivalvia	Mactridae
638	MYSEPLAN	Mysella planiata	Mollusca	Bivalvia	Montacutidae
639	MYSELLA	Mysella spp.	Mollusca	Bivalvia	Montacutidae
640	CRENDECU	Crenella decussata	Mollusca	Bivalvia	Mytilidae
641	CRENGLAN	Crenella glandula	Mollusca	Bivalvia	Mytilidae
642	CRENELLA	Crenella spp.	Mollusca	Bivalvia	Mytilidae
643	GEUKDEMI	Geukensia demissa	Mollusca	Bivalvia	Mytilidae
644	ISCHRECU	Ischadium recurvum	Mollusca	Bivalvia	Mytilidae
645	MODIOLUS	Modiolus spp.	Mollusca	Bivalvia	Mytilidae

NO	CODE	GENUS SPP.	PHYLYUM	CLASS	FAMILY
646	MUSCNIGE	<i>Musculus niger</i>	Mollusca	Bivalvia	Mytilidae
647	MUSCULUS	<i>Musculus</i> spp.	Mollusca	Bivalvia	Mytilidae
648	MYTILIDA	Mytilidae	Mollusca	Bivalvia	Mytilidae
649	MYTIEDUL	<i>Mytilus edulis</i>	Mollusca	Bivalvia	Mytilidae
650	NUCULANI	Nuculanidae	Mollusca	Bivalvia	Nuculanidae
651	NUCULA	<i>Nucula</i> spp.	Mollusca	Bivalvia	Nuculidae
652	PECTINID	Pectinidae	Mollusca	Bivalvia	Pectinidae
653	BARNTRUN	<i>Barnea truncata</i>	Mollusca	Bivalvia	Pholadidae
654	PHOLADID	Pholadidae	Mollusca	Bivalvia	Pholadidae
655	SOLECFAM	Solecurtidae	Mollusca	Bivalvia	Solecurtidae
656	TAGELUS	<i>Tagelus</i> spp.	Mollusca	Bivalvia	Solecurtidae
657	SOLENIDA	Solenidae	Mollusca	Bivalvia	Solenidae
658	TELLINID	Tellinidae	Mollusca	Bivalvia	Tellinidae
659	THRACIID	Thraciidae	Mollusca	Bivalvia	Thraciidae
660	THYASIRI	Thyasiridae	Mollusca	Bivalvia	Thyasiridae
661	BIVALDEP	Bivalvia: Other - Deposit Feeders	Mollusca	Bivalvia	Unidentified
662	BIVALSUS	Bivalvia: Other - Suspension Feeders	Mollusca	Bivalvia	Unidentified
663	BIVALVIA	Bivalvia: Other - Unidentified	Mollusca	Bivalvia	Unidentified
664	UNIONIDA	Unionidae	Mollusca	Bivalvia	Unionidae
725	BUCCINID	Buccinidae	Mollusca	Gastropoda	Buccinidae
726	CAECIDAE	Caecidae	Mollusca	Gastropoda	Caecidae
727	CAECUM	<i>Caecum</i> spp.	Mollusca	Gastropoda	Caecidae
728	CREPCONV	<i>Crepidula convexa</i>	Mollusca	Gastropoda	Calyptraeidae
729	CREPCOFO	<i>Crepidula convexa-fornicata</i> complex	Mollusca	Gastropoda	Calyptraeidae
730	CREPFORN	<i>Crepidula fornicata</i>	Mollusca	Gastropoda	Calyptraeidae
731	CREPMACU	<i>Crepidula maculosa</i>	Mollusca	Gastropoda	Calyptraeidae
732	CREPPLAN	<i>Crepidula plana</i>	Mollusca	Gastropoda	Calyptraeidae
733	CREPIDUL	<i>Crepidula</i> spp.	Mollusca	Gastropoda	Calyptraeidae
734	ANACHIS	<i>Anachis</i> spp.	Mollusca	Gastropoda	Columbellidae
735	COLUMBLD	Columbellidae	Mollusca	Gastropoda	Columbellidae
736	CYLICHNE	<i>Cyllichnella</i> spp.	Mollusca	Gastropoda	Cyllichnidae
737	EPITONIUM	<i>Epitonium</i> spp.	Mollusca	Gastropoda	Epitonidae
738	CRATENA	<i>Cratena</i> spp.	Mollusca	Gastropoda	Facelinidae
739	HYDROBIA	<i>Hydrobia</i> spp.	Mollusca	Gastropoda	Hydrobiidae
740	HYDROBII	Hydrobiidae	Mollusca	Gastropoda	Hydrobiidae
741	LYMNAFAM	Lymnaeidae	Mollusca	Gastropoda	Lymnaeidae
742	NASSARIUM	<i>Nassarius</i> spp.	Mollusca	Gastropoda	Nassariidae
743	NATICA	<i>Natica</i> spp.	Mollusca	Gastropoda	Naticidae
744	NATICIDA	Naticidae	Mollusca	Gastropoda	Naticidae
745	NUDIBRAN	Nudibranchia	Mollusca	Gastropoda	Nudibranchia
746	PLANORBI	Planorbidae	Mollusca	Gastropoda	Planorbidae
747	FARGOA	<i>Fargoa</i> spp.	Mollusca	Gastropoda	Pyramidellidae
748	ODOSTOMI	<i>Odostomia</i> spp.	Mollusca	Gastropoda	Pyramidellidae
749	PYRAMIDE	Pyramidellidae	Mollusca	Gastropoda	Pyramidellidae
750	TURBONIL	<i>Turbonilla</i> spp.	Mollusca	Gastropoda	Pyramidellidae

