

**MULTIVARIATE ANALYSES OF THE IMPACT OF
OFFSHORE MARINE MINING ON THE BENTHIC
MACROFAUNA OFF THE WEST COAST OF
SOUTHERN AFRICA**

by

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MASTER OF SCIENCE

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*To my parents,
Derek and the late Deborah Savage.*

For encouraging me to follow my heart.

DECLARATION

This thesis reports the results of original research which I carried out under the auspices of the Marine Biology Research Institute, University of Cape Town. All assistance that I received has been fully acknowledged. This work has not been presented for a degree at any other university.

Signed by candidate

Signature Removed ..

Candida Savage

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Date

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The strategy for analysing multivariate data presented by Field *et. al.* (1982) was tested for its sensitivity in detecting the effects of offshore marine mining on macrobenthic communities. The technique has proven to be particularly sensitive and robust in elucidating changes in the structure of marine communities following organic pollution events. The primary aim of this study was to investigate its applicability in discerning community changes in an area exposed to physical disturbance of the seabed. Statistical testing, using analysis of similarities, reveals a highly significant difference between mined and unmined samples. Statistical testing also detects natural spatial heterogeneity across the 6 study areas. Aggregation of the data to higher taxonomic levels did not result in the loss of information, and in fact, improved the resolution of the community patterns. Multivariate analyses were therefore performed using the community data aggregated to genus-level. Hierarchical agglomerative clustering reveals two major groups of samples, the mined and the unmined samples. Within these two clusters, cluster analysis and non-metric multi-dimensional scaling distinguish between areas 1 and 2, areas 3 and 4, and areas 5 and 6. Area 2 provided a reference site where no mining is likely in the foreseeable future and area 1 was mined between the two sampling cruises, providing an indication of the changes induced by the mining process. Cluster analysis shows a shift in the grouping of samples from area 1. The unmined samples from area 1 grouped with the reference station (area 2) in the first survey. After the area was mined, the samples grouped with the mined samples from areas 3 and 4, indicating a shift in community structure. Multidimensional scaling ordination confirmed the groupings detected by cluster analysis and hence the groups of clusters can be accepted as real. Samples 3.5 and 3.7 from the *Rockfish* cruise and samples 4.6 and 4.9 from the *Pentow Salvor* cruise were conspicuous as outliers in both the cluster and ordination analyses. Geological results show that samples 3.5 and 4.9 also exhibit anomalously high proportions of gravel in the sediment, which possibly influences the community composition. Several species contributed to the overall dissimilarity between mined and unmined samples. The Amphipoda *Ampelisca anomala* and *Hippomedon longimanus* were reduced in abundance after mining. Furthermore, the Polychaeta *Prionospio pinnata*, *Haploscoloplos kerguelensis* and the Lumbrineris genus also appear to be sensitive to the effects of mining and were reduced in number. Organisms which showed an increase in relative abundance in mined areas included *Macoma crawfordi*, *Nassarius vinctus*, *Tricolia capensis* and *Terebellides stroemii*. There is a net increase in the proportion of Gastropoda and Bivalvia in the mined samples, which is possibly a reflection of the altered stratigraphy in mined areas. During the mining process, the fine sand component of an area is suspended in the water column and gradually disperses over a wide area. The net result is an increase in the relative proportion of the larger gravel and mud fractions. A meta-analysis of phylum-level community data was used to assess the severity of disturbance caused by marine mining *vis-a-vis* disturbance studies conducted on the N.E. Atlantic Shelf. The Namibian samples were consistently distinct from the samples collected off the N.E. Atlantic Shelf. It was hypothesized that this difference may reflect the anomalously oxygen-poor conditions on the continental shelf off the west coast of Southern Africa..

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CHAPTER 1

GENERAL INTRODUCTION

“The beginning is the signal part of any work...for that is the time at which the character is being formed and most readily receives the desired impressions.”

Plato

GENERAL INTRODUCTION

The analysis of changes in benthic community structure has been widely used for detecting and monitoring the biological effects of marine pollution. To date, however, no documented studies have tested the validity of using multivariate techniques for elucidating changes in soft-bottom benthic communities following physical disturbance of the sea bed. Field *et. al.* (1982) outlined a strategy for analysing multivariate data which has proven to be particularly sensitive and robust in revealing even subtle shifts in community structure following an organic pollution event (Warwick and Clarke 1991). The current study uses samples obtained from an offshore diamond mining area to test the applicability of using multivariate methods for detecting the effects of physical disturbance on the macrobenthos.

Soft-bottom macrobenthos have probably been the most widely used component of the marine biota in environmental impact studies (Warwick 1993). Marine benthos are arbitrarily divided into macrofauna (>1000µm), meiofauna (100-1000µm) and microfauna (1-100µm) (Parsons *et. al.* 1977). Soft-bottom macrobenthos are predominantly sessile and their long generation time means that the community structure reflects environmental conditions integrated over a long time (Gray *et. al.* 1990). The disadvantages of using macrobenthos in environmental impact studies are mainly pragmatic concerns. The equipment requires a relatively large research vessel and the identification process is time consuming, making benthic studies expensive. However, a multidisciplinary environmental impact study, commissioned by De Beers Marine (Pty) Limited in 1994, provided a good opportunity for collecting benthic samples from a physically disturbed area with no putative organic pollution. I was therefore

able to test the sensitivity of multivariate methods in revealing changes in benthic community structure due to physical disturbance.

Description of the mining operation

Mining takes place on the continental shelf off the Namibian coast in waters between 85 and 200 metres below mean sea level. Two mining processes are used, the underwater crawler and the large rotating drill, which can be considered equivalent in their severity of disturbance (M.Mittelmeyer, *pers. comm.*). Both methods use high-powered air-lift suction to deliver the gravel to the anchored mining vessel. To achieve the "airlift", compressed air is pumped down to the drill apparatus on the sea-floor. The air is then allowed to bubble up a thick-walled pipe and the difference between external and internal fluid densities creates a suction. This partial vacuum sucks up gravel from the sea-floor which is screened and treated on board for diamonds. The processed gravel is then released overboard in the form of tailings. During the mining process all sediments are removed to the level of bedrock, excepting the largest boulders. Sedimentological studies showed that the unmined sediment was a stratified sequence of gravels overlain by very fine sand. As a consequence of mining, the sequence is disturbed and the sediment is returned to the sea floor as a mixture. The fine sand component remains suspended in the water column and gradually disperses over a wide area by the prevailing currents. The net result is an increase in the relative percentages of the larger mud and gravel components (Rogers 1995).

A wide variety of numerical and statistical techniques have been developed for handling community data. The choice of an analysis method ultimately depends on the aims of the

study, but also on the nature of the data and the validity of the statistical assumptions (Heip *et. al.* 1988). The available methods can broadly be classified as (Warwick and Clarke 1991):

1. Univariate methods which reduce the relative abundances of the species in each sample to a single coefficient, for example a diversity index.
2. Distributional methods which summarise the relative abundances in each sample by a curve or histogram, for example a k-dominance curve.
3. Multivariate methods. Benthic communities are inherently multivariate (Field *et. al.* 1982) with a large number of species which vary in their sensitivity to disturbance. The most appropriate method of analysis would therefore be one that takes account of the varying sensitivities of species. Multivariate methods base their comparisons of two or more samples on the extent to which these samples share particular species as well as their relative importance in terms of abundance or biomass. The primary objective of multivariate analysis is to reduce the raw data set to a low dimensional graphical form in order to discern the most salient patterns in the community data.

Univariate and distributional methods are species-independent and two communities with entirely different taxonomic compositions could have the same diversity indices or dominance curves. Conversely, multivariate methods are species-dependent and exploit the fact that various organisms respond differently to disturbance, which makes it a much more sensitive technique than univariate or distributional methods (Warwick and Clarke 1991). Despite their greater sensitivity, multivariate methods in themselves are only indicative of community

change. They do not indicate whether the change is detrimental or not (Warwick and Clarke 1991). Use is made, therefore, of a meta-analysis which compares the current study to a range of other macrobenthic studies representing various levels of disturbance.

Thesis layout

Following this General Introduction which establishes the background and objectives of the current study, chapter 2 describes the field work and multivariate methods used. The various tools which account for the flexibility of the multivariate method are discussed and reasons for the chosen transformations and similarity coefficients are given. The sampling strategy is discussed in some detail and a method for estimating the number of replicates necessary to adequately represent the benthic community is presented.

The five aims of the study presented below are treated as separate chapters. Each chapter commences with an introduction to the statistical or numerical analysis dealt with in that chapter and then discusses the results. Chapter 3 uses formal statistical testing to assess whether mined samples are significantly different from unmined samples in terms of their biotic composition. The paradigm is that the groups of samples are identified *a priori* based on their putative level of disturbance. Analysis of similarities (ANOSIM), a statistical test analogous to ANOVA, was used to test the null hypothesis of no difference between disturbed areas and undisturbed areas.

Chapter four is essentially a descriptive stage in the analysis. Two complementary multivariate methods, namely hierarchical agglomerative clustering and ordination techniques, are used to

present the community data in a graphical form which is easy to interpret. The resultant dendrograms and multidimensional scaling (MDS) plots are used to obtain a low-dimensional picture of how the samples interrelate.

Chapter 5 attempts to relate the observed patterns from the multivariate analysis back to the biological characteristics of the community. The SIMPER (an acronym for “similarity percentages”) program assesses the relative importance of each species to the overall multivariate analysis. It is thereby possible to establish a list of indicator species which are characteristic of disturbed areas.

Having allowed the biological information to “tell its own story”, the sedimentology will be examined to determine any relations to the biotic pattern. Chapter 6 attempts to link environmental variables such as particle size, percentage organic carbon and percentage organic nitrogen to the observed community changes by superimposing the environmental parameters on the biological ordination.

A final stage in the analysis is to assess the relative level of severity of disturbance using a method recently proposed by Warwick and Clarke (1993a). A ‘meta-analysis’ is performed to compare pollution-induced disturbance studies with the samples collected from the mined areas.

A final concluding chapter summarises the most salient findings of the current study with particular emphasis on the applicability of using multivariate methods to detect changes in soft-bottom macrobenthos following physical disturbance to the sea bed.

Within this framework the main aims of the study were:

1. To test the null hypothesis that there is no difference in community composition between mined and unmined areas.
 2. To ascertain macrobenthic community distribution patterns in mined and unmined areas using graphical multivariate methods.
 3. To determine which species are primarily responsible for the dissimilarity between mined and unmined areas, with the aim of establishing a baseline list of indicator species.
 4. To investigate the link between sedimentology of the area and the benthic community structure.
 5. To compare the severity of disturbance caused by offshore marine mining to disturbance caused by organic pollution using a meta-analysis.
-

CHAPTER 2

METHODS

“Though this be madness, yet there is method in’t.”

Shakespeare (Hamlet)

METHODS

2.1 STUDY AREA

De Beers Marine operates in concession areas off the west coast of southern Africa which extend from the Olifants river mouth in the south to Luderitz in the north. Mining activity is limited to the Namibian continental shelf off the Orange River at depths of between 110-135m. Six sampling stations were selected north of the Orange river 20-30km off the Namibian coast. The southern sites, stations 5 and 6, were situated at 110m depth and were separated from the northern sites by approximately 30km. Stations 1 to 4 were at a mean depth of 130m (see Figure 2.1).

The six stations were sampled over two consecutive years, in June 1994 and February 1995. Five stations were mined at different times in the past providing a quasi-time series of post-mining recovery and there was one reference station where no mining is likely in the foreseeable future. Between the two sampling cruises, area 1 was mined, providing a reference point for an area before and after sampling. The six study sites with the different mining histories and their temporal states at the time of the sampling cruises are described in Table 2.1.

Figure 2.1. Map of study area off the west coast of Southern Africa. The six sampling stations are positioned in a grid drawn to scale where each block represents a 5km*5km (25km²) area.

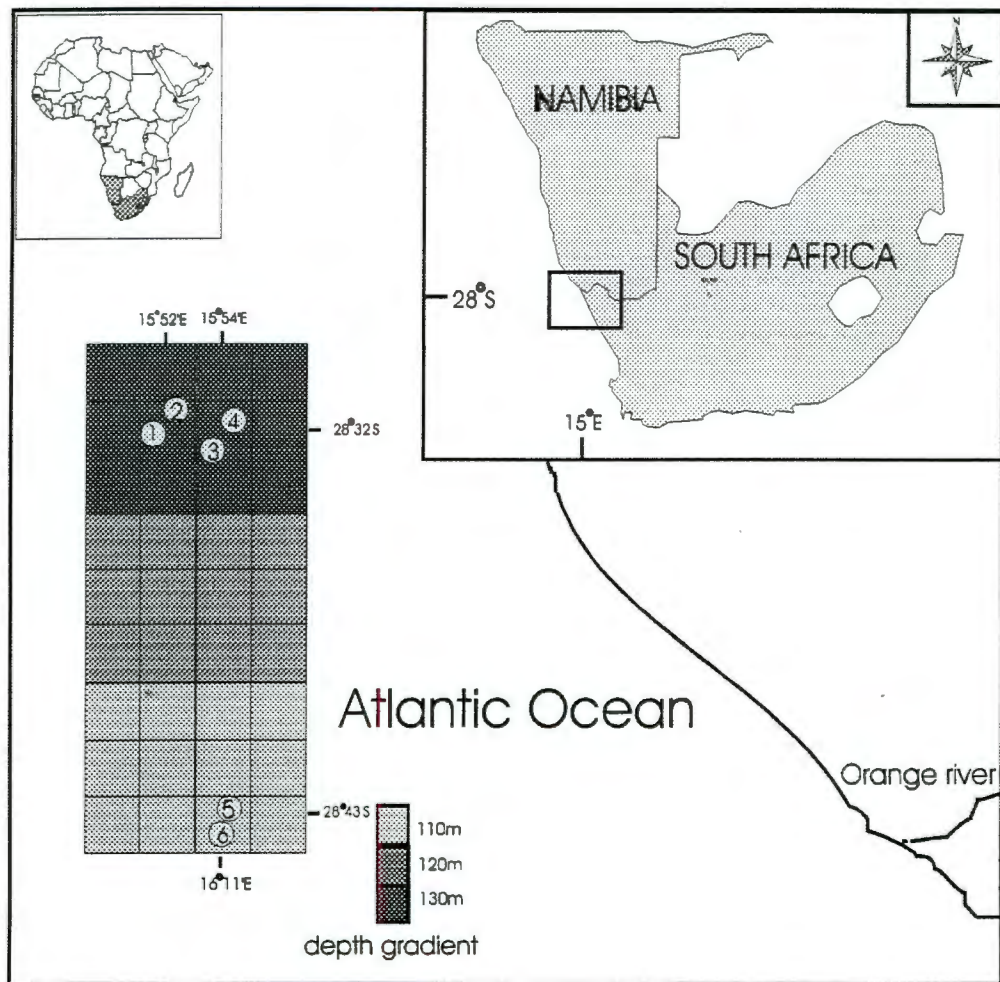


Table 2.1. Condition of samples and their temporal states of post-mining recovery at the time of sampling.

DATE MINED	AREA	TEMPORAL STATE OF RECOVERY AT TIME OF 1 ST CRUISE (JUNE 1994)	TEMPORAL STATE OF RECOVERY AT TIME OF 2 ND CRUISE (FEB. 1995)
Never	2	unmined	unmined
January 1995	1	unmined	0-1 month
May 1994	3	0-1 month	9 months
November 1993	4	6 months	15 months
November 1992	5	18 months	27 months
October 1990	6	43 months	50 months

During each sampling cruise a 0.2m² Van Veen grab was used to collect representative data of the diversity and density of the benthic macrofauna. The exact position of each grab sample is approximate as ocean currents and swell often cause the grab to drift off the proposed coordinates. This is dealt with in greater detail under the sub-heading sampling strategy below. During the first cruise (on board the *Rockfish*) ten samples were taken from each station with a total of 60 samples. The same six areas were revisited nine months later (on the *Pentow Salvor*) when an additional six samples were taken per area. Each sample is represented by a 2-digit number. The first digit represents the station number and the second digit the replicate sample taken at a particular station, for example 6.4 means the fourth sample taken at station 6. Sample numbers preceded by 'R' refer to samples collected during the first (*Rockfish*) cruise, similarly 'S' denotes samples collected during the second (*Pentow Salvor*) cruise. Samples are numbered according to the grab attempt number and are therefore not necessarily consecutive.