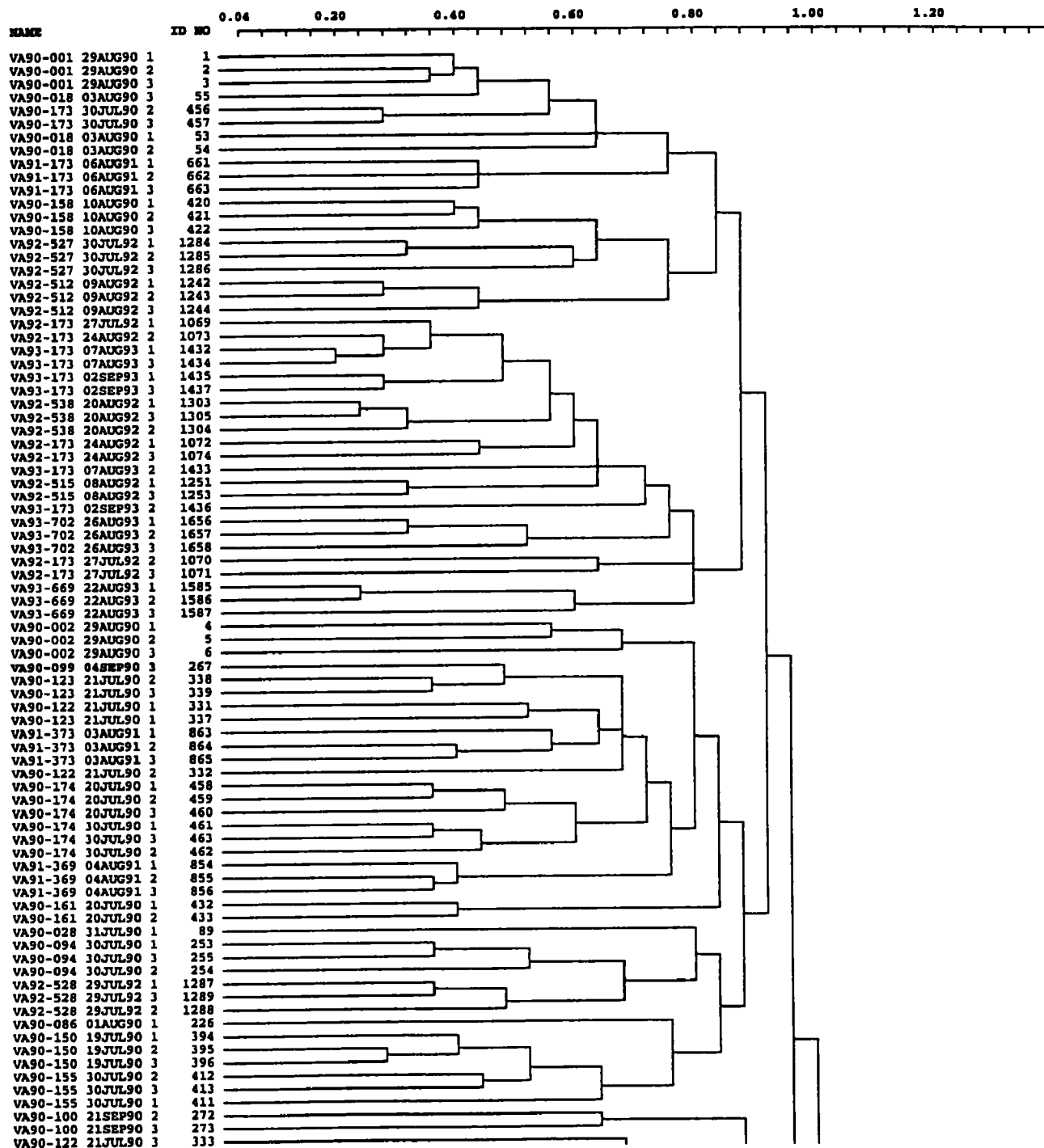
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751	SCAPHFAM	Scaphandridae	Mollusca	Gastropoda	Scaphandridae
752	TURRIFAM	Turridae	Mollusca	Gastropoda	Turridae
753	GASTROPO	Gastropoda: Other	Mollusca	Gastropoda	Unidentified
754	VITRINEL	Vitrinellidae	Mollusca	Gastropoda	Vitrinellidae
755	VIVIPARI	Viviparidae	Mollusca	Gastropoda	Viviparidae
858	CHAEAPIC	Chaetopleura apiculata	Mollusca	Polyplacophora	Chaetopleuridae
859	POLYPLAC	Polyplacophora	Mollusca	Polyplacophora	Unidentified
778	NEMATODA	Nematoda	Nematoda	Nematoda	Unidentified
864	TURBELLA	Turbellaria	Platyhelminthe	Turbellaria	Unidentified
860	PORIFERA	Porifera	Porifera	Porifera	Unidentified
<b>Taxa in the EMAP-E Species List but not present</b>					
868	NAISCOMM	<i>Nais communis</i>	Annelida	Oligochaeta	Naididae
866	AMPHABDI	<i>Amphioptus abdita</i>	Echinodermata	Ophiuroidea	Amphiuridae
867	HIATARCT	<i>Hiatella arctica</i>	Mollusca	Bivalvia	Hiatellidae



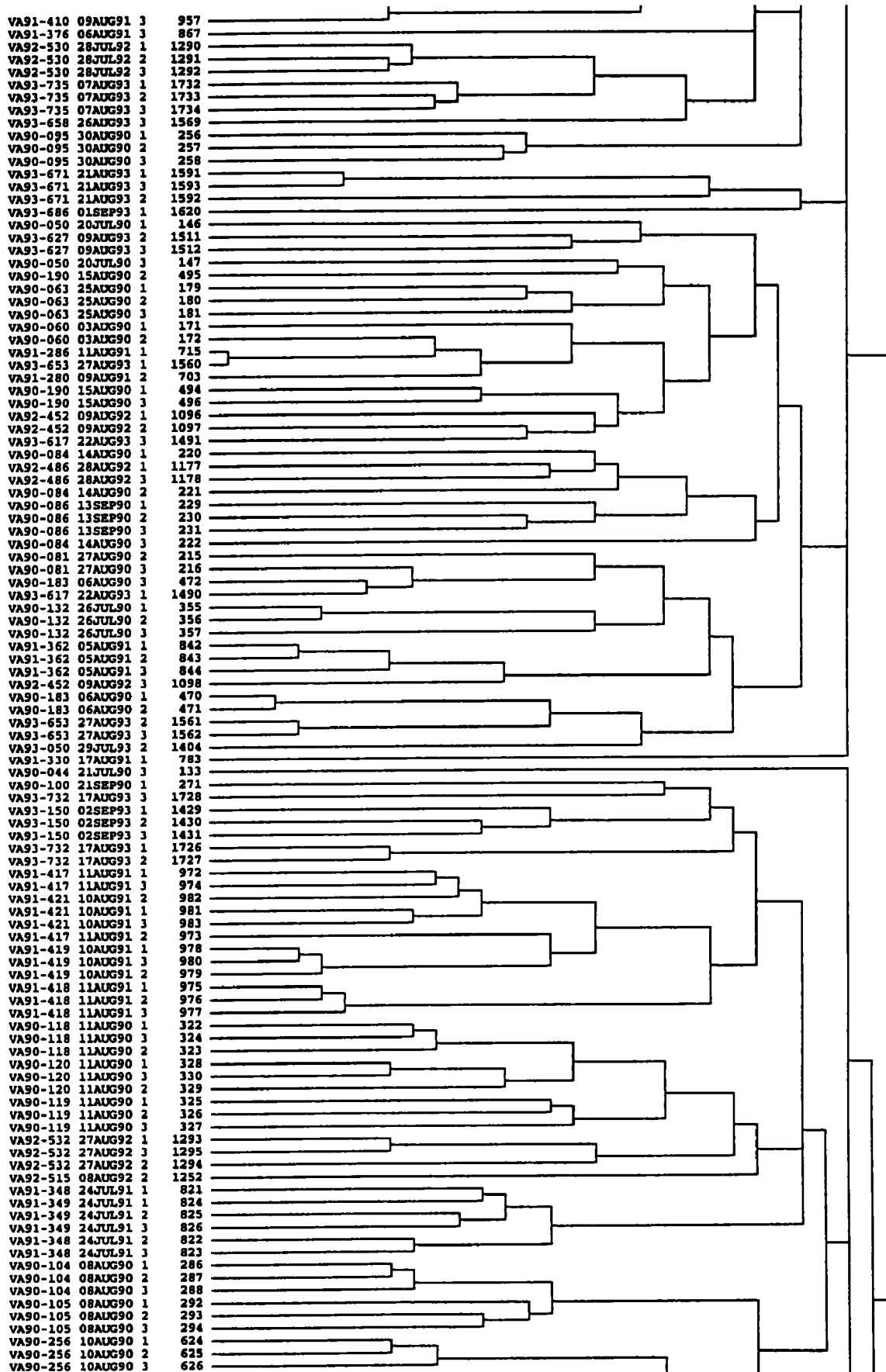
## APPENDIX IV SAMPLE CLUSTER ANALYSIS

A cluster analysis of the 1918-sample EMAP-E VP benthic data at CNESS (CNESS,  $m=25$ , UPGMA Sorting). All samples with fewer than 25 individuals were dropped (a requirement with a random sample size of 25). The pared data set consisted of 1736 samples and 466 species. New Bedford Harbor STA 099, a degraded estuarine station (Schimmel et al. 1993, Table B-2) is bolded. This degraded EMAP-E VP sampling site exhibits considerable variation among months and years.