2.2 BENTHIC FAUNAL ANALYSIS

2.1.1 Field Work

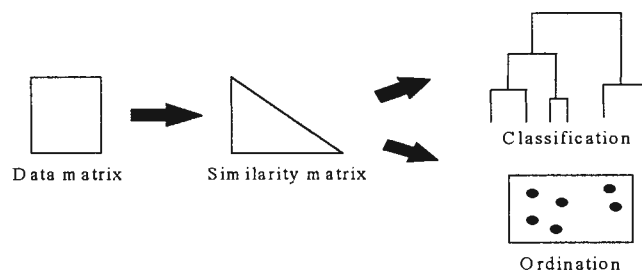
On board the sampling vessel the volume of each grab sample was estimated and a representative sample of the surficial sediment was taken for geological analyses. Each grab sample was sieved through a set of sieves and all organisms retained on the 1mm² sieve were fixed in 10% formalin and kept for further analysis.

Once in the laboratory, the samples were thoroughly rinsed in freshwater to remove all traces of formalin as this degrades soft muscle tissue and leaches the organisms' colour, and transferred to 1% phenoxatol. The samples were hand sorted to extract the organisms from the sediment and any organisms considered dead at the time of sampling were excluded from the study. The macrofauna were identified to the lowest possible taxon and then blot-dried and weighed.

2.1.2. Numerical analysis

Field *et. al.* (1982) outlined a strategy for analysing multispecies data. The starting point for the multivariate analysis is the concept of similarity between any pair of samples, in terms of the biological samples they contain. It is thus a biologically-motivated definition of what constitutes similarity or dissimilarity between two communities (Clarke and Warwick 1994), and thus multivariate techniques are much more sensitive than univariate methods to changes in community structure. Similarities are calculated between every pair of samples and these values entered into a triangular matrix of similarity. This similarity matrix is the basis for the clustering and ordination analyses.

Figure 2.2. Schematic diagram representing the stages in the multivariate analysis of benthic community data.



The community data were analysed using the computer package PRIMER (Plymouth Routines In Multivariate Ecological Research), which was designed with a bias towards studies of soft-bottom benthos. The primary objective of PRIMER is to reduce the complexity of the data by graphical representation of the biological relationships between the samples. The program thereby highlights patterns in community structure that are often not readily apparent in the raw data.

The inherent flexibility of the multivariate method is afforded by the range of options available for prior treatment of the data. The choice of transformation and the similarity coefficient affects the relative contributions of each species to the overall analysis.

Transformation of raw data. Similarity between samples can be defined in several ways, each giving different weight to different aspects of the community. For example, some definitions might concentrate on the similarity in abundance of the most common species whereas others emphasize the abundance of rare species. Such similarities do not take cognisance of the similarity of the overall community composition. It is therefore desirable to transform the data prior to calculating the similarity matrix. Forms of transformation range from no transformation, square root or logarithmic transformation, to the reduction of the data to presence-absence values for each species (Clarke and Green 1988). At the former end of the spectrum emphasis is focussed on the species that numerically dominate most samples, at the latter end the rarer species will be given more weighting (Clarke and Green 1988). The current study uses 4th root-transformation:

$$Y_{ij} = \sqrt{\sqrt{X_{ij}}} = X_{ij}^{\frac{1}{4}} \quad (\text{Field } et. al. 1982).$$

Fourth root-transformation down-weights the importance of the very abundant species so that the less dominant, and even the rare, species play some role in determining similarity of two samples.

Similarity coefficient. Macrobenthic survey data typically consist of matrices where many species are absent from the majority of samples, typically more than half the entries are zeros. Transformation of the data should not change this, and a similarity matrix which is not affected by joint absences is computed (Field *et. al.* 1982). The coefficient of similarity which has proved to be particularly robust with marine biological data is the Bray-Curtis or Czekanowski coefficient (Bray and Curtis 1957). The Bray-Curtis coefficient defines the similarity between the j^{th} and k^{th} samples, S_{jk} , as:

$$S_{jk} = 1 - \delta_{jk}$$

$$\text{where } \delta_{jk} = \frac{\sum_{i=1}^s |Y_{ij} - Y_{ik}|}{\sum_{i=1}^s (Y_{ij} + Y_{ik})} \quad (\text{Field } et. al. 1982)$$

Y_{ij} represents the entry in the i^{th} row and j^{th} column of the data matrix (i.e. the abundance or biomass of the i^{th} species in the j^{th} sample) (Field *et. al.* 1982).

Classification. Cluster analysis (or classification) aims to find the “natural groupings” of samples such that samples within a group share a more similar suite of species than samples in different groups. The current study makes use of hierarchical agglomerative clustering

techniques which produce a dendrogram which successively fuses the samples into groups, and the groups into larger clusters, starting with the highest mutual similarities then gradually lowering the similarity level at which groups are formed.

The classification technique has four drawbacks:

- The hierarchy is irreversible, therefore, once samples are grouped together their identity is lost;
- The dendrograms only show inter-group relationships and the level of similarity reflects the average inter-group value;
- The sequencing of samples is arbitrary, so unrelated samples may be placed next to each other;
- Cluster analysis tends to over-emphasize discontinuities and may force a graded series into discrete classes (Field *et. al.* 1982).

It is therefore important to employ an additional method of presentation, such as ordination techniques. If the two complementary methods agree, discontinuities can be accepted as real (Field *et. al.* 1982).

Ordinations. The PRIMER package uses non-metric multidimensional scaling (MDS) as the preferred method of ordination. MDS is perhaps the most robust ordination technique available, using only rank order information (for example, Station A is more similar to Station B than it is to Station C) (Gray *et. al.* 1988). MDS ordination produces a 2-dimensional or 3-dimensional plot which represents the best possible reconciliation between all inter-station distances. The distances between points on the plot are a measure of their relative degree of (dis)similarity. Points which are close together will represent stations that are similar in species

composition, while the further apart any two stations are, the more dissimilar the stations will be. Because ordination methods reduce inherently high-dimensional data to a low-dimensional plot, some distortion is involved. A stress function is therefore computed which assesses how well the sample relationships are represented in the 2-D plot. The lower the stress value, the more accurate the representation of samples in the MDS.

Formal statistical testing. The patterns in community structure can be verified by statistical testing which identifies changes on a spatial and temporal scale. Formal significance tests for differences between sites were performed using the ANOSIM permutation test (Clarke and Green 1988).

Finding species responsible for grouping. Following the division into station groups from the classification and ordination results, the species having the greatest contribution to this division were extracted using the similarity percentages (SIMPER) program available in the PRIMER package.

Environmental factors. Any attempt to explain changing biological patterns should be accompanied by a suite of environmental variables. The current study measured the percentage composition of mud, sand and gravel and the average percentage organic carbon and nitrogen. The relative contribution of these environmental factors in influencing the community structure was assessed by superimposing each factor on the biological MDS plot.

2.3. GEOLOGICAL ANALYSES

2.2.1. Textural analysis

The textural analysis and the particle size analysis was conducted at the Marine Geoscience Unit at the University of Cape Town by Dr. David Li and under the auspices of Dr. John Rogers.

The surficial sediment was examined to measure the percentage composition of mud, sand and gravel. Interstitial salt was removed from the sediment by osmosis. The samples were dialysed overnight in cellophane tubing suspended in a bucket of running water. The sediment was then wet-sieved through a 63-micron sieve to separate the silt+clay fractions (<63-microns) from the sand+gravel (>63-microns) fractions. The sand+gravel fractions were dried overnight at 105°C and weighed. The gravel component was further separated from the sand by dry-sieving through a 2mm sieve. The gravel fraction was then weighed and the sand fraction derived by subtraction.

The silt+clay fraction was transferred to a 1-litre perspex cylinder and, after vigorous stirring, a 25ml aliquot was removed. This aliquot was dried overnight and thereafter weighed. A pipetting factor of 40 was then used to multiply the aliquot weight to determine the weight of silt+clay. This weight was then added to that of sand and gravel to calculate the total weight and the percentages of the individual fractions. A triangular Gravel-Sand-Mud diagram devised by Folk (1954) was then used to classify each sample texturally.

2.2.2 Particle size analysis

Each sand fraction was split to a weight of 2-3g, weighed and then settled in a settling tube. The weight accumulating on a pan suspended from an electronic balance was recorded at 1.5 second intervals. The results produced an arithmetic cumulative curve, a probability plot and a frequency curve. The cumulative percentages at $1/10$ phi intervals were printed out to calculate the percentages of individual phi-fractions.

$$\text{phi} = -\log_2 (\text{particle diameter (mm)}) \quad (\text{Rogers 1995}).$$

The particle size analysis of the silt+clay fraction was determined using a computer-linked Sedigraph 5000D, which sends a beam of x-rays through a glass-sided cell through which the silt+clay fraction is pumped. As the silt and clay particles settle out, relatively more x-rays are detected. The relatively high organic content of the samples could cause the samples to flocculate within the cell. Therefore, the organic matter was removed using hydrogen peroxide in a water bath, in a process taking up to 6 weeks.

2.2.3 Measurement of organic matter, calcium carbonate and nitrogen

Representative samples were analysed for the total carbon and total nitrogen and for the total organic carbon and the total organic nitrogen by the C.S.I.R. (Council for Scientific and Industrial Research) at Stellenbosch. The samples were dried at 50°C to prevent the loss of volatiles and then crushed. A subsample of the crushed material was analysed for the total carbon and total nitrogen content using a CHN analyser. A second subsample was acidified

with concentrated HCl and dried before analysing for the acid-insoluble total organic carbon and total organic nitrogen content.

A factor of 1.8 was used to estimate the percentage of organic matter. Using atomic masses of 40 for calcium, 12 for carbon and 16 for oxygen, a molecular mass of 100 is obtained for CaCO_3 . Therefore, if the percentage of inorganic carbon is known, by applying a factor of $100/12$, the percentage of CaCO_3 can be calculated.

2.4 SAMPLING STRATEGY

The design problem

“ No one would now dream of testing the response to a treatment by comparing two plots, one treated and the other untreated.”

R.A. Fisher and J. Wishart 1930 (in Hurlbert 1984)

Macrobenthic communities typically exhibit a high degree of spatial patchiness on a local scale. Benthic studies therefore frequently encounter problems in selecting a suitable control from a heterogeneous environment and typically suffer from ‘pseudoreplication¹’ problems (Hurlbert 1984). The need for adequate temporal replication was addressed by Bernstein and Zalinski (1983) and Stewart-Oaten *et. al.* (1986) in their BACI (Before/After, Control/Impacted) design. The design was further improved by Underwood (1992) who included spatial replicates. An appropriate sampling scheme should include replicated sampling in time and replicated sampling at appropriate spatial scales.

The current study attempts to overcome the 'pseudoreplication' problem by having local reference replicates from each sampling station which provide a reference point for the amount of natural heterogeneity between sites. As discussed above, 10 replicates were taken per study site during the first cruise and a further 6 replicates per site were taken the following year. Several grab samples from each station were taken outside, yet adjacent to, the mined areas, thus providing an indication of the benthic community structure in undisturbed areas.

The exact positions of grab samples are approximate as ocean currents and swell often cause the grab to drift off the co-ordinates. The sample positions, however, can be plotted to within 20m accuracy using a Global Positioning System (GPS) and by noting the prevailing current direction during sampling. The co-ordinates for each grab sample were plotted onto a map of the mined areas by a surveyor from De Beers Marine. Furthermore, the particle size analysis provides clues as to the level of disturbance for each replicate sample. Unmined areas are characterised by a unimodal size frequency distribution whereas mined areas typically exhibit a polymodal distribution (Rogers 1995). Therefore, by concurrently plotting the sample positions on a map of the mined areas and using the sediment size frequency distribution, we were able to determine the condition of each replicate sample; i.e. whether it was mined or unmined. The condition of each replicate from both cruises is tabulated in Table 2.2.

¹'pseudoreplication' is defined as the testing for treatment effects with an error term inappropriate to the hypothesis being considered (Hurlbert 1984). In other words, a hypothesis with generality is developed, but the measurements made are too small to cover the whole hypothesis.

Table 2.2. List of mined and unmined replicates from the *Rockfish* and *Pentow Salvor* cruises. According to the GPS positions of the stations.

CONDITION		ROCKFISH CRUISE	PENTOW SALVOR CRUISE
UNMINED	Site 1	1.1 1.2 1.3 1.4 1.5 1.6 1.7 1.8 1.9 1.10 1.11	1.15
	Site 2	2.1 2.2 2.3 2.4 2.5 2.6 2.7 2.8 2.9 2.10	2.2 2.3 2.4 2.5 2.6 2.7
	Site 3	3.1 3.3 3.5 3.6 3.7 3.8 3.10	3.5
	Site 4	4.1 4.3 4.4 4.5	
	Site 5	5.1 5.4 5.5 5.6 5.7 5.8 5.9 5.10	5.2 5.3 5.5 5.6 5.9 5.11
	Site 6	6.6 6.7	6.2 6.4 6.6
MINED	Site 1		1.1 1.5 1.11 1.14 1.17
	Site 2		
	Site 3	3.2 3.4	3.1 3.2 3.3 3.4 3.7
	Site 4	4.2 4.6 4.7 4.8 4.9 4.10	4.2 4.6 4.8 4.9 4.13 4.14 4.15
	Site 5	5.3	
	Site 6	6.8 6.9 6.10	6.1 6.3 6.5

Several replicates were uncertain in terms of their exact position and hence mining status and are subsequently excluded from the study. These replicates are R6.1, R6.2, R6.3, R6.4 and R6.5. The above classification for each replicate was used for defining the *a priori* condition of each replicate for the statistical tests in chapter 3.

Another design problem inherent in macrobenthic studies is assessing how many replicates are appropriate to adequately represent the community structure. The heterogeneity of benthic communities coupled with the intensity of labour in terms of sampling effort and taxonomic work, make benthic surveys expensive and time-consuming. The number of replicates taken is therefore often a compromise between pragmatic considerations and statistical robustness and one needs to exercise some valued judgements in terms of sampling efficiency. Two sampling

variables were considered in this study; the level of taxonomic identification (discussed in chapter 4) and the number of samples necessary to represent patterns in community structure. The question of ‘how many replicates are enough?’ is particularly appropriate in the current study where some sites were represented by very few impacted replicates.

Karakassis (1995) proposed a mathematical method to calculate the minimum sampling area based on macrobenthic species richness. The total number of species, S_{∞} , within a benthic community is calculated by plotting the cumulative number of species in k samples by the cumulative number of species in $k+1$ samples and solving the regression line for $y = x$ (Karakassis 1995). Essentially, one is calculating the upper limit of the asymptote in a species-area curve. Thus, the method examines the rate at which different species are incorporated into the data set with increasing sampling effort (Karakassis 1995).

The algorithm is based on presence-absence data and consists of the following steps:

- A random numbers generator is used to execute different random permutations of the sampling units (i.e. for each species the sites where it occurs is randomized but the total (proportion) of that species remains constant).
- The cumulative number of species (S_{ik}) present in k quadrats in the i^{th} permutation of the sampling units is computed (Karakassis 1995).
- The mean species content for all k quadrats is calculated using:

$$\bar{S}_k = \frac{1}{P} \sum_{i=1}^P S_{ik}$$

- The regression line for the pairs $(\bar{S}_k, \bar{S}_{k+1})$ is plotted using:

$$\bar{S}_{k+1} = a + b\bar{S}_k$$

- The equation of the regression line is solved for $\bar{S}_k = \bar{S}_{k+1}$

$$S_\infty = \frac{a}{1-b} \text{ (Karakassis 1995).}$$

A computer program was written in Tru Basic v2.0 to generate the above algorithm (see Appendix B). The abundance matrices from the combined cruise data were converted to presence-absence data and the program run using 150 permutations for the 59 unmined samples and the 32 mined samples, respectively. The minimum number of samples required in order to obtain a reliable estimate of S_∞ for the unmined stations was 31 samples. The estimated number of samples for the mined stations was less, with S_∞ being adequately represented with 23 samples. The lowered number of samples necessary to estimate S_∞ for the mined stations suggests that the accumulation of species in relation to sampling effort is less than the cumulative number of species in unmined stations. This result reflects a certain amount of “community uniformity” (Karakassis 1995) in the mined stations.

The program was also run using the 10 unmined reference samples from area 2 to assess whether 10 samples is sufficient to account for inherent heterogeneity within an area. The species accumulation curve became asymptotic, which suggests that the full species complement of the area was not sampled. Unfortunately, this is an inherent problem in benthic communities which typically exhibit a high degree of spatial patchiness.