### CNESS Distance (NESSm = 25)



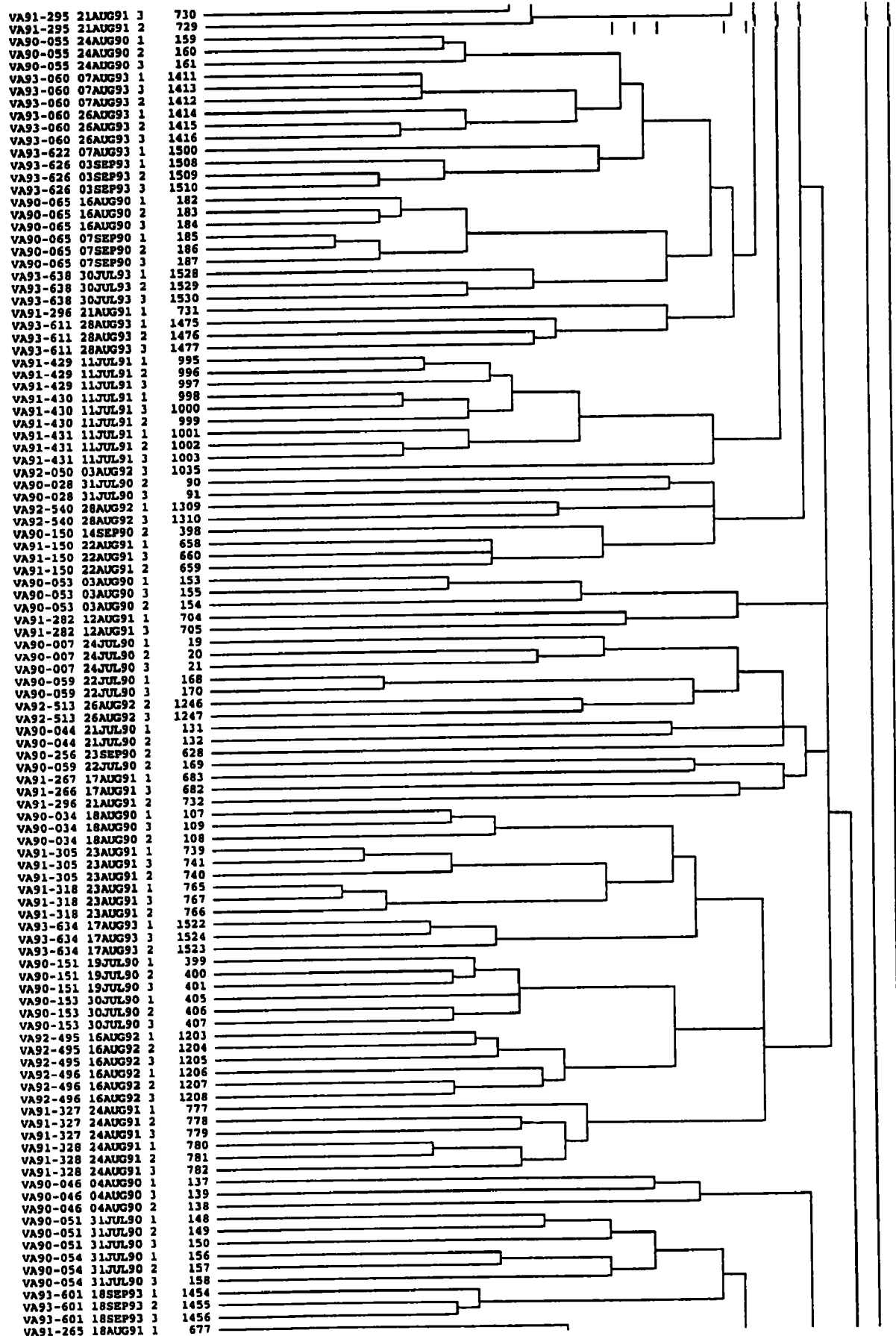
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VA93-714	19AUG93	1	1685
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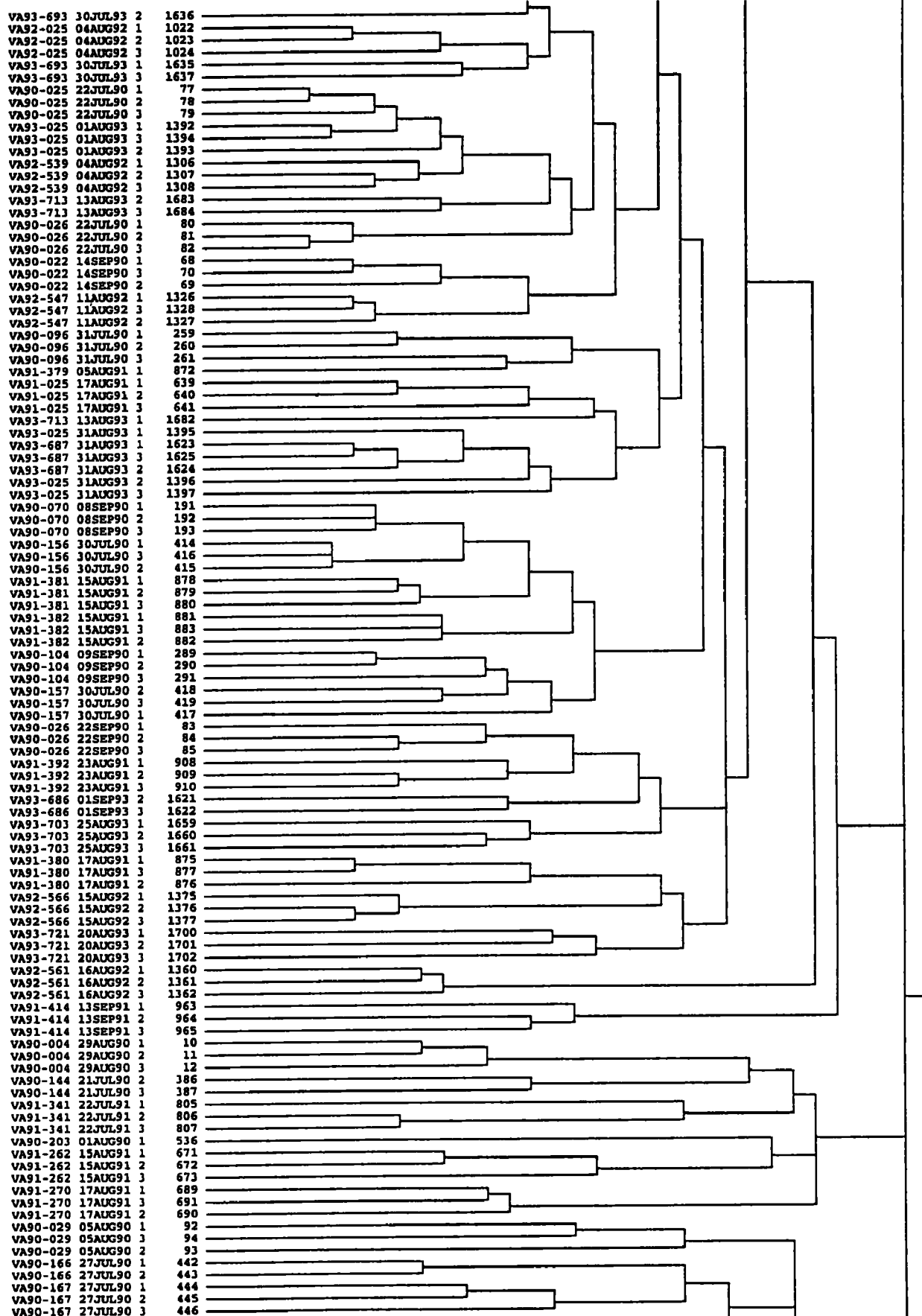
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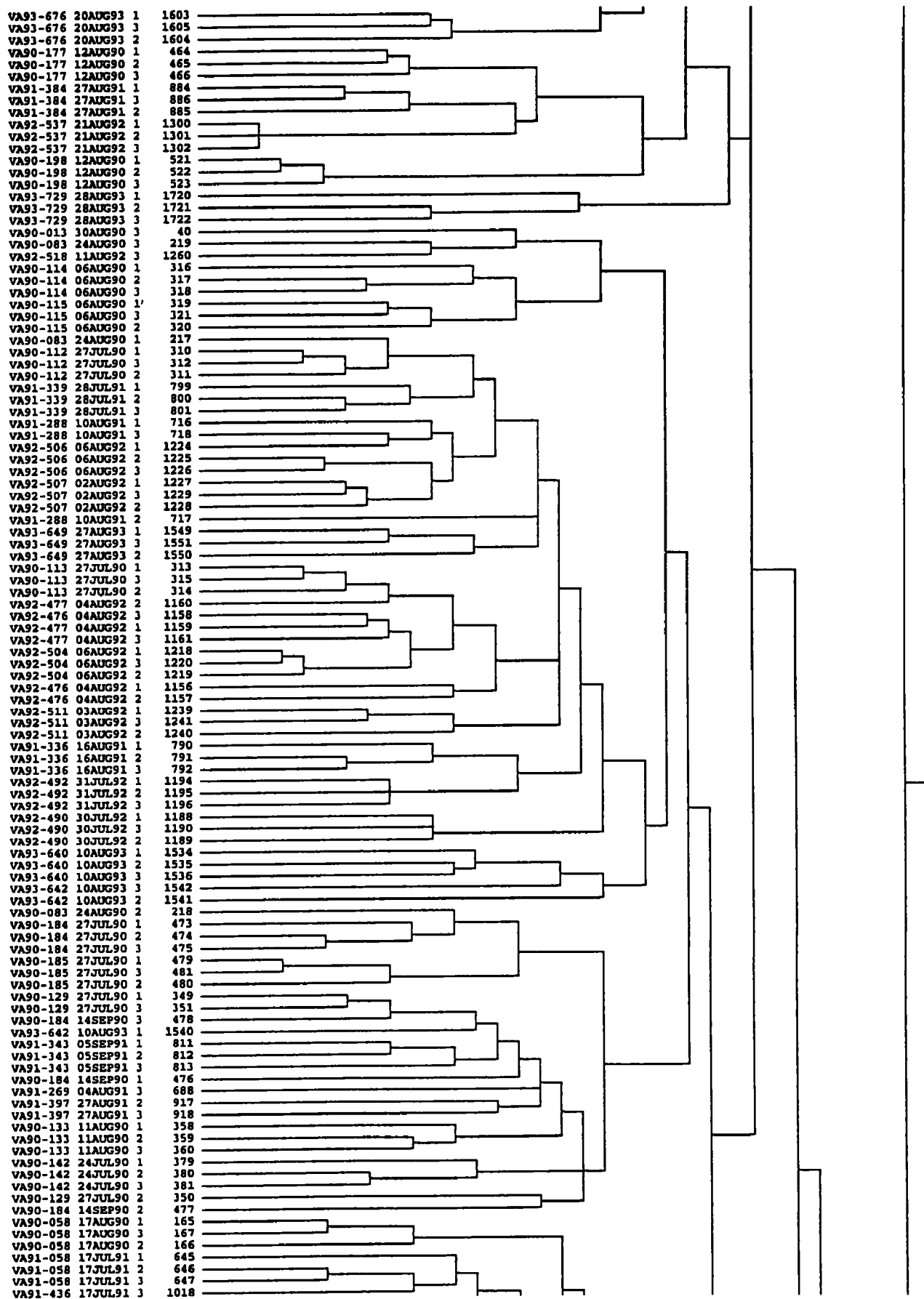
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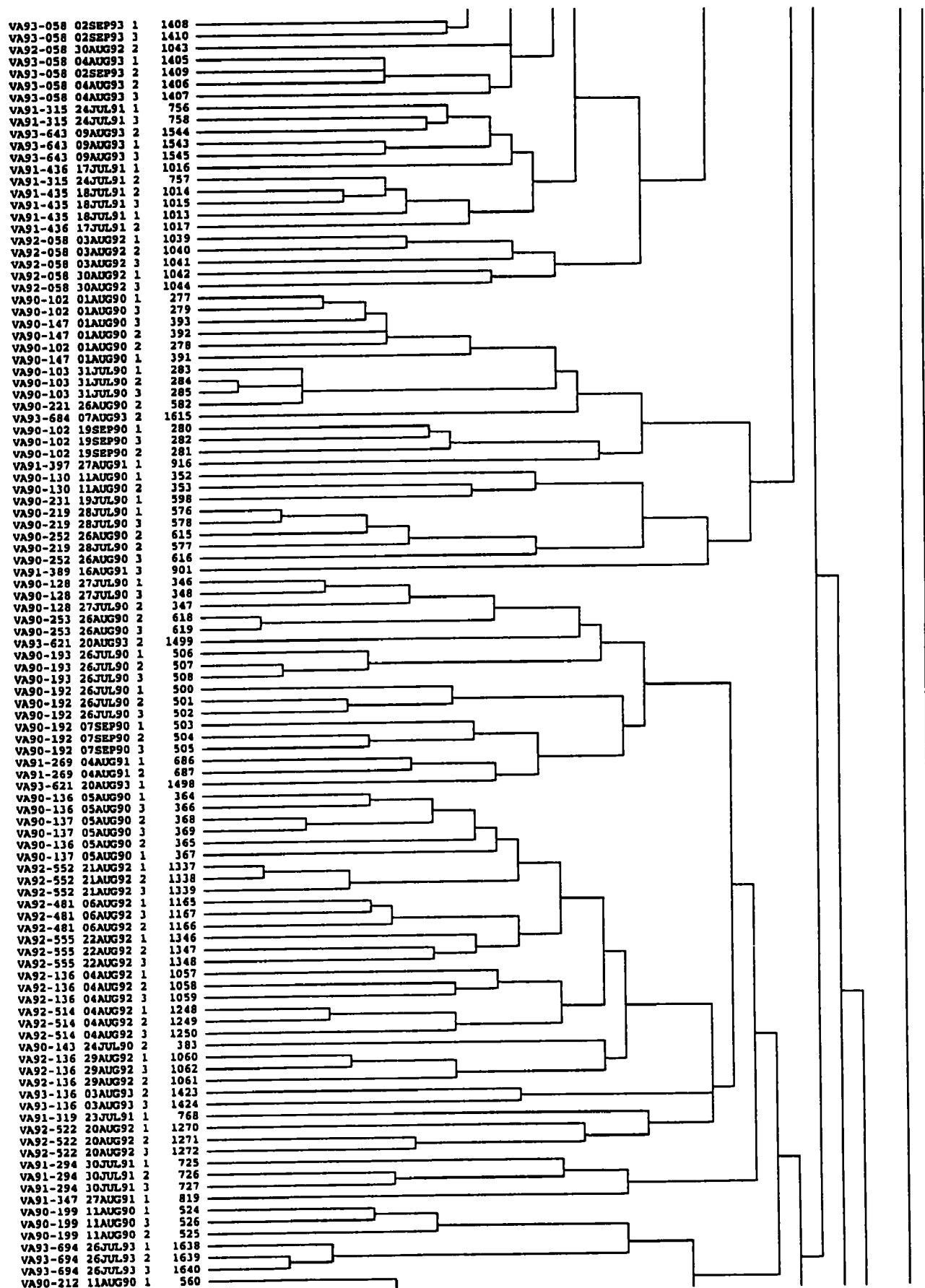