CHAPTER 3

FORMAL MULTIVARIATE STATISTICAL TESTING

***“He uses statistics as a drunken man uses a lamp-post-
for support rather than illumination.”***

Andrew Lang

FORMAL MULTIVARIATE STATISTICAL TESTING

Descriptive multivariate analyses, such as clustering and ordination, display the relationships among stations in an informal, graphical way that highlights the patterns in the community data. It is also necessary to demonstrate that significant differences genuinely exist between samples. This chapter employs a non-parametric randomisation test to examine the differences in community structure between mined and unmined areas based on *a priori* knowledge of the groups of samples. Testing for significant differences between stations that are grouped together by a cluster analysis or ordination leads to a circular argument. The statistical testing chapter is therefore presented before the results of the multivariate analyses are discussed in order to avoid bias in the grouping of stations.

The species abundance and biomass matrices, with their predominance of zero values, do not lend themselves to standard statistical tests based on multivariate normality (Clarke and Warwick 1994). Most multivariate analyses make no assumptions about the structure of the samples and a formal statistical test is needed which makes the same assumptions (or lack thereof) that underlie the clustering and ordination methods (Clarke and Green 1988). This ANOSIM test (analysis of similarities), by analogy with the ANOVA test (analysis of variance), is a non-parametric statistical test based on the principles of permutation and randomisation (Hope 1968 as cited in Clarke and Green 1988). The starting point for the ANOSIM test is the triangular matrix of similarities and in particular the corresponding rank order similarities between samples (Clarke and Green 1988).

A test statistic is computed, reflecting the average difference in rank similarities between and within mined and unmined stations. If \bar{r}_w is defined as the average of all the rank similarities among replicates **within** stations, and \bar{r}_B is the average of all rank similarities arising from pairs of replicates **between** stations, then a suitable test statistic is:

$$R = (\bar{r}_B - \bar{r}_w) / (M / 2)$$

where $M = n(n-1)/2$ and n is the total number of samples (Clarke 1993). The R statistic will usually lie between 0 and 1 and when it approximates 0, the null hypothesis is true (Clarke 1993). Under the null hypothesis, H_0 , of no differences between mined and unmined samples, there will be a negligible effect on average to the R statistic if the labels identifying which samples belong to which “treatments” (mined or unmined) are arbitrarily reshuffled (Clarke 1993); this is the principle of the permutation test. The test statistic is compared with its value under a large number of random permutations so that all possible allocations of the sample labels are examined and the R statistic recalculated each time (Clarke and Warwick 1994). The significance level is then calculated by referring the observed value of R to its permutation distribution (Clarke 1993). For example, if 95% of the random relabellings fall outside the expected labels for the original data, the null hypothesis is rejected at the $p < 0.05$ significance level. It is worth noting that one-way and two-way designs are not restricted to balanced designs (Clarke 1993).

3.1 ONE-WAY LAYOUT

The simplest statistical design which tests for differences between mined and unmined samples is the one-way layout. The null hypothesis, H_0 , of 'no differences between disturbed and undisturbed samples was tested for each cruise separately and for the combined cruise data.

Rockfish cruise. A total of 60 samples were collected from 6 sites during the first sampling cruise on board the *Rockfish*. Forty-four samples came from areas that had not been mined and a further 12 samples fell within mined areas, the remaining 4 samples were uncertain in terms of their condition and were excluded from the analysis (refer to Table 2.2 in *Methods*). Note that the putative condition of the samples is known *a priori*. The abundance data were 4th root-transformed and Bray-Curtis similarities calculated. The R statistic was calculated and its value compared under 5000 permutations using the ANOSIM program in PRIMER. The Global R value at 0.333 rejects the null hypothesis at the significance level $P < 0.001\%$. It was concluded therefore that there was a highly significant difference in community structure between mined and unmined replicates from the *Rockfish* sampling cruise.

Pentow Salvor cruise. Similarly, the data for the second cruise were 4th root-transformed and the Bray-Curtis coefficient of similarity used. The 17 unmined samples and 20 mined samples were tested for significant differences using 5000 permutations. The Global R = 0.233 at significance level $P < 0.001\%$ rejected the null hypothesis and it was concluded that disturbed and undisturbed *Pentow Salvor* samples were significantly different.

Combined cruise data. A one-way ANOSIM test was performed on the abundance data for the combined cruise data. The underlying premise before the data could be combined is that there is no temporal variability. The issue of temporal variability is dealt with in the two-way crossed ANOSIM below. For the moment, temporal variability will be assumed to be negligible. A total of 60 unmined replicates and 31 mined replicates were tested for significant differences using a one-way layout. There was a highly significant difference (Global R = 0.292) at the $P < 0.001\%$ significance level. The null hypothesis was rejected and it is inferred that benthic communities in mined and unmined samples are markedly distinct.

3.2 PERMUTATION TEST FOR THE ONE-WAY LAYOUT

The mined and unmined replicates were collected from six different study sites in an area spread over 40km. The mosaic nature of benthic communities has been noted above in the sampling strategy, and it is hence desirable to ascertain how much intrinsic site-to-site variability there is between samples. The null hypothesis is that there is 'no difference in community structure among sites'. The test statistic computes the observed differences between sites and compares this with differences among samples within sites (Clarke 1993). The R statistic is a global test indicating if there is a significant difference between sites. To assess where these differences lie, pairwise tests are performed between every pair of sites (Clarke and Green 1988). The two cruises were analysed separately and one-way tests were performed on each "treatment". Four separate one-way permutation tests were done: on the *Rockfish* unmined samples, the *Rockfish* mined samples, the *Pentow Salvor* unmined samples and the mined *Pentow Salvor* samples. The results are tabulated in Table 3.1 below.

Table 3.1. The results of the one-way ANOSIM tests for inter-site variability for (a) the *Rockfish* cruise and (b) the *Pentow Salvor* cruise. The sites which produced significant differences at the 5% significance level in the pairwise tests are presented in the last column.

SAMPLES USED	NULL HYPOTHESIS (H ₀)	GLOBAL R	SIGNIFICANCE LEVEL	SIGNIFICANT DIFFERENCE AT 5% SIGNIFICANCE LEVEL
a) <i>Rockfish</i> unmined samples	There is no variability across sites from the undisturbed condition. i.e. natural variability is negligible	0.386	< 0.001 %	1 vs 2 1 vs 4 1 vs 5 1 vs 6 2 vs 5 2 vs 6 4 vs 5
mined samples	There is no variability across sites from the disturbed condition.	0.548	0.002 %	NONE
b) <i>Pentow Salvor</i> unmined samples	There is no variability across sites from the undisturbed condition. i.e. natural variability is negligible	0.451	0.001%	2 vs 4 2 vs 5
mined samples	There is no variability across sites from the disturbed condition.	0.173	0.036%	1 vs 2 1 vs 4 2 vs 4

The results of the one-way ANOSIM tests show that for both the unmined and the mined condition there is some site-to-site variability, and the pairwise tests show which sites are primarily responsible for this difference. In all the above tests, with the exception of the mined samples collected on the *Rockfish* cruise, the null hypothesis was rejected and it is concluded

that there is inherent variability across sites. One of interesting findings is that the disturbed samples collected on the first (*Rockfish*) cruise did not show any inter-site variability. It would appear as if the natural variability among sites has been destroyed and replaced by a new benthic community, which hosts the same species composition across a broad spatial scale. This result, however, may be an artifact of the small sample size for *Rockfish* mined samples.

One of the primary challenges in this study is to estimate how much variability among sites is due to natural differences among communities and how much change can be attributed to physical disturbance as a consequence of marine mining. This question can be addressed using a two-way crossed design which has the advantage that it can elicit the effect of one factor which is normally hidden in the MDS plot by a second dominating factor (Clarke and Warwick 1994).

3.3 TWO-WAY CROSSED DESIGN

The two-way crossed design arises when there are matched control and impacted samples taken at a number of sites. The term “crossed” implies that for each condition there are replicate samples taken from all sites, so the two factors, sites and “treatments”, are said to be crossed (Zar 1984). Two-way crossed ANOSIM tests will be used to test for spatial and temporal variability, respectively.

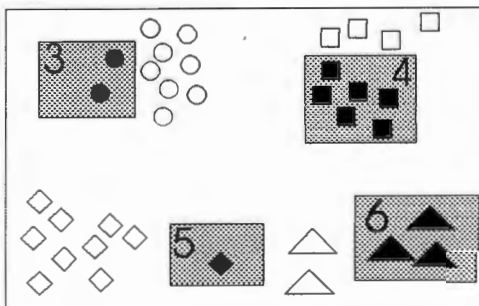
3.3.1 Two-way crossed ANOSIM to test for spatial variability

Rockfish cruise. There are two levels of spatial replication. There are 4 sites that were subjected to the effects of offshore marine mining with several replicates at each site (See Figure 3.1). Sites 1 and 2 were unmined at the time of the first sampling cruise so are excluded from the test since there are no replicates representing the mined condition. Matched replicates were taken inside mined patches and from adjacent unmined areas, so the effect of marine mining can be tested against a background of changing community structure across a wide spatial scale. There are two factors: the presence or absence of disturbance by marine mining and the possible inter-site variability of the different study sites. Two null hypotheses are appropriate:

H₁: There are no disturbance effects, allowing for possible site effects.

H₂: There are no site effects, allowing for the possible disturbance effects.

Figure 3.1. Schematic diagram of the sampling design for the two-way crossed ANOSIM test for the *Rockfish* cruise data. The shaded symbols represent samples collected in mined areas and the unshaded symbols refer to the corresponding unmined samples.



The first hypothesis (H_1) was addressed by extending the one-way ANOSIM test discussed above to a constrained randomisation test (Clarke 1993). The abundance data were 4th root-transformed and Bray-Curtis similarities calculated. An R statistic is calculated for each separate site, analogous to a one-way ANOSIM for disturbance effects. The resulting R_1 to R_4 values are then averaged to give the test statistic \bar{R} (Clarke 1993). This was then compared to \bar{R} values arising from all possible permutations of sample labels (disturbed or undisturbed) within each site (Clarke 1993). The null hypothesis (H_1) was rejected (Global $R = 0.535$; significance level $p < 0.004\%$) and it was hence concluded that there is a significant difference between disturbed and undisturbed replicates (averaged across all sites).

The second question (H_2) could then be examined. Due to the symmetry in the crossed analysis of similarities test (Clarke 1993) the second null hypothesis of “no site effects, allowing for possible treatment effects” can be tested by reversing the roles of treatments and sites in the above test. \bar{R} is now an average of two R statistics, R_C calculated for “control” samples and R_D calculated for disturbed samples. In 5000 permutations, Global $R = 0.342$ and the null hypothesis was rejected ($P < 0.001\%$). It was therefore concluded that there is a highly significant difference between sites averaged across the disturbance factor. It should be cautioned, however, that the above test has the potential to reject the null hypothesis either when there is a consistent treatment effect across all sites or when this difference is strongly present in some sites but not others (Clarke 1993). Therefore, use is made of the pairwise tests which highlight which sites were primarily responsible for the difference. The following pairs of sites showed significant differences at the $P < 0.001\%$ significance level:

3 vs 5

4 vs 5

4 vs 6.

It would appear therefore, that disturbance effects are not the only source of spatial variability. There are also inherent differences between the study sites which act synergistically with the mining effects to produce the observed significant differences among samples. The natural variability among sites could be attributed to a range of factors. The sites are in different temporal states of post-mining recovery and the spatial variability could reflect different successional states in the community. Another possible influence is the varying sedimentology of the different sites and this relationship is examined in chapter 6.

Pentow Salvor cruise. A two-way crossed ANOSIM could not be performed on the *Pentow Salvor* data, due to the paucity of data. There were not enough replicates to generate sufficient permutations, and hence not enough power to generate significant results.

3.3.2 Two-way crossed ANOSIM to test for temporal variability

The two-way crossed design can also be employed to separate the effects of natural fluctuations in time from changes attributed to disturbance effects. This scenario arises when replicate samples are taken at several sites a number of times (Clarke and Warwick 1994). The null hypotheses that there are “no disturbance effects” (but allowing for possible changes in time) and “no time changes” (but allowing for disturbance effects) are then tested (Clarke and Warwick 1994). The test was illustrated using the abundance data for site 6 collected from both cruises, as site 6 had the greatest number of replicates representing both mined and

unmined conditions. The null hypothesis of “no disturbance effects” was rejected ($R = 0.1$; $P < 0.0026\%$), however, the 2nd null hypothesis of “no time changes” was not rejected. The Global R value = 0.168 at a significance level, $P = 0.23\%$ showed that the null hypothesis could not be rejected and hence temporal variability for site 6 was considered negligible. This result cannot be applied to all sites. Nevertheless, it gives weight to the assumption that there is no temporal variation during the duration of the current study. This has implications in terms of combining the cruise data in further analyses.

In conclusion, we can now attempt to answer the question proposed earlier in the chapter, namely how do we separate the changes in community structure due to natural fluctuations from alterations as a consequence of marine mining? It is evident that anthropogenic disturbance does not act alone on the benthic community. There are also natural changes on a spatial scale which determine differences in the biological communities. The spatial variability may be a function of the different successional stages of post-mining recovery, which would be an indirect effect of the mining process. It is likely, however, that both natural fluctuations and induced disturbance effects act synergistically to influence the patterns in benthic community structure.

CHAPTER 4

GRAPHICAL MULTIVARIATE ANALYSIS OF BENTHIC COMMUNITY PATTERNS

“What is the use of a book,” thought Alice, “without pictures?”

Lewis Carroll (Alice in Wonderland)

DESCRIPTION OF BENTHIC COMMUNITY PATTERNS USING MULTIVARIATE ANALYSES

Multivariate methods are a powerful tool for discerning patterns in community data and providing an objective summary of the data. The graphical output facilitates comprehension of the community and relationships not recognisable in the raw data become more readily apparent. Cluster analysis divides stations into homogeneous groups such that similar samples are grouped together and dissimilar samples are separated. The complementary non-metric MDS ordination technique is used to verify putative sample groups from the classification. The ordination produces a low-dimensional plot of the arrangement of samples such that similar samples are close by and dissimilar samples far apart.

4.1 TAXONOMIC RESOLUTION

The level of taxonomic discrimination necessary to detect changes in community structure was addressed in the problem of sampling design. Identification of benthic organisms is very time-consuming and requires a high degree of taxonomic expertise and standardization (Warwick 1988b; Warwick 1993). An important consideration in benthic surveys is determining the taxonomic resolution necessary to detect patterns in community structure. Taxonomic sufficiency is required only to the level that indicates the community response (Ellis 1985). Recently, there has been a flood of publications on analysing data sets at successively higher groupings (species, genus, family, phylum). An important finding is that the analysis is robust to aggregation of the species data and the effects of disturbance were

often detected at very high taxonomic levels (Ellis 1985; Heip *et. al.* 1988; Warwick 1988a, b, c; Ferraro and Cole 1990; Gray *et. al.* 1990; Warwick *et. al.* 1990; James *et. al.* 1995). It was further suggested that there may be theoretical advantages to conducting analyses on taxa-aggregated data. Multivariate analyses based on higher taxa may more closely reflect anthropogenic disturbances than those based on species data, the latter being more affected by natural environmental variation (Warwick 1988a, b).

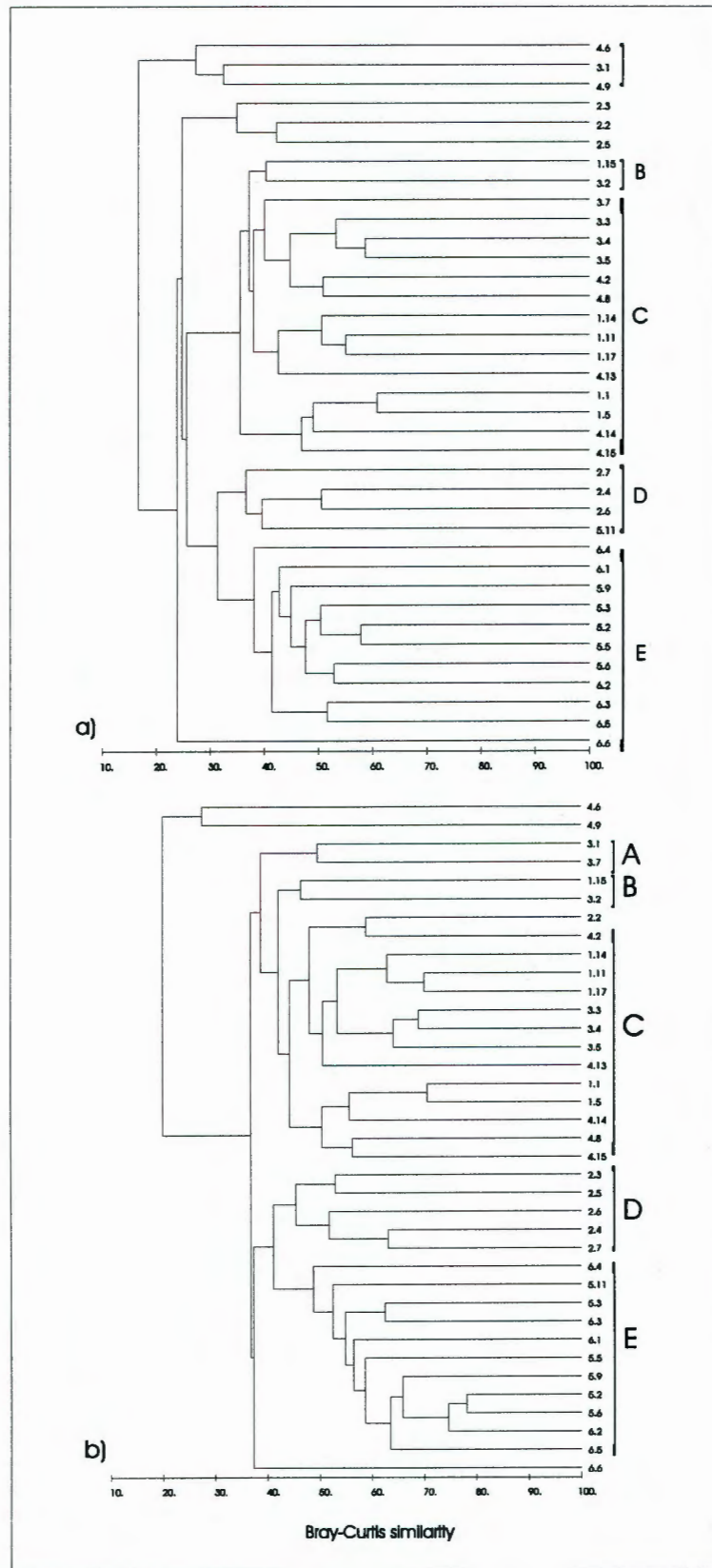
The level of “taxonomic sufficiency” was illustrated using the abundance data from the *Pentow Salvor* cruise. The data were 4th root-transformed and the Bray-Curtis measure used to generate a similarity matrix and then non-metric multidimensional scaling was applied to the matrix. The data were analysed at Species, Genus and Family level and the results presented in Figure 4.1.

Cluster analysis reveals two major groups at the 40% similarity level in the Genus and Family-level analysis. The cluster analysis at Species level also reveals two main groups, although the level of similarity is lowered to approximately 30%. The MDS graph for the Species-level analysis exhibits a large amount of noise and the groups formed by cluster analysis are not readily apparent. Conversely, the MDS ordination at Genus and Family level show much concordance with one another and with the respective dendrograms. Figure 4.1 suggests that aggregating the community data to higher taxonomic levels than species does not result in a significant loss of information. In fact, analysing the community at higher taxonomic levels reduces the amount of “noise” in the data which is a consequence of natural environmental variability. The main analyses are therefore performed using the data aggregated to genus level.

4.2 BIOMASS DATA

Changes in benthic community data are commonly measured using abundance of the organisms. The current study measured abundance and biomass data at each station. The component of the data that best represents the community patterns under investigation was assessed at the outset of this study by performing cluster and multi-dimensional scaling on the abundance and biomass data for the *Pentow Salvor* cruise. The results of the multivariate analyses on the abundance data are presented in Figure 4.2 and Figure 4.3, respectively.

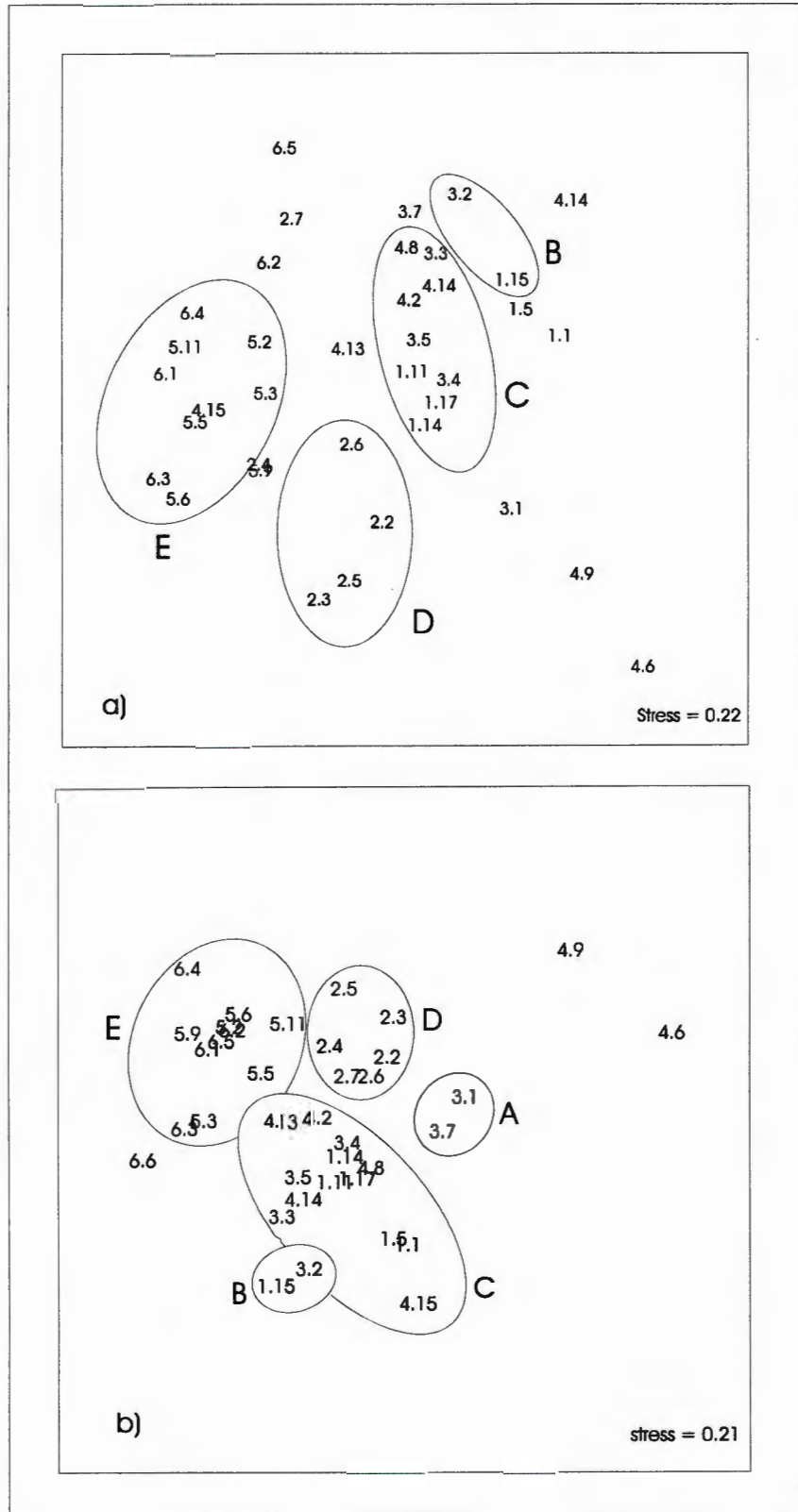
Figure 4.2. Results of hierarchical agglomerative clustering for the genus-level *Pentow Salvor* cruise data using the (a) biomass data and (b) the abundance data.



The cluster analysis of the biomass data closely resembles that for the abundance data. Both dendrograms reveal 5 groups (B-E) at approximately 30% similarity level. Cluster analysis groups together samples 3.1 and 3.7 (Group A) in the abundance data. Group A is absent from the biomass analysis and sample 3.1 now groups with two outliers, 4.6 and 4.9. Apart from this anomaly, the two dendrograms show remarkable similarities. Group B contains samples 1.15 and 3.2. Group C clusters the mined samples from areas 1, 3 and 4 together. Group D contains unmined samples from area 2, excepting sample 5.11 which groups with area 2 in the biomass data. Group E is a composite of mainly unmined samples from areas 5 and 6.

The non-metric multi-dimensional scaling ordination of the biomass data shows close parallels with the ordination of the abundance data (See Figure 4.3). The groups of samples revealed in the cluster analysis are substantiated in the complementary MDS plot with groups B, C, D and E forming clusters in two-dimensional space. The abundance and biomass data place samples 4.6 and 4.9 as outliers, distinct from the other samples. The ordination of the biomass data also plots sample 3.1 as an outlier, which qualifies the results of the cluster analysis.

Figure 4.3. MDS plot for the *Pentow Salvor* using (a) the biomass data (stress=0.22) and (b) the abundance data (Stress = 0.21). The groups of samples revealed by the cluster analysis are encircled and identified as Groups A-E.

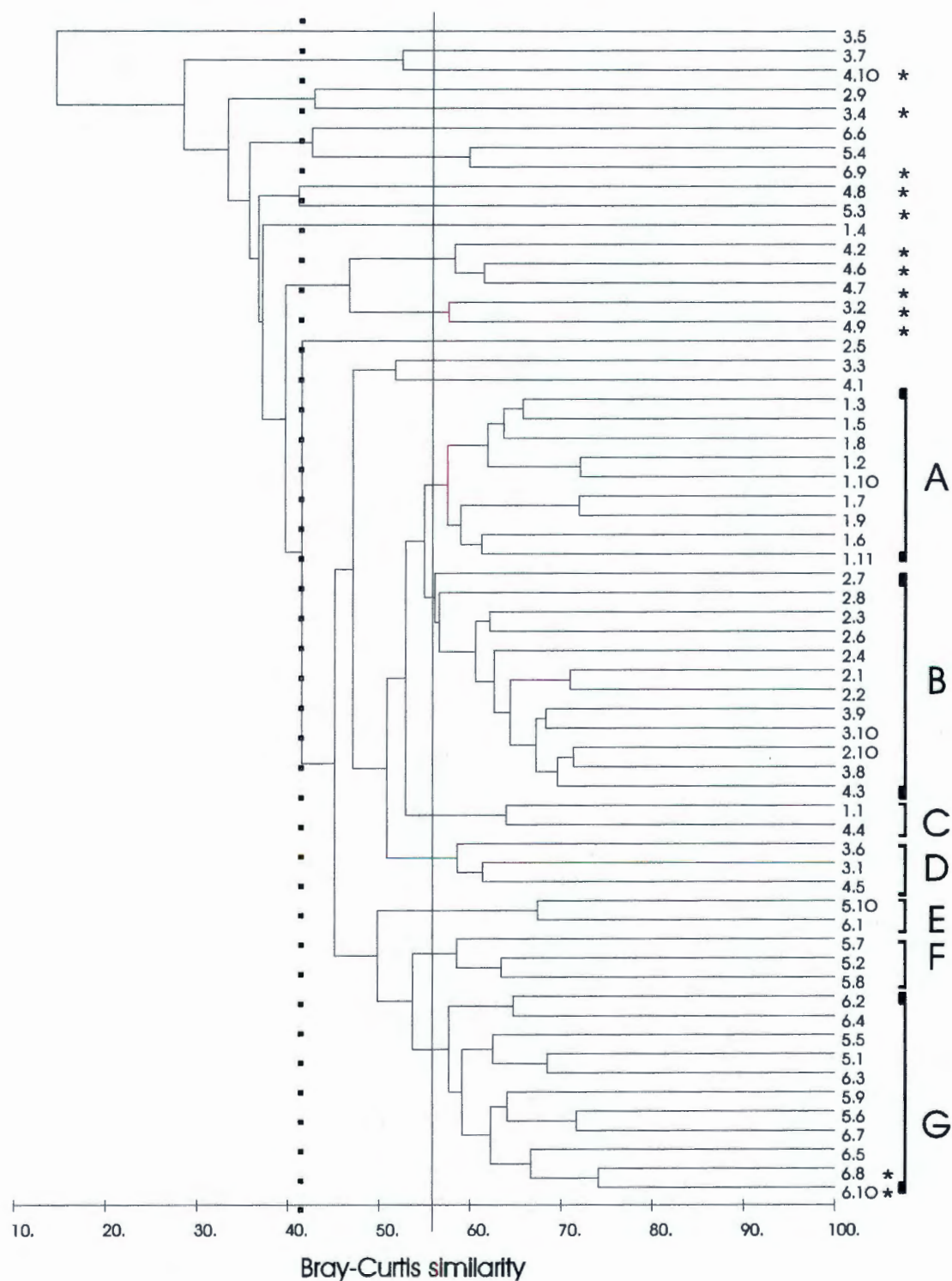


The cluster and ordination analyses for the abundance and biomass *Pentow Salvor* data show similar patterns and one can therefore assume that either aspect of the biological data can be used to reveal patterns in the community data. The current study uses the abundance data to discern changes in community structure, excepting the meta-analysis which uses both abundance and biomass data to derive a production value (see Chapter 7).

4.3 MULTIVARIATE ANALYSES OF THE *ROCKFISH* COMMUNITY DATA

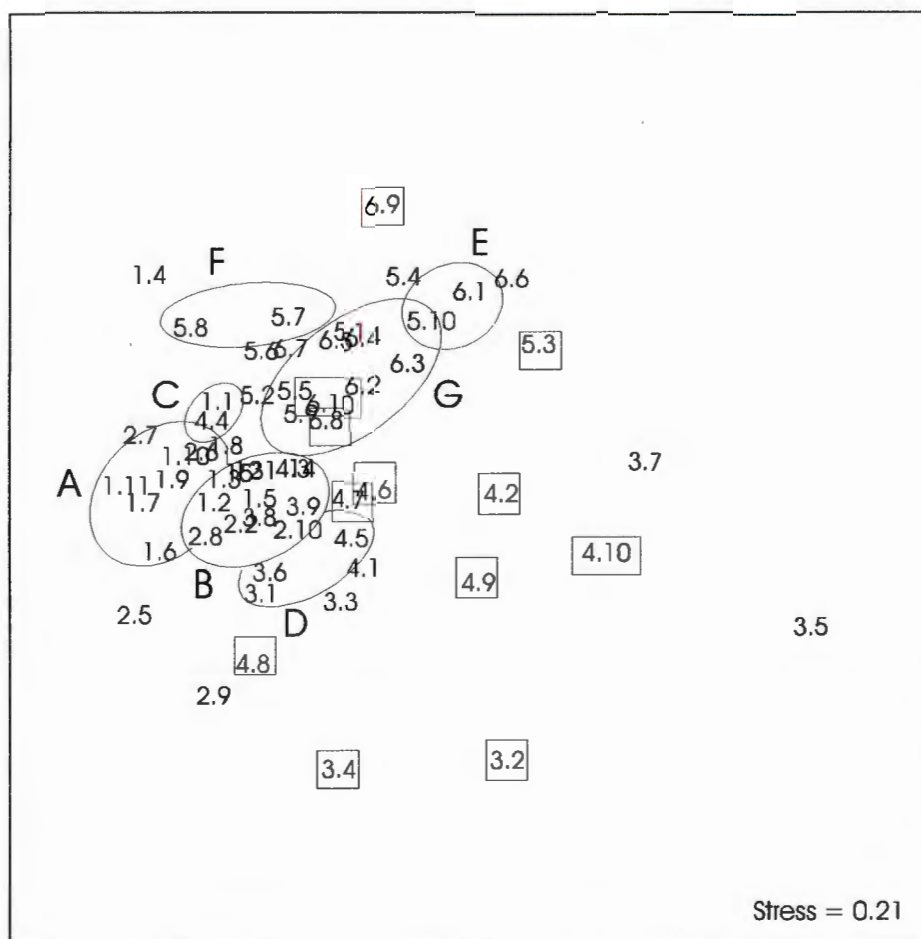
The *Rockfish* abundance data, aggregated to genus level, was 4th root-transformed and the Bray-Curtis coefficient of similarity used to compute similarity between samples. Hierarchical agglomerative clustering produces a dendrogram which is pictured in Figure 4.4.