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VA90-258	10AUG90	2	632	
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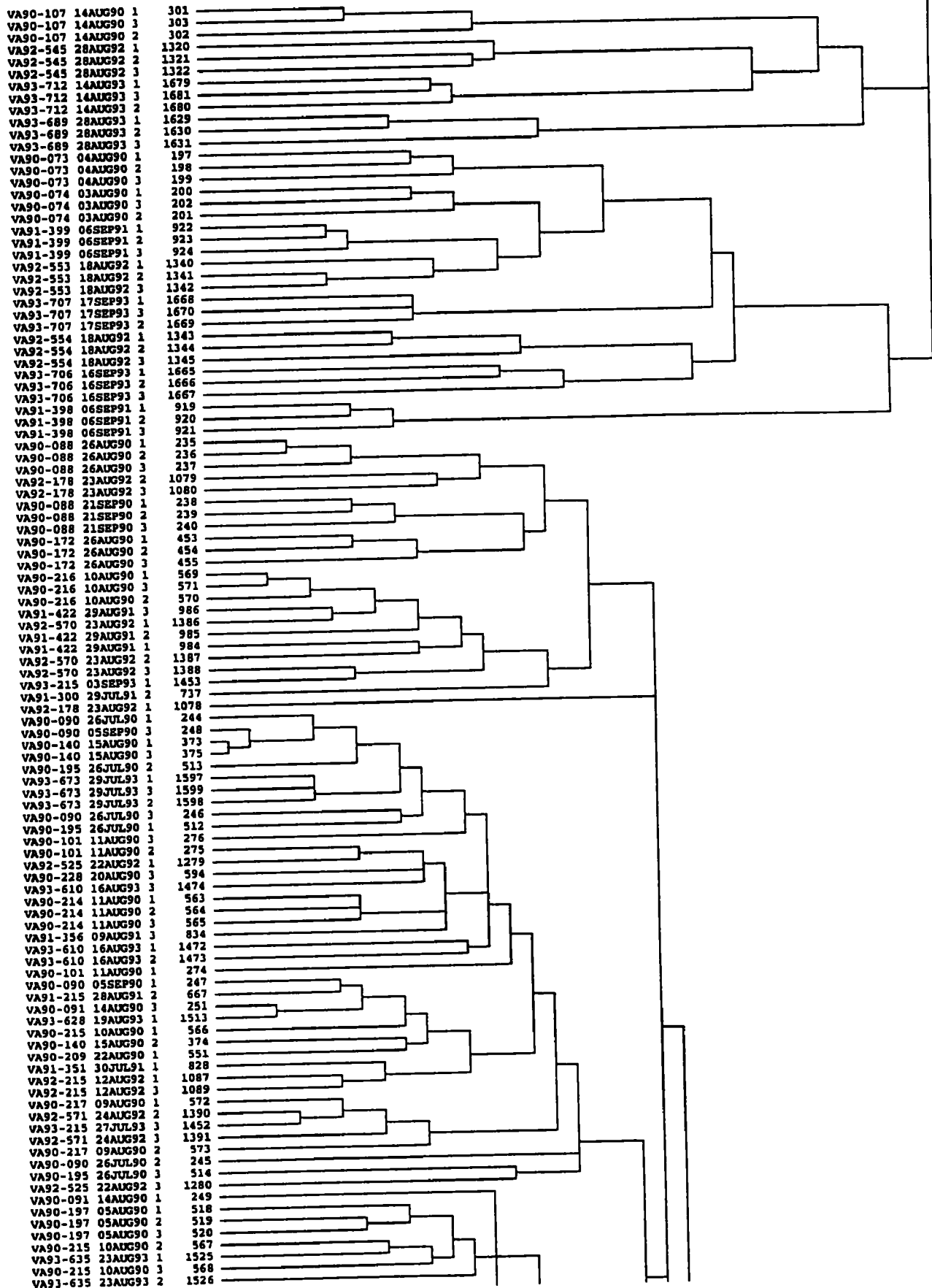