Figure 4.4. Dendrogram of the abundance data aggregated to genus-level for the *Rockfish* sampling cruise. Mined samples are represented by *. The groups of samples discernable at the 56% similarity level (represented by a solid line) are identified as groups A to G. A dotted line through 42% similarity level distinguishes between the group of unmined samples (A-G) and the mainly mined samples.



Seven groups of samples, labelled A to G, are revealed by the cluster analysis at 56% similarity level. The mined samples, represented by an asterisk, form ungrouped samples distinct from all the other groups, with the exception of 6.8 and 6.10. Samples 3.5, 3.7, 2.9, 6.6, 5.4 and 1.4 were classified as unmined and yet are positioned adjacent to the mined samples in the dendrogram. This group of samples is heterogeneous with a large range of faunistic variation. Conversely, Group A represents a very homogeneous group of samples and is composed entirely of samples from area 1. If the similarity level is extracted back, hypothetically, to approximately 54%, Groups A and B cluster together. It is interesting to trace the change in the grouping of samples from area 1 (Group A) which was sampled before and after mining. The relative shift in positioning of Group A in the dendrogram is discussed in section 4.4. Groups C and D contain unmined samples from areas 3 and 5. Groups E, F, and G contain unmined samples from the southern areas 5 and 6 and the two mined samples, 6.8 and 6.10. At a coarser level of similarity (42% similarity), the unmined samples all form a single group of samples, which share similarities in terms of their species composition that are distinct from the mined samples, excepting 6.8 and 6.10. The relationships revealed in the cluster analysis are substantiated by the MDS in Figure 4.5

Figure 4.5. MDS ordination for the *Rockfish* abundance data (stress = 0.21). Mined samples are framed and the groups of samples identified in the cluster analysis are encircled and represented by groups A-G.



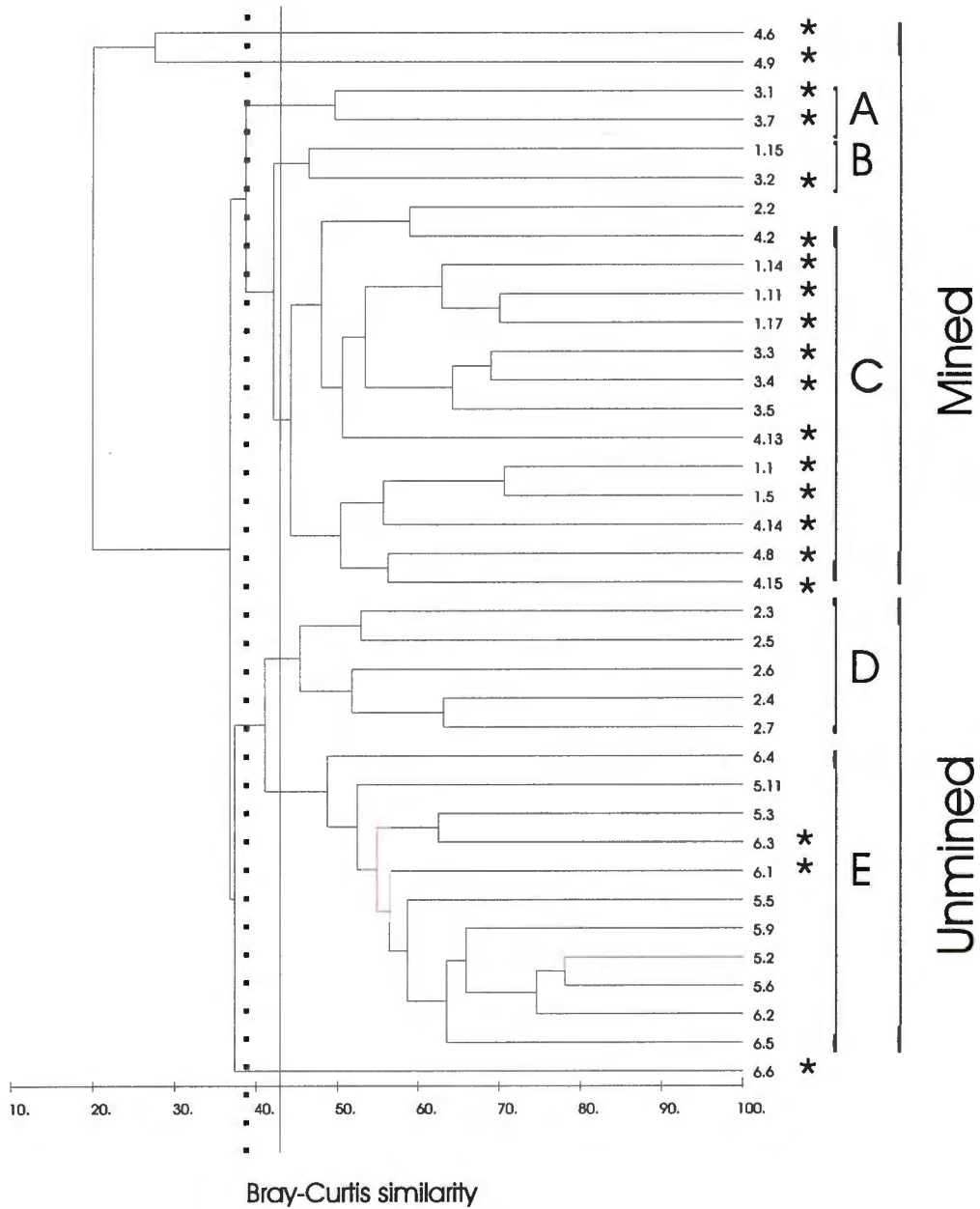
The results of the ordination closely resembles that for the dendrogram and hence relationships between samples can be accepted as real. The community data from the first sampling cruise can be explained by seven groups of unmined samples. The unmined samples from area 1 are positioned relatively close to those from area 2 and similarly, the unmined samples from areas 3 and 4 group together. The mined samples are represented as outliers with no affinity to the other unmined samples, with the exception of samples 6.8 and 6.10, which group with the unmined samples from area 6. It would appear therefore that the distinction between areas 1 to 4 on one hand and areas 5 and 6 on the other is due primarily to natural variability between the southern and northern areas. The difference between the unmined samples in

areas 1 to 4 is most likely a reflection of natural variability on a spatial scale of hundred's of metres. Samples 3.5 and 3.7 were classified *a priori* as unmined samples, based on the GPS positions; however, the cluster analysis and the ordination place these two samples with the mined group of samples. This anomaly may be due either to sampling error with small grab samples, or may be explained by a misclassification of the samples initially. Sediment particle size analysis reveals that sample 3.5 is predominantly composed of gravel which would suggest that it was collected from a mined area (see Figure 6.1 in Chapter 6). Unfortunately, no sedimentological study was conducted on sample 3.7.

4.4 MULTIVARIATE ANALYSES OF THE *PENTOW SALVOR* COMMUNITY DATA

The community data from the second sampling cruise (*Pentow Salvor*) was aggregated to genus level and the Bray-Curtis coefficient used to compute similarity on the 4th root-transformed abundance data. The results of hierarchical agglomerative clustering are presented in Figure 4.6.

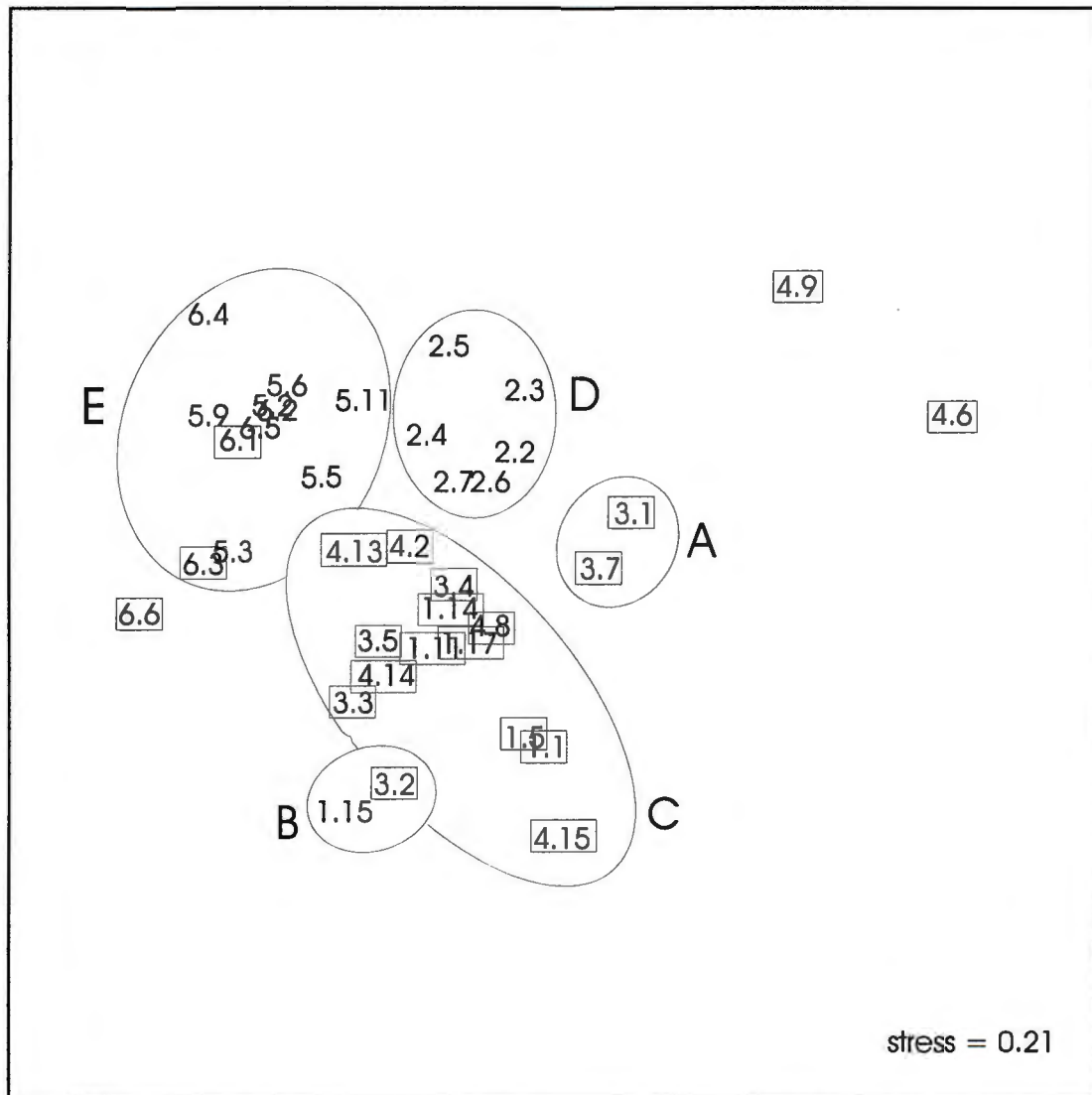
Figure 4.6. Cluster analysis for the *Pentow Salvor* abundance data aggregated to genus level. Mined samples are represented by *. A solid line through 43% similarity level groups 5 groups of samples together (A-E) based on their faunistic attributes. A dotted line through 38% similarity level distinguishes between two general groups of samples, the mined and the unmined samples.



The dendrogram reveals two major groups of samples at the 38% similarity level. The unmined samples, excepting 6.1, 6.3 and 6.6, are depicted as a homogeneous group of samples distinct from the mined samples. Analogous to the *Rockfish* data, the mined samples

from area 6 group with the unmined samples from that area, which seems to suggest that the difference between the southern sites and northern sites is greater than the changes in community structure caused by offshore marine mining. Nevertheless, the clear distinction between the mined and unmined samples illustrates the importance of offshore mining in causing significant changes in benthic community structure. Two samples, 4.6 and 4.9 show marked differences in terms of their biotic composition from any other samples and group together as outliers. At the 43% similarity level, cluster analysis differentiates 5 groups: 3 clusters which contain largely mined samples and 2 groups containing mainly unmined samples. Group A contains two mined samples from area 3. Group B contains a mined sample from area 3 and an unmined sample from area 1. Group C is composed of mined samples from areas 1, 3 and 4, plus mined sample 3.5. Group D contains the unmined reference samples from area 2 and Group E is composed of samples from the southern sites 5 and 6. Interestingly, area 1, which was unmined in the first survey, clustered with the reference samples from area 2 in the *Rockfish* data. When the area was re-sampled approximately 1 month after mining, there was a notable change in community structure and the samples now clustered with the mined samples from areas 3 and 4.

Figure 4.7. MDS ordination of the Pentow Salvor abundance data (stress = 0.21). The groups of samples identified by cluster analysis are encircled and identified as groups A-E and mined samples are emphasised by a framed sample number.



The mined samples 4.6 and 4.9 emerge as very distinct outliers in terms of their faunistic attributes. Reasons for this anomaly are explored in Chapter 6 when environmental parameters are superimposed on the biotic MDS plot. The groups of samples identified in the dendrogram also group together in the ordination plot. The mainly mined samples (Groups A, B and C) are located along the lower half and to the extreme right of the MDS plot while

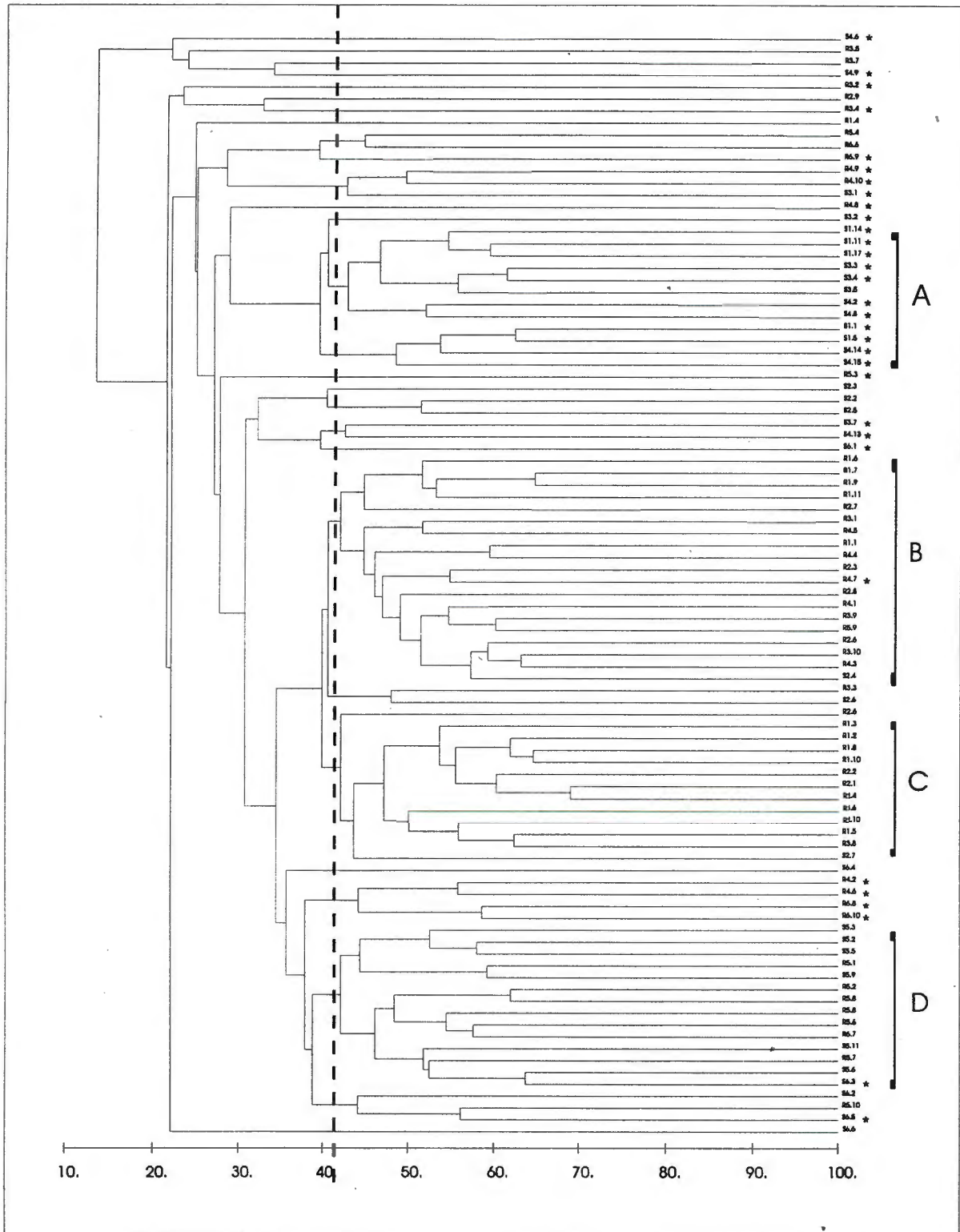
largely unmined samples (Groups D and E) are positioned in the upper left hand positions of the ordination.

4.5 MULTIVARIATE ANALYSES OF THE COMBINED CRUISE COMMUNITY DATA

The abundance data, aggregated to genus-level, was combined for the *Rockfish* and *Pentow Salvor* sampling cruises. The data were 4th root-transformed and the Bray-Curtis coefficient of similarity computed. Hierarchical agglomerative clustering reveals 4 major groups at the 42% similarity level (see Figure 4.8).

The 4 main groups discernable at 42% similarity level can broadly be classified as a mined group of *Pentow Salvor* samples (Group A), 2 groups of unmined *Rockfish* samples (Groups B and C) and a group of unmined samples from both cruises (Group D). The mined samples from the first (*Rockfish*) survey generally form an unrelated set of samples which do not show affinities to each other or to any other samples in terms of the biological organisms they contain. The mined samples from the second (*Pentow Salvor*) cruise, however, cluster together (identified as Group A), indicating that this group of samples exhibit faunistic similarities. The results of the cluster analysis for the combined cruise data suggest that the difference between mined and unmined samples is greater than the difference attributed to site-to-site variability in the northern areas 1 to 4.

Figure. 4.8. Cluster analysis for the combined cruise data aggregated to genus-level. Mined samples are represented by *. A dashed line through 42% similarity level distinguishes 4 main groups of samples identified as A-D, based on their faunistic attributes.



The MDS ordination for the combined cruise data reveals 3 major groups of samples. Groups A and D identified in the cluster analysis are discernable in the 2-D plot, however, Groups B and C now form a single group of samples. Group (B+C) generally contains all the unmined samples from the *Rockfish* cruise. A notable feature of the above MDS is that the outliers identified in the individual cruise analyses, namely R4.6, R4.9, S3.5 and S3.7, are still positioned as distinct outliers in the combined cruise analysis. The high stress function for the combined cruise data (stress=0.26) indicates that there is distortion in representing the multi-dimensional community data in two dimensions, presumably due to the large sample size, and hence caution must be exercised when interpreting the inter-sample relationships revealed in the ordination.

Multivariate analyses have proven to be particularly sensitive in revealing changes in community structure as a consequence of marine mining. Samples from area 1, which was unmined in the first survey, clustered with the reference samples from area 2. However, after the area had been exposed to marine mining, the samples showed a shift in terms of their faunistic attributes and showed affinities to groups of mined samples. The consistency in results for the cluster analysis and the MDS techniques suggest that multivariate methods are robust in revealing inter-sample relationships. Multivariate analyses also reveal the subtle differences among the 6 study areas due to natural variability. It was hence demonstrated that the technique for analysing multivariate community data outlined by Field *et. al.* (1982) can be used as a tool to study the effects of physical disturbance on the macrobenthic community.

CHAPTER 5
INDICATOR SPECIES

“Life is a mosaic, and each tiny piece must be cut and set with skill.”

E.B Pusey

INDICATOR SPECIES

Having described the benthic community patterns using two complementary techniques, it is now appropriate to determine which species are primarily responsible for influencing the sample groupings in the cluster and MDS analyses. The dendrograms and ordination plots divided the samples into two very distinct groups, the unmined and the mined samples. At this stage in the analysis, it is important to refer back to the biological data and find which species are characteristic of disturbed sites and which species are reduced in abundance following disturbance of the sediments. These results can subsequently be used to establish a list of indicator species for physically disturbed areas off the west coast of southern Africa.

To date, macrobenthic studies have established lists of indicator species from organic pollution events. Pearson and Rosenberg (1978) reviewed the use of indicator species and devised a sequence of changes which takes place in macrobenthic communities following organic pollution in the area. Firstly, the most sensitive species are lost, then as the severity of pollution increases the community is gradually reduced to only a few tolerant species (Pearson and Rosenberg 1978). The best adaptive strategy for an animal in an organically enriched area is therefore to increase its tolerance to chemical stress. The effect is entirely different for physical disturbance of the benthos, where organisms are destroyed or removed from an area. The mining process essentially denudes areas of sediment to bedrock level, destroying all benthos during the operation. The current chapter compares the species composition in mined areas to unmined areas and thereby establishes a list of species which characteristically recolonize the defaunated sediments off the Namibian coast.

The SIMPER (“similarity percentages”) program in PRIMER calculates the contribution each species makes to the overall groupings of samples. Conceptually, the program calculates the average dissimilarity, $\bar{\delta}$, between all pairs of inter-group samples (i.e. every sample in the mined group versus every sample in the unmined group), and then breaks this average down into the component contributions of each species. The Bray-Curtis dissimilarity, δ_{jk} , between any two samples j and k can be defined as:

$$\delta_{jk} = \sum_{i=1}^p \delta_{jk(i)}$$

where

$$\delta_{jk(i)} = \frac{100|Y_{ij} - Y_{ik}|}{\sum_{i=1}^p (Y_{ij} + Y_{ik})} \quad (\text{Clarke 1993})$$

Y_{ij} is the abundance of the i^{th} species in the j^{th} sample and p is the number of species (Clarke 1993). Thus $\delta_{jk(i)}$ can be thought of as the contribution of the i^{th} species to δ_{jk} (Clarke 1993). By averaging δ_{jk} over all sample pairs (j, k), with j in the first group and k in the second, the average dissimilarity, $\bar{\delta}$, between groups 1 and 2 is computed (Clarke 1993).

The SIMPER program is restricted to a 160*100 matrix, therefore, before any analyses could be run, species represented by 2 or fewer individuals were removed from the abundance matrices. Three separate analyses were performed using the untransformed abundance data for the *Rockfish* sampling cruise (Table 5.1), the *Pentow Salvor* cruise (Table 5.2) and the combined cruise data (Table 5.3), respectively. These tables list the average abundance of each species in the mined group and the average abundance in the unmined group. The percentage contribution of each species is listed in the 3rd column and the 4th column represents the cumulative percentage for the species. The arbitrary cut-off percentage of 45%

was chosen to limit the species list to a manageable size. Beyond 45% (cumulative percentage) individuals were contributing approximately 1% or less to the sample groupings and their contribution was considered negligible.

Table 5.1. The percentage contribution of each species to the grouping of samples for the 1st sampling cruise (*Rockfish*) data. The arbitrary cut-off percentage of 45% similarity was chosen. The most abundant group is highlighted in bold type. Average dissimilarity between mined and unmined groups =70.29%

SPECIES	TAXONOMIC GROUP	MINED GROUP	UNMINED GROUP	PERCENT	CUMULATIVE PERCENT
<i>Prionospio pinnata</i>	Polychaeta	8.92	51.89	3.47	3.47
<i>Ampelisca anomala</i>	Amphipoda	4.42	12.59	3.36	6.82
<i>Macoma crawfordi</i>	Bivalvia	39.33	18.86	3.17	9.99
<i>Nassarius vinctus</i>	Gastropoda	13.00	3.73	2.97	12.97
<i>Hippomedon longimanus</i>	Amphipoda	6.08	7.84	2.91	15.87
<i>Lumbrineris spp.</i>	Polychaeta	3.17	10.14	2.80	18.68
<i>Terebellides stroemii</i>	Polychaeta	31.33	2.77	2.80	21.47
<i>Euphausiacea</i>	Euphausiacea	0.83	3.05	2.27	23.74
<i>Lumbrineris heteropoda difficilis</i>	Polychaeta	0.58	2.93	2.19	25.93
<i>Lumbrineris albidenta</i>	Polychaeta	0.67	4.80	2.09	28.02
<i>Marginella capensis</i>	Gastropoda	1.25	3.02	2.07	30.09
<i>Goneplax angulata juveniles</i>	Brachyura	5.08	3.34	2.02	32.11
<i>Acidostoma obesum</i>	Amphipoda	12.67	0.27	1.89	34.01
<i>Dosinia spp.</i>	Bivalvia	1.42	1.66	1.89	35.89
<i>Laonice cirrata</i>	Polychaeta	1.25	2.07	1.80	37.69
<i>Ampelisca brevicornis</i>	Amphipoda	0.58	1.91	1.77	39.46
<i>Nephtys spp.</i>	Polychaeta	1.67	0.41	1.77	41.23
<i>Haploscoloplos kerguelensis</i>	Polychaeta	0.08	3.32	1.66	42.89
<i>Diopatra monroi</i>	Polychaeta	4.67	1.59	1.61	44.50

The principal contributor was the polychaete, *Prionospio pinnata*, which was approximately six times more abundant in unmined areas and contributed 3.47% to the separation between

mined and unmined samples. Other species which were more abundant in unmined areas were the amphipods, *Ampelisca anomala* and *Hippomedon longimanus*; the polychaetes, *Lumbrineris spp.*, *Lumbrineris heteropoda difficilis* and *Lumbrineris albidenta*. Indicator species which were characteristic of disturbance included the bivalve, *Macoma crawfordi*, the gastropod, *Nassarius vinctus* and the polychaete, *Terebellides stroemii*.

Table 5.2. The percentage contribution of each species to the grouping of samples for the 2nd sampling cruise (Pentow Salvor) data. The arbitrary cut-off percentage of 45% was chosen. Average dissimilarity between mined and unmined groups = 71.48%.

SPECIES	TAXONOMIC GROUP	MINED GROUP	UNMINED GROUP	PERCENT	CUMULATIVE PERCENT
<i>Ampelisca anomala</i>	Amphipoda	1.75	6.00	2.64	2.64
<i>Nassarius vinctus</i>	Gastropoda	19.40	20.65	2.61	5.25
<i>Tricolia capensis</i>	Gastropoda	5.55	0.35	2.42	7.66
<i>Terebellides stroemii</i>	Polychaeta	2.50	3.53	2.34	10.01
<i>Prionospio pinnata</i>	Polychaeta	11.75	31.65	2.33	12.33
<i>Nassarius speciosus</i>	Gastropoda	3.50	0.41	2.26	14.59
<i>Macoma crawfordi</i>	Bivalvia	14.05	12.06	2.24	16.83
<i>Haploscoloplos kergulensis</i>	Polychaeta	2.80	4.29	2.20	19.03
<i>Lumbrineris spp. juveniles</i>	Polychaeta	2.85	3.47	2.19	21.22
<i>Hippomedon longimanus</i>	Amphipoda	5.10	1.29	2.00	23.22
<i>Calocaris barnardi</i>	Anomura	0.95	3.94	1.93	25.15
<i>Lumbrineris spp.</i>	Polychaeta	0.95	1.94	1.82	26.96
<i>Diopatra monroi</i>	Polychaeta	2.65	5.71	1.77	28.74
<i>Solariella agulhasensis</i>	Gastropoda	2.35	0.24	1.65	30.38
<i>Nassarius pyramidalis</i>	Gastropoda	1.65	0.12	1.64	32.02
<i>Nassarius plicatellus</i>	Gastropoda	1.55	0.59	1.62	33.64
<i>Lumbrineris heteropoda difficilis</i>	Polychaeta	0.75	1.12	1.59	35.23
<i>Leucothoe richardi</i>	Amphipoda	0.85	0.94	1.59	36.82
<i>Lumbrineris tetraura</i>	Polychaeta	1.80	0.94	1.58	38.40
<i>Laonice cirrata</i>	Polychaeta	1.00	0.65	1.58	39.98
<i>Goneplax angulata</i>	Brachyura	0.90	0.82	1.58	41.55
<i>Marginella capensis</i>	Gastropoda	0.95	0.47	1.54	43.10

As with the *Rockfish* data, *Ampelisca anomala* and *Prionospio pinnata* were characteristic of undisturbed areas while *Macoma crawfordi* was more prevalent in disturbed samples. Several anomalies, however, emerge from this data set. *Nassarius vinctus* is now more common in unmined samples, whereas it was distinctly more abundant in mined areas in the *Rockfish* data. The difference in mean abundance between the mined and unmined group for *Nassarius vinctus* in the *Pentow Salvor* data is negligible (19.40 versus 20.65), and the importance of this species is most likely because of its high densities rather than the distinction in abundance between the two groups. A similar anomaly was noted for *Terebellides stroemii* which has shifted to being more abundant in the unmined samples. A possible explanation for this observation is that a batch of larvae may have settled just before the 1st survey but not before the 2nd sampling cruise. The surveys would then reflect different recruitment stages in the life cycles of these species. The *Pentow Salvor* data set included the gastropod, *Tricolia capensis*, as an important indicator being five times more abundant in mined areas.

Table 5.3. The percentage contribution of each species to the grouping of samples for the combined cruise data. The arbitrary cut-off percentage of 45% was chosen. Average dissimilarity between mined and unmined groups = 72.19%

SPECIES	TAXONOMIC GROUP	MINED GROUP	UNMINED GROUP	PERCENT	CUMULATIVE PERCENT
<i>Ampelisca anomala</i>	Amphipoda	2.81	10.77	3.10	3.10
<i>Nassarius vinctus</i>	Gastropoda	16.71	8.62	2.94	6.04
<i>Prionospio pinnata</i>	Polychaeta	11.23	46.13	2.89	8.93
<i>Macoma crawfordi</i>	Bivalvia	22.45	17.90	2.67	11.60
<i>Hippomedon longimanus</i>	Amphipoda	4.77	6.46	2.55	14.15
<i>Terebellides stroemii</i>	Polychaeta	13.45	3.13	2.47	16.62
<i>Lumbrineris spp.</i>	Polychaeta	1.84	7.79	2.40	19.02
<i>Goneplax angulata juveniles</i>	Brachyura	2.00	2.49	2.13	21.15
<i>Euphausiacea</i>	Euphausiacea	0.42	2.36	2.01	23.16
<i>Haploscoloplos kerguelensis</i>	Polychaeta	1.45	3.11	1.99	25.15
<i>Lumbrineris heteropoda difficilis</i>	Polychaeta	0.74	2.36	1.94	27.09
<i>Tricolia capensis</i>	Gastropoda	4.52	0.34	1.94	29.02
<i>Marginella capensis</i>	Gastropoda	1.03	2.33	1.85	30.88
<i>Laonice cirrata</i>	Polychaeta	1.13	1.66	1.73	32.61
<i>Lumbrineris albidenta</i>	Polychaeta	0.58	3.64	1.71	34.33
<i>Ampelisca brevicornis</i>	Amphipoda	0.29	1.79	1.65	35.97
<i>Dosinia spp.</i>	Bivalvia	0.74	1.26	1.58	37.55
<i>Diopatra monroi</i>	Polychaeta	3.29	2.85	1.54	39.09
<i>Goneplax angulata adults</i>	Brachyura	0.71	0.80	1.49	40.58
<i>Nassarius speciosus</i>	Gastropoda	2.13	0.15	1.48	42.06
<i>Lumbrineris tetraura</i>	Polychaeta	1.13	2.00	1.36	43.42
<i>Nephtys hombergi</i>	Polychaeta	0.48	1.18	1.35	44.77

There is some general agreement for the 1st, 2nd and combined cruise analyses in terms of indicator species. For each analysis, several species contributed to the overall dissimilarity between the two groups, but the primary contributors came from the Amphipoda, Polychaeta, Bivalvia and Gastropoda taxa. There were no perfect indicators which were abundant in one group and entirely absent in the other. The principal contributors are generally those species

that are abundant in one group and rare in the other group. *Ampelisca anomala* and *Prionospio pinnata* were consistently more abundant in the unmined group. *Hippomedon longimanus* was also more abundant in the unmined group (except in the *Pentow Salvor* data set). The *Lumbrineris* genus and *Haploscoloplos kerguelensis* exhibited consistently higher densities in the unmined samples. Indicator species for physically disturbed samples include *Macoma crawfordi*, *Nassarius vinctus*, *Tricolia capensis*, and *Terebellides stroemii*. It is interesting to note that there is a shift in the community composition to a greater proportion of bivalves and gastropods in the mined areas. The mining process removes the fine silt and clay component, which, when dumped at the surface as “tailings”, probably drifts away, whereas pebbles and shells tend to be scattered over the mined area. The net result is an increase in average grain size. The possible relationship between sediment particle size and the taxa present is investigated in the following chapter.