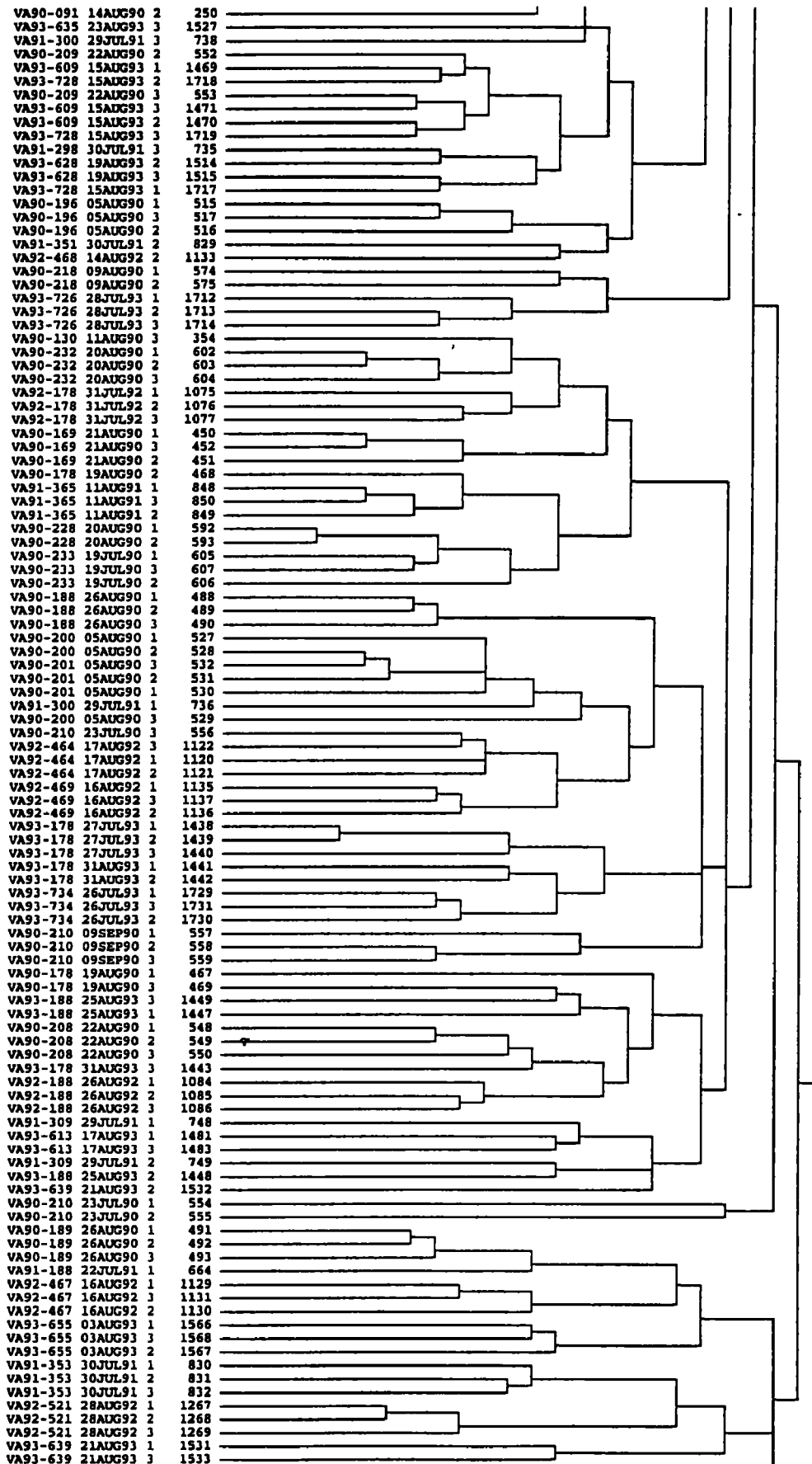
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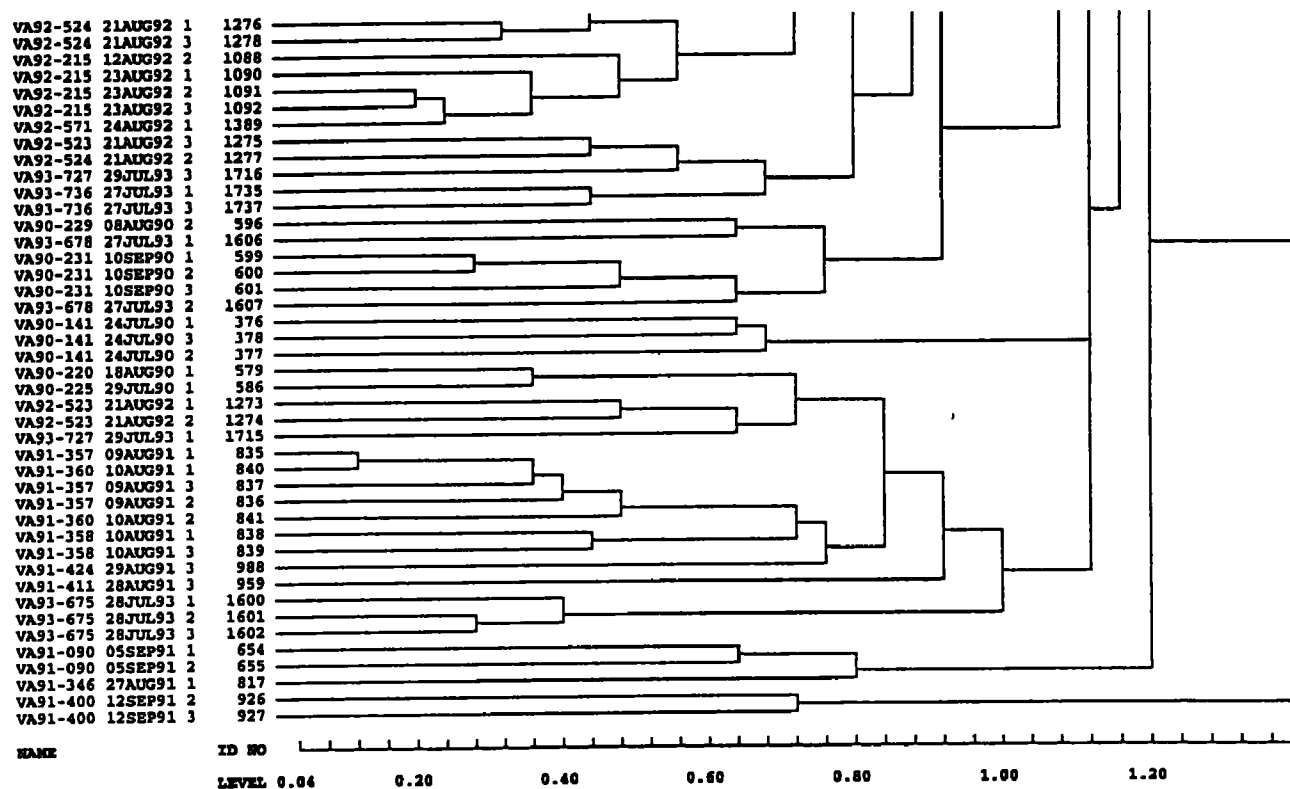
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VA90-207	22AUG90	2	546
VA90-207	22AUG90	3	547
VA90-253	26AUG90	1	617
VA91-347	27AUG91	3	820
VA90-220	18AUG90	2	580
VA92-471	18AUG92	3	1143
VA92-471	18AUG92	1	1141
VA92-471	18AUG92	2	1142
VA90-194	26JUL90	1	509
VA90-194	26JUL90	2	510
VA90-194	26JUL90	3	511
VA91-298	30JUL91	1	734
VA90-139	26JUL90	1	370
VA90-139	26JUL90	3	372
VA90-139	26JUL90	2	371
VA92-519	05AUG92	1	1261
VA92-519	05AUG92	2	1262
VA92-519	05AUG92	3	1263
VA91-346	27AUG91	3	818
VA91-356	09AUG91	1	833
VA91-188	22JUL91	2	665
VA91-188	22JUL91	3	666
VA91-333	22JUL91	1	784
VA91-326	23JUL91	2	775
VA91-326	23JUL91	1	774
VA91-326	23JUL91	3	776
VA92-502	27JUL92	1	1212
VA92-502	27JUL92	3	1214
VA92-502	27JUL92	2	1213
VA93-188	02AUG93	1	1444
VA93-188	02AUG93	3	1446
VA93-188	02AUG93	2	1445
VA93-651	01AUG93	2	1556
VA93-651	01AUG93	3	1557
VA91-333	22JUL91	2	785
VA91-333	22JUL91	3	786
VA90-093	23AUG90	2	252
VA91-403	21AUG91	1	934
VA91-403	21AUG91	3	936
VA91-403	21AUG91	2	935
VA90-143	24JUL90	1	382
VA90-223	11SEP90	3	584
VA90-225	29JUL90	2	587
VA90-225	29JUL90	3	588
VA92-560	22AUG92	3	1359
VA91-350	28AUG91	1	827
VA90-227	08AUG90	1	589
VA90-227	08AUG90	2	590
VA90-227	08AUG90	3	591
VA90-229	08AUG90	1	595
VA90-229	08AUG90	3	597
VA92-526	22AUG92	1	1281
VA92-526	22AUG92	2	1282
VA92-526	22AUG92	3	1283
VA93-678	27JUL93	3	1608
VA91-424	29AUG91	1	987