The presence of certain species indicates that certain minimal environmental conditions have been met. The corollary, however, does not hold. The absence of a species does not demonstrate the absence of disturbance (Warwick 1993). A species may be absent due to:

- sampling error, particularly for very low density species,
- the environmental conditions are unsuitable,
- the species has not had the opportunity to get into the area, but may well survive if it were introduced, or
- the functional niche was assumed by another species (Cairns 1979).

The question of why some species dominate in disturbed areas while others are reduced in relative importance is still uncertain. Generally, two explanations have been proposed for this dominance:

- superior tolerance of stressful conditions (Filice 1959; Reish 1979 as cited in Grizzle 1984); and
- superior invasion abilities (Pearson and Rosenbergh 1978; Gray 1979, 1980, 1981 as cited in Grizzle 1984).

It is likely that the tolerance hypothesis would be an important adaptive strategy for an animal in a chemically stressed environment. Conversely, in physically disturbed areas, such as the mined areas off Namibia, the dominant adaptive strategy would most likely be an ability to invade newly-disturbed areas. Such “opportunistic” or “r-selected” species would have a rapid reproductive rate, short life-span and quick generation time (Gray 1981).

It is difficult to draw parallels between the above species list and those derived from organic pollution studies as most of these latter studies were conducted in the northern hemisphere where the benthos is composed of different species, but similar genera. Nevertheless, the above species list can be used as a baseline survey of indicator species for physically disturbed areas off the west coast of southern Africa.

CHAPTER 6

**LINKING OBSERVED COMMUNITY PATTERNS TO
ENVIRONMENTAL PARAMETERS**

“In nature, no factor ever varies alone.”

McIntosh

LINKING OBSERVED COMMUNITY PATTERNS TO ENVIRONMENTAL PARAMETERS

Multivariate analyses have so far been used to characterise changes in community structure following disturbance by marine mining and these differences were formally tested using analysis of similarities tests. It is now desirable to examine whether faunistic differences between sites are correlated with the sedimentological characteristics of disturbed and undisturbed areas. The current chapter therefore seeks the best possible reconciliation between environmental parameters in an attempt to assess the relative importance of each variable in influencing community structure.

There are two possible approaches for examining the relationship between faunal patterns and environmental data. The first approach, proposed by Field *et. al.* (1982), analyses one variable at a time. The biological data are analysed first and then the environmental data is tested for concordance. By superimposing environmental parameters on the 2-D ordinations from the faunistic data, the extent of correlation of the variables with the group differences is illustrated. The underlying premise is that samples that are similar in terms of a suite of environmental parameters would reflect similar species composition (Clarke and Ainsworth 1993). The two analyses are kept separate to avoid any interactive assumptions. This asymmetric approach was the accepted method in a number of practical studies (Gray *et. al.* 1988, 1990; Warwick *et. al.* 1990; Warwick and Clarke 1993a).

The second approach, advocated by Clarke and Ainsworth (1993), provides the theoretical basis underlying the BIO-ENV program in PRIMER. Analogous to the first approach, the biotic and abiotic similarity matrices are computed separately, however, the abiotic matrix is computed repeatedly using all possible combinations of the environmental variables. A rank correlation is then computed for every combination of variables and the degree of improvement or deterioration in each match is recorded (Clarke and Ainsworth 1993). The set of variables that 'best explain' the biotic structure is ascertained by this rank correlation (Clarke and Ainsworth 1993). The advantage of this latter method is that it considers all variables and all combinations of variables simultaneously. The method, however, is more applicable to macrobenthic studies where there is a gradient of pollution and several related contaminant chemicals are measured. Conversely, the effects of offshore marine mining were apparent using particle size composition of the sediment and the average percentage organic matter. The environmental factors were hence unrelated and use is made therefore of the former approach whereby the environmental data is superimposed on the biotic data one at a time.

6.1 PARTICLE-SIZE ANALYSIS AND SEDIMENT STRATIGRAPHY

Detailed textural and particle-size analyses characterised the sediment samples into % mud, % sand and % gravel. The composition of the sediment samples and the average percentage organic carbon and organic nitrogen are listed in Appendix C.

Geological results were available for all the faunal samples collected during the 2nd (*Pentow Savior*) sampling cruise, however, only a subset of the *Rockfish* samples had matching

environmental data. Thus several samples were excluded from the biological MDS for the *Rockfish* data. Non-metric MDS ordinations were performed employing Bray-Curtis similarities on 4th root-transformed abundance data for the *Rockfish* and *Pentow Salvor* data, respectively. The resulting ordinations performed at the genus level are presented in Figure 6.1 below.

The *Rockfish* abundance data clustered into three main groups. Areas 1 and 2 were positioned on the left of the MDS plot with areas 3 and 4 forming an adjacent group. The biota from areas 5 and 6 separated out along the vertical axis of the ordination. The geological results support the biological findings. Sediments from areas 1 and 2 were different from those of areas 3 and 4, which, in turn, were different from those from areas 5 and 6 (Rogers 1995). Sediment from areas 1 and 2 were predominantly composed of sand. Areas 3 and 4 consisted of a polymodal distribution of mud and sand. Area 5 was largely composed of sand and area 6 exhibited modes in both the sand and mud size range. Sample 3.5, which was identified as an outlier in the dendrogram and the MDS in Section 4.3, is the only sample dominated by gravel. It seems likely, therefore, that sediment particle-size is an important factor in influencing species composition in an area.

Figure 6.1. *Rockfish* sampling cruise (a) MDS plot for the biotic data (stress = 0.18). The samples grouped by cluster analysis are designated by the outline around each group. (b) The most abundant particle size-class of each sample superimposed on the biotic ordination, where M = mud; S = sand; G = gravel and a combination (eg. M/S) refers to an approximate 50:50% contribution of each size class.

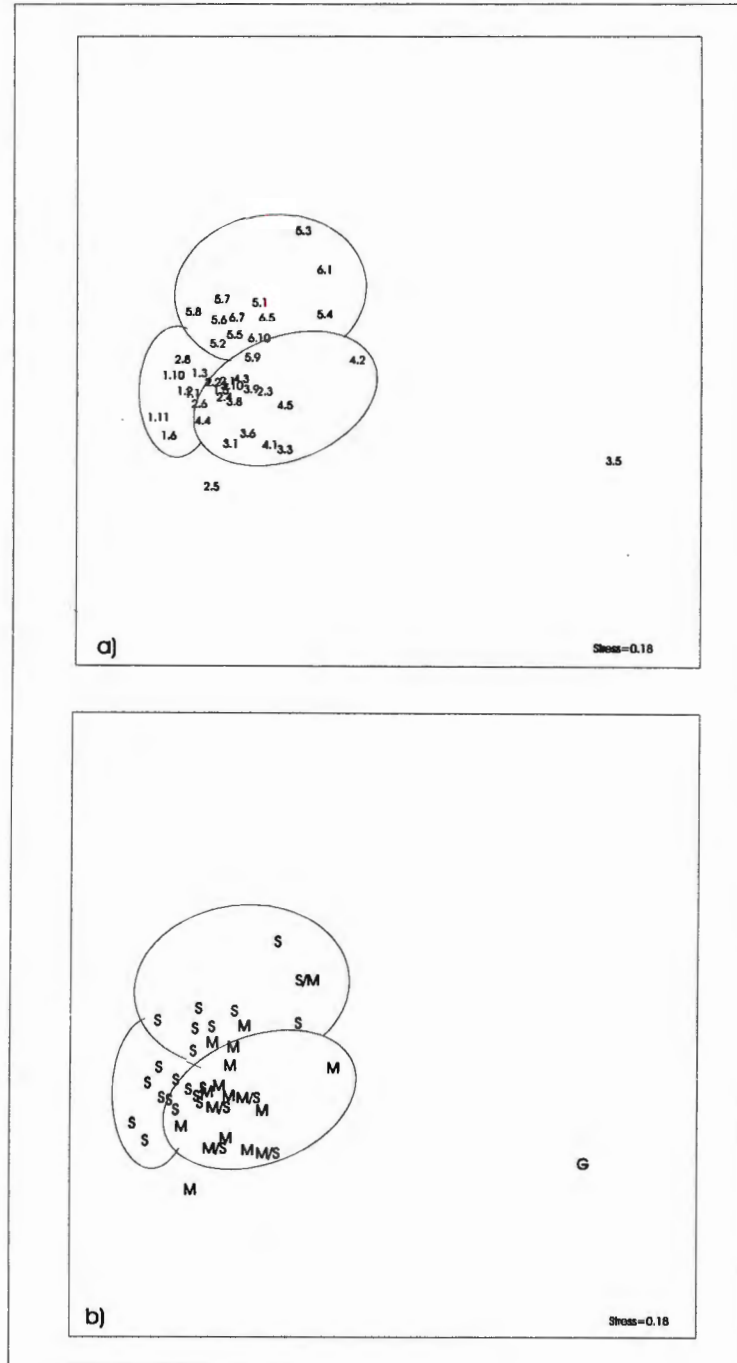
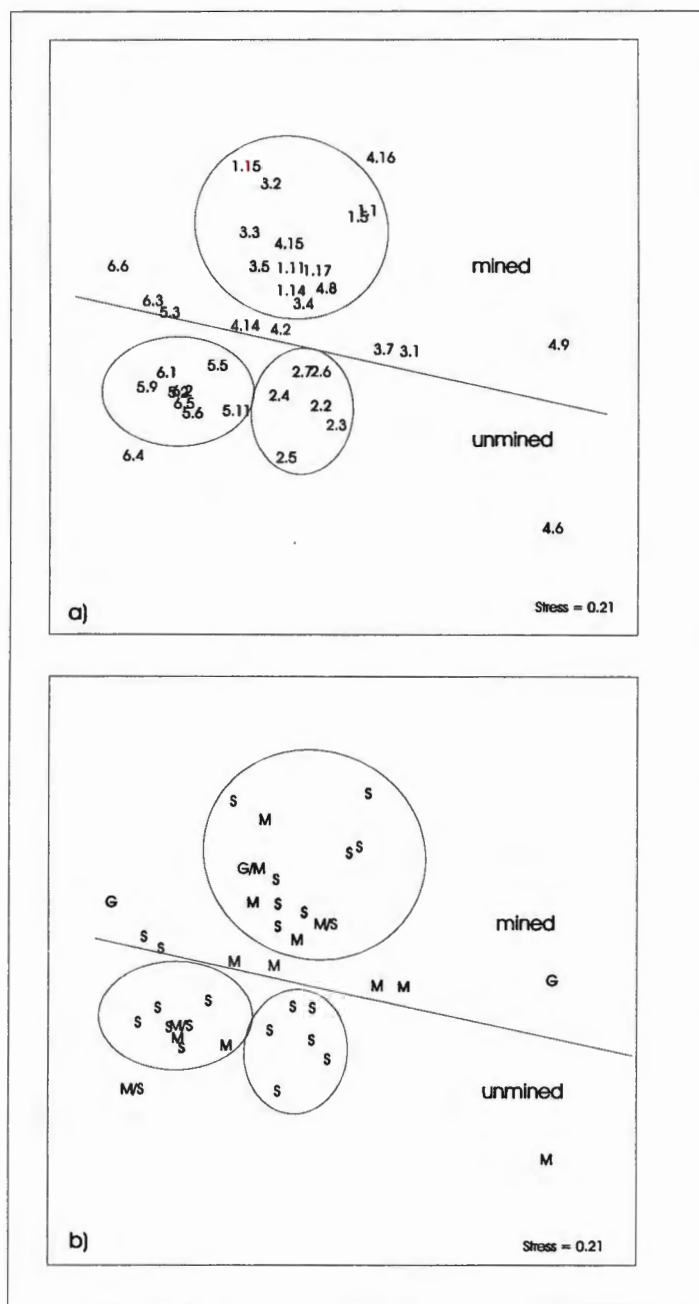


Figure 6.2. *Pentow Salvor* sampling cruise. (a) MDS ordination for the biological data (stress = 0.21). (b) The dominant particle size-class superimposed as a character on the biotic data, where M = mud, S = sand, and G = gravel and a combination (eg. M/S) refers to an approximate 50:50% contribution of each particle-size class. A diagonal line divides the MDS roughly into mined and unmined samples.



The MDS ordination of the *Pentow Salvor* cruise data produced a more complex picture than that of the first sampling cruise. A line passing mid-way through the graph, 6.2, divides the ordination into two halves with the top half generally representing the mined samples originating from areas 1, 3, 4 and 6 and the lower half consisting of the unmined samples from areas 2 and 5. There is a second axis which separates the northern sites (areas 1 to 4) from the southern sites (areas 5 and 6), with the southern sites being positioned to the extreme left of the ordination. Within the unmined group there are 2 clusters of samples. Area 2 forms a distinct group which is dominated by sand particles and the other unmined group contains samples from areas 5 and 6. These samples are predominantly composed of particles in the sand size-class with some samples also containing relatively higher proportions of mud. The samples positioned immediately above the horizontal division (4.13, 4.2, 3.7, 3.1) are principally composed of mud. The mined group of samples were collected over a fairly broad spatial scale (areas 1, 3 and 4) and they contain a polymodal distribution of particles. The main contributing particle-size is a combination of sand and mud, although there is also an infusion of particles in the gravel size-class. It is interesting to note that the outlier, 4.9, is again predominantly composed of gravel. The other outlying sample, 4.6, however, has mud as the most abundant sediment type.

The main sedimentological features that emerged from this study area are described below. Premined stratigraphy consists of a basal mud overlain by a shelly sandy gravel, capped by slightly gravelly muddy sand (Rogers 1995). Detailed particle-size analysis of the sand fractions revealed that unmined sediment is distinguished by a single, well-sorted mode in the 125-micron (3 phi) boundary of the very fine to fine sand on the Wentworth scale (Table 6.1). In contrast, the surficial sediment in the mined areas is characteristically polymodal and

poorly-sorted with modes ranging from fine sand (3 phi) to very coarse sand (0 to -1 phi) (Rogers 1995). It would appear, therefore, that the tripartite stratigraphy (clay overlain by shelly sandy gravel and surficial slightly gravelly sandy mud) is thoroughly mixed by the mining process.

Table 6.1. The phi-scale used for defining Wentworth grades.

PARTICLE SIZE	WENTWORTH GRADE
-1 to 0 phi (2 to 1mm)	very coarse sand
0 to 1 phi (1000 to 500 microns)	coarse sand
1 to 2 phi (500 to 250 microns)	medium sand
2 to 3 phi (250 to 125 microns)	fine sand
3 to 4 phi (125 to 63 microns)	very fine sand

Unfortunately there were not enough sediment samples available from mined areas in the *Rockfish* data to draw conclusions about pre- and post-mining changes in sedimentology. However, the trend emerging from the *Pentow Salvor* data is that unmined areas are characteristically sandy and mined areas are composed of relatively larger proportions of both gravel and mud.

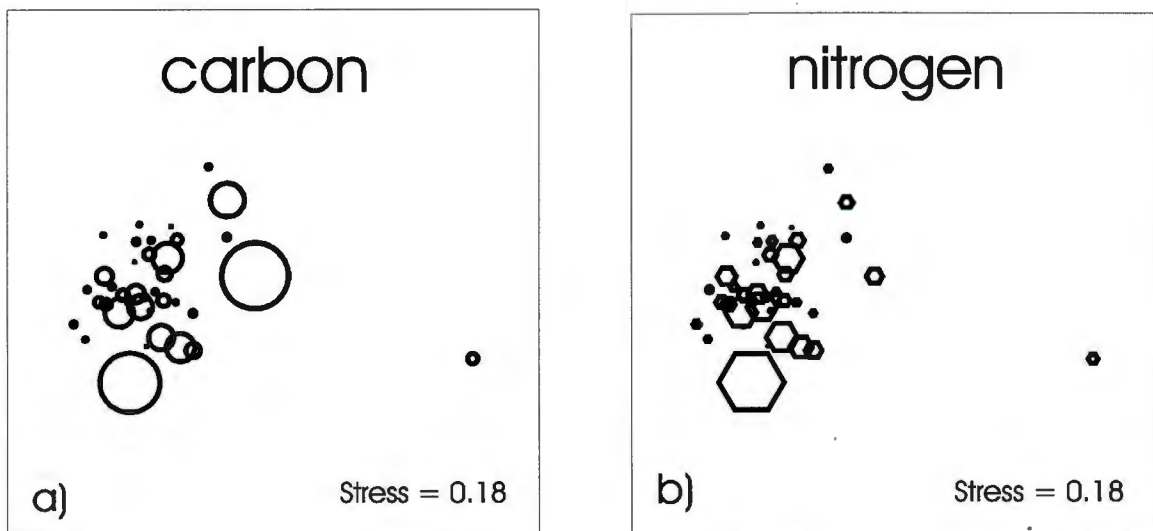
The proportions of mud, sand and gravel are of importance for the distribution of many organisms since porosity and interstitial space are directly controlled by the relative abundance of different sized particles (Gray 1981). There is a general tendency for deposit feeders to predominate in clay-silt sediments and filter feeders to predominate in sandy sediments (Mann 1982). One would, therefore, predict that mining, which removes the sand component and returns the sediment as a mixture of gravel (-1 to 0 phi) and mud (3 to 4 phi),

would cause a shift in community structure towards an increase in the abundance of deposit-feeding organisms. This requires further testing.