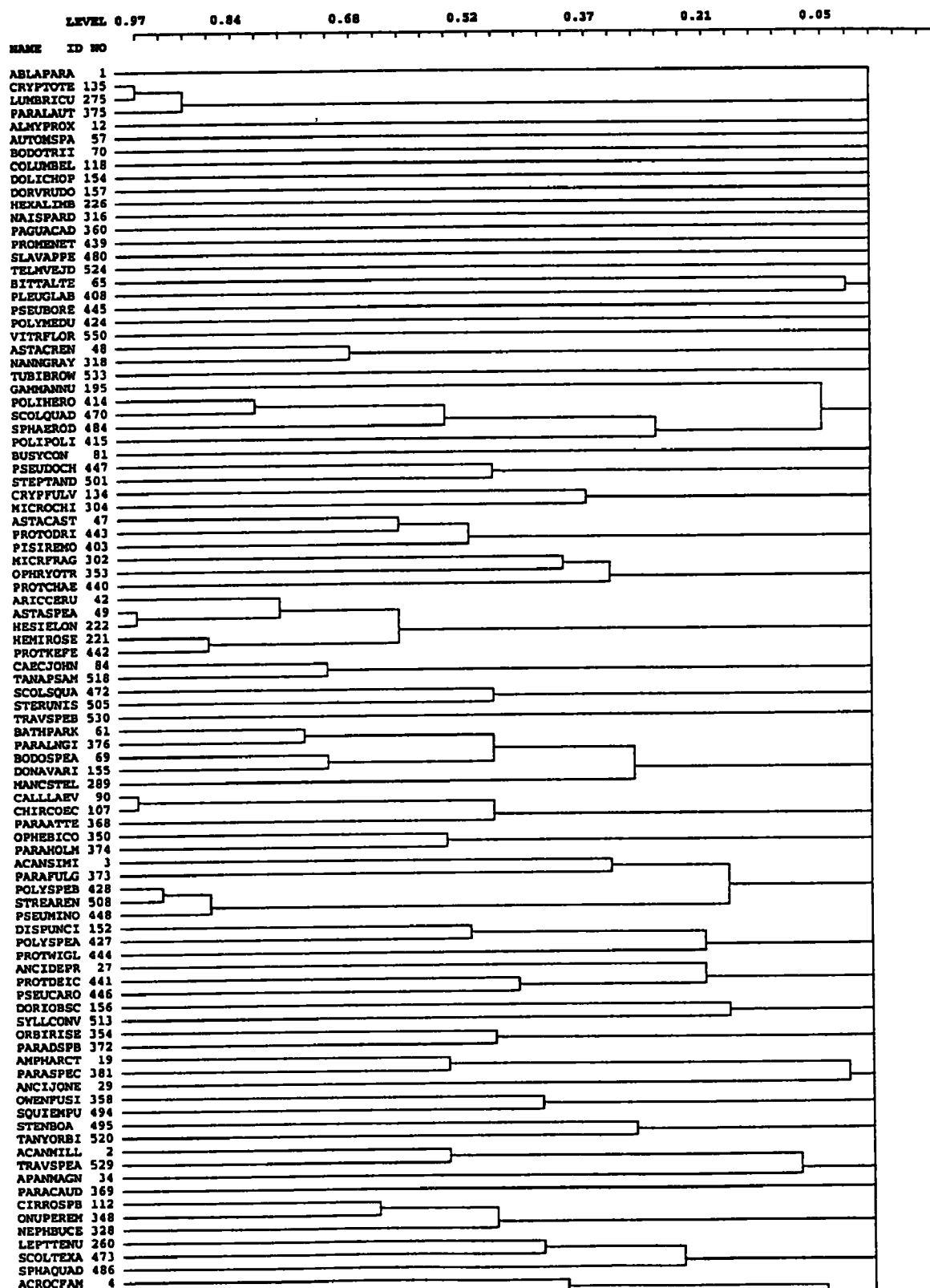


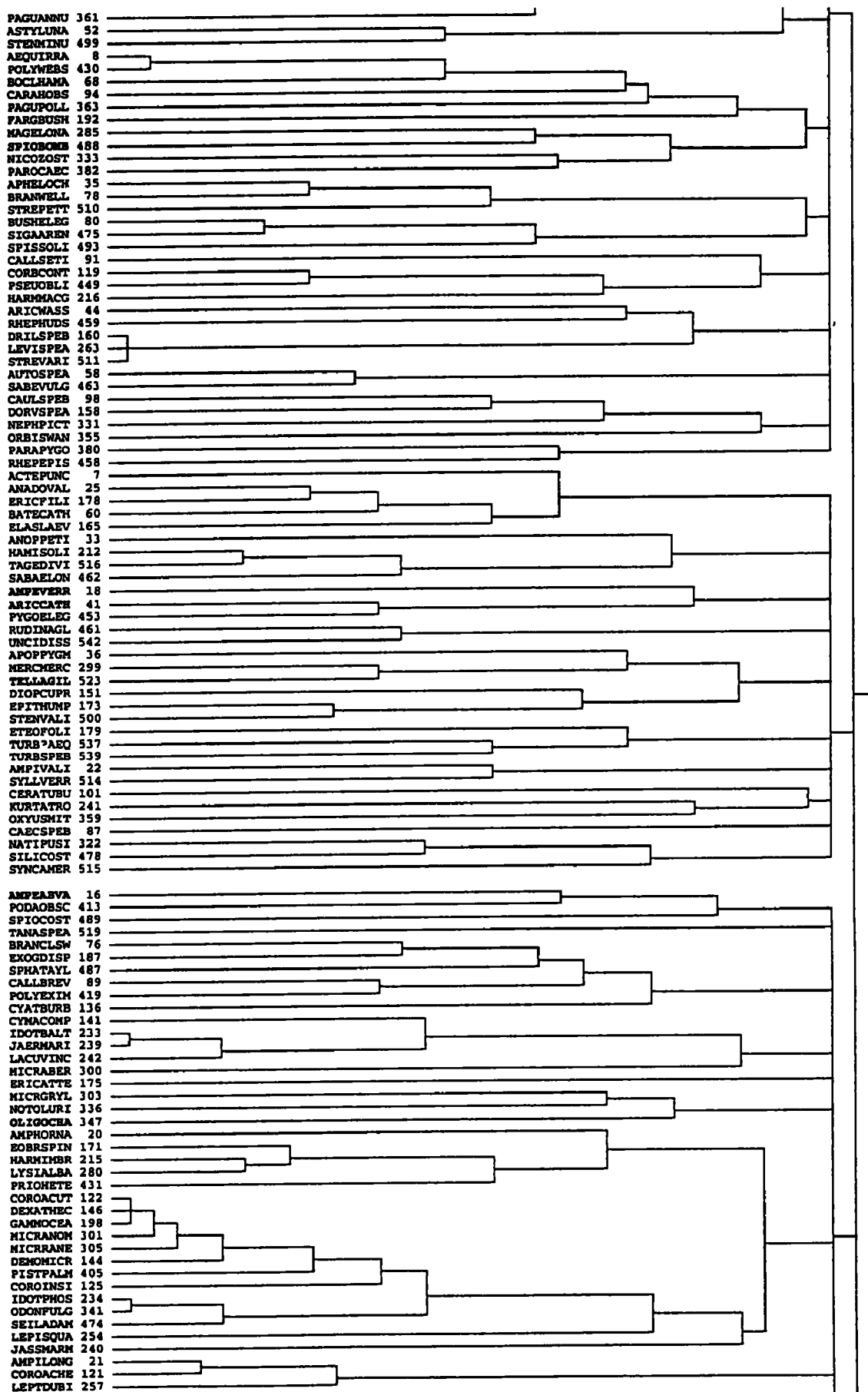


## APPENDIX V SPECIES CLUSTERS FOR ALL 551 EMAP-E VP TAXA

All EMAP-E VP taxa were clustered using the species-clustering methods described in Trueblood *et al.* (1994). Species are clustered using single linkage clustering of  $\cos \theta$ , where  $\theta$  is the angle between pairs of species vectors in the Gabriel covariance biplot (Figure 15).

### Pearson's R





STVASPEA	66
ODOSSPEA	343
LUMSTENI	276
SOLEVELU	481
ARABSPEA	38
LEMBSHIT	250
MICRSIMI	377
PARALONG	377
NEANAREN	323
NEOPSAYI	327
CAULBIOC	97
DODECACE	153
EUMISANG	185
UROSCINE	547
PLATDUM	407
POLYAGGR	416
RAETACF	455
ENOPSANG	169
NEANVIRE	325
LIBIEMAR	264
LYONAREN	278
MARPBELL	291

ANACLAFR	23
PETRPHOL	387
PHYLAEN	395
GLYCAMER	203
NASSTRIV	320
MUCRMUCR	310
PAGULONG	362
CYLIBIDE	140
SCOLBOUS	467
PROCVICI	438
EPITRUPI	174
MACOTENT	283
OPHIUROI	352
MALNSPEB	287
PECTGOUL	384

BOONBISU	71
ILYAABSO	235
ETEOHETE	180
STREBENE	509
LEITROBU	249
MICRSCEZ	306
MYAAREN	313
SPIOSETO	492
BOONIMPR	72
MELINITI	298
POLYCORN	418
PARAAEST	367
CRASVING	132
DULIAPPE	162
PANOHERB	366
NEANSUCC	324
COROSIMI	128
EKOGSPEA	189
UNCISERR	545
COROTUBE	129
ERICBRAS	176
PIONSPEB	401
CRANSEPT	131
PARACYPR	371
PROCCORN	435
EUPCLAUD	186
LEPISUBL	255
LYONHYAL	279
SCOLRUBR	471

ACTEORYZ	6
BRADVILL	75
HUTCHACR	229
PANDGOUL	365
PITAMORR	406
SIPUNCUL	479
NINONIGR	334
NUCUDELP	340
NOTOSPIN	338
PARGBART	191
MELIMACU	297
POLYHAEM	423
SCOLHEBE	469
TYPOAL_1	541
AGLACIRC	9
BYBLSERR	82
GONIGRAC	208
COROCRAS	124
CERAPINN	100
ASTAUNDA	50
CYCLBORE	138
HIPPSERR	227
CALYPSPA	92
SCOLCAPE	468
SPIOFILI	490
CIRRSPEA	113
PHOTPOLL	392
UNCIINER	543
CHONINPU	109
OPHEACUM	349
ORCHIMNU	356
PHYLMUCO	397
EKOQVERU	190
EUCHELEG	182
ISCHANGU	217
LAONKROY	247
AMPEAGAS	17
UNCIIRRO	544
COROBONN	123
PHOTDENT	391
STERCAND	503
PHYLMACU	396
EKOHEBE	188