6.2 AVERAGE PERCENTAGE ORGANIC CARBON AND NITROGEN

One of the clearest indicators of the difference between sediments in the mined areas and the unmined areas is the abundance of organic matter. The average percentage carbon and average percentage nitrogen values were superimposed on the biotic data to assess the degree of concordance between the two ordinations.

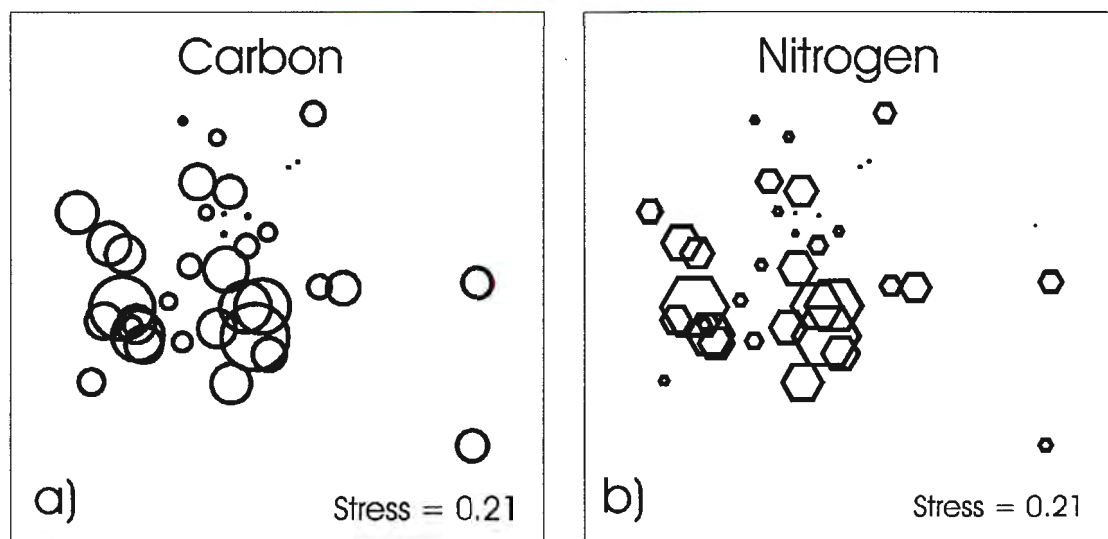
Figure 6.3. *Rockfish* sampling cruise. a) The average % organic carbon superimposed as a circle on the biotic plot, where the size of the circle reflects the relative magnitude of the percentage carbon value. b) The average percentage organic nitrogen superimposed as a hexagon on the biological data.



One of the trends that emerges from Figure 6.3 is that generally samples exhibiting a high average % carbon value also show high average % nitrogen values, except samples 4.2 and

6.1 which have high carbon values but average nitrogen concentrations. Sample 2.5 has an anomalously high carbon (4.25%) and nitrogen (0.52%) concentration. The reason for this is unclear. The outlier, sample 3.5, is not characteristically different from the other samples in terms of organic content values, and one can therefore assume that its distinctiveness is due to its high gravel content rather than as a consequence of organic matter content.

Figure 6.4. *Pentow Salvor* sampling cruise. a) The average % organic carbon superimposed as a circle on the biotic plot, where the size of the circle reflects the relative magnitude of the percentage carbon value. b) The average percentage organic nitrogen superimposed as a hexagon on the biological data.



Akin to the *Rockfish* data, samples yielding high organic carbon values showed high nitrogen values. The most obvious pattern that emerges from Figure 6.4 is that the unmined samples (in the lower half of the ordination) exhibited higher average % carbon and average % nitrogen values than their mined counterparts. The unmined areas have total organic carbon values approximating 4%, which using a factor of 1.8, converts to organic matter contents of about 7%. In stark contrast, mined areas have total organic matter values of 2-3% (Rogers 1995).

The spectrum of nitrogen values mirrors that of organic matter values. Unmined areas have much higher total nitrogen values (0.62%) compared to mined areas (<0.005%).

The reasons for the depauperate organic matter values in the mined areas are largely unclear. Organic matter resides in the fine particle fraction. Mining removes this fraction and it takes time to accumulate from planktonic detritus and mining tailings.

In retrospect, there is strong correlative evidence for the importance of sediment particle size in determining community structure, but this does not demonstrate a cause-and-effect relationship between environmental parameters and community structure. Nevertheless, one can assume that the results are consistent with the assumption that grain size is a contributing factor to the niche parameters that influence community patterns.

A further consideration is establishing whether the relationship between the biotic and abiotic data is as a consequence of anthropogenic disturbance or whether they correlate more closely with differences in natural environmental variables. The nature of the mining process affects the stratigraphy of the sediment so it is difficult, if not impossible, to divorce the two sources of variability. However, the results of the ANOSIM statistical tests show a significant difference between mined and unmined areas. The most likely explanation is that mining disturbs the natural stratigraphy and particle size distribution of an area and these altered sediments in turn influence the structure of the benthic community in the area.

CHAPTER 7

META-ANALYSIS: COMPARATIVE ANALYSIS OF DISTURBANCE

*“Not chaos-like, together crushed and bruised,
But as the world harmoniously confused:
Where order in variety we see,
And where, though all things differ, all agree.”*

Pope (Windsor Forest)

META-ANALYSIS: comparative levels of disturbance.

Changes in benthic community structure are usually measured relative to local controls. However, for management purposes, it is often desirable to assess the severity of disturbance *vis-a-vis* other pollution events on a global scale. One of the drawbacks of multivariate analyses is that they detect differences between communities, but are unable to gauge the level of community stress on a global scale. Species composition varies markedly from place to place depending on local environmental constraints, and this variability would mask any species-dependent response to stress. Furthermore, a high degree of standardization in terms of taxonomic expertise would be required to make studies comparative on a global scale. Therefore, in order to make several macrobenthic studies from a variety of stations comparable, they must be described on a common scale.

Traditionally measures which were species-independent, such as dominance curves and diversity indices, were used for comparative purposes. However, diversity does not behave predictably in response to environmental stress (Warwick and Clarke 1993a). Diversity may increase, decrease or remain the same with increasing levels of disturbance (Warwick and Clarke 1993a). Furthermore, Abundance/Biomass comparison (ABC) curves only recognise three broad categories of disturbance (unpolluted, moderately polluted and grossly polluted) (Warwick and Clarke 1993a) and they tend to overemphasise the single dominant species (Clarke 1990). What is needed is an index of community stress which utilises the full multivariate information and therefore retains a lot more information and is more sensitive than univariate methods in detecting community changes (Warwick and Clarke 1991).

Warwick and Clarke (1993a, 1993b) proposed three possible approaches to measure the severity of disturbance using multivariate techniques:

- Breakdown of seriation (Clarke *et. al.* 1993)
- Increased variability as a symptom of stress (Warwick and Clarke 1993b)
- Meta-analysis using phylum-level data (Warwick and Clarke 1993a).

The first two methods are discussed briefly below and then the latter method, the meta-analysis, is discussed in detail incorporating the results from the current study.

7.1 BREAKDOWN OF SERIATION IN COMMUNITY STRUCTURE

Intertidal and shallow-water benthic communities typically exhibit zonation patterns in the form of sequential changes in community structure with increasing water depth (Petersen 1991). These zonation patterns are determined by a range of environmental gradients including light availability, competition and predation (Sheppard 1982, Done 1983, as cited in Clarke *et. al.* 1993). Clarke *et. al.* (1993) defined the term 'seriation' as 'a sequential pattern of community change' and proposed that the degree of breakdown in this seriation pattern provides an indication of the level of disturbance (Clarke *et. al.* 1993). The technique was tested on a study of the effects of dredging on an intertidal coral-reef assemblage at Ko Phuket, Thailand.

7.2 INCREASED VARIABILITY AMONG REPLICATES

Warwick and Clarke (1993b) noted that the variability among samples collected from impacted sites was far greater than that from control areas. A comparative Index of Multivariate Dispersion (IMD) was devised which measured the relative variability between impacted and control samples (Warwick and Clarke 1993b). This index was computed for four different types of marine communities: meiobenthos subjected to organic enrichment, macrobenthos from the Ekofisk oil field, North Sea, corals from S. Tikus Island, Indonesia following the 1982-3 El Nino event, and reef-fish inhabiting a coral reef which had been subjected to mining. In each case the standard deviation for a mean increased with increasing levels of perturbation (Warwick and Clarke 1993b). Warwick and Clarke (1993b) were therefore able to show that variability in itself is characteristic of disturbed situations.

7.3 META-ANALYSIS

Meta-analysis refers to the combined analysis of a range of several individual case-studies which in combination provide a broader perspective on the problem under investigation (Warwick and Clarke 1993a). Warwick and Clarke (1993a) compared 50 samples from 8 locations in the NE Atlantic shelf at which the pollution status was known. The comparative severity of pollution events was therefore assessed against each other on a regional scale. The variability in species composition on a regional scale can be overcome by working at higher taxonomic levels (Warwick and Clarke 1993a). It has already been shown that pollution effects are detectable at high taxonomic levels and very little, if any, information is lost by aggregating the data back to phylum level. Warwick and Clarke (1993a) used the following 20 phyla in the species aggregation (Table 7.1).

Table 7.1. The 20 phyla used in the species aggregation, following the classification of Howston (1987). Phyla not encountered in this study are designated by *.

1. Porifera *	11. Annelida
2. Cnidaria	12. Chelicerata
3. Platyhelminthes	13. Crustacea
4. Nemertea	14. Mollusca
5. Nematoda	15. Brachiopoda *
6. Priapulida	16. Bryozoa *
7. Entoprocta *	17. Phoronida
8. Pognophora *	18. Echinodermata
9. Sipuncula	19. Hemichordata
10. Ehiura *	20. Chordata

The macrobenthic studies used in Warwick and Clarke's (1993a) baseline study were selected due to the availability of abundance and biomass data and because they represented a range in their degree of disturbance. The 8 locations off the NE Atlantic shelf are described below.

- **Garroch Head, Firth of Clyde, sewage-sludge dump-ground (G1...G12)**

A transect of 12 stations were sampled in 1983 on a west-east transect across a sewage-sludge dump-ground in the Firth of Clyde, Scotland (Pearson and Blackstock 1984 as cited in Warwick and Clarke 1993a). These stations are denoted as G1...G12. Stations in the middle of the transect show signs of gross pollution (Pearson 1987, Warwick et. al. 1987, as cited in Warwick and Clarke 1993a).

- **Loch Linnhe (L63...L73) and Loch Eil (E63...E73), West Scotland**

Two West Scottish sea-lochs, Loch Linnhe and Loch Eil, were sampled over a period spanning 1963 to 1973, when a pulp-mill was commissioned (Pearson 1975). Loch Linnhe samples (L63...L73) and Loch Eil samples (E63...E73) show increasing pollution effects in later years, with the exception of recovery noted in Loch Linnhe in 1973 coinciding with a decrease in pollution loading.

- **Frierfjord, Oslofjord stations (FA...FG)**

Samples were collected from six stations in Frierfjord/Langesundfjord, Oslofjord (Norway).

The stations were ranked in order of increasing stress A-G-E-D-B-C, according to thirteen different criteria.

- **Amoco-Cadiz oil spill, Bay of Morlaix (A77...A81)**

Twenty-one sampling stations were aggregated into five years for the meta-analysis: 1977 = pre-spill, 1978 = immediate post-spill, and 1979-81 = recovery following oil spill.

- **Skaggerrak (SK1, SK3)**

Two stations were sampled at Skaggerrak, one at a depth of 100m and the other station at 300m. The 300m station showed signs of natural disturbance due to the dominance of the sediment-reworking bivalve, *Abra nitida* (Warwick and Clarke 1993a).

- **Northumberland, England (NR)**

An undisturbed site off the coast of Northumberland, NE England.

- **Carmarthen Bay, Wales (CR)**

An undisturbed site in Carmarthen Bay, S. Wales.

- **Keil Bay (KL)**

Twenty-two sets of samples were averaged to produce a mean production value for an undisturbed station in Kiel Bay, Germany.

The abundance and biomass matrices of phylum-level data were then merged into a production matrix using the following allometric equation:

$$P = \left(\frac{B}{A} \right)^{0.73} \times A$$

where P is production,

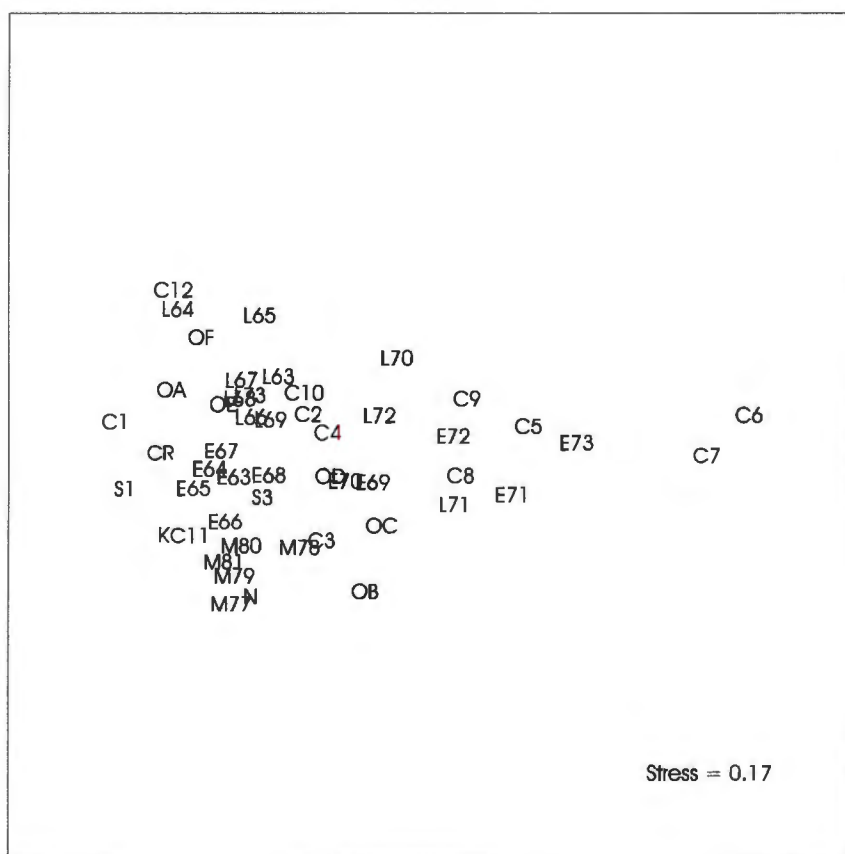
B is biomass, and

A is the abundance of a species.

B/A is the mean body-size and 0.73 is the average exponent of the regression of annual production on body-size for macrobenthic invertebrates (Warwick and Clarke 1993a). The data from each study are standardised by expressing the production of each phylum as a proportion of the total production for each sample.

An ordination using the standardized, 4th root-transformed data and the Bray-Curtis coefficient of similarity was performed on the production matrix for all 50 samples from the NE Atlantic Shelf (Figure 7.1).

Figure 7.1. MDS ordination of phylum-level production data from the 50 macrobenthic stations on the NE Atlantic Shelf, with Clyde (C1...C12); Linnhe (L63...L73); Eil (E63...E73); Oslofjord (OA...OG); Morlaix (M77...M81); Skagerrak (S1, S3); Northumberland (N); Carmarthen (CR) and Kiel (K). Stress = 0.17.



The MDS for the NE Atlantic samples takes the form of a wedge with the principal horizontal axis representing a scale of disturbance. The most disturbed sites (the two stations closest to the Clyde sewage-sludge dump centre, namely C6 and C7) are located to the extreme right of the wedge and the undisturbed samples are clustered to the left. The relative positions of the

stations on the horizontal axis are thus a measure of their relative severity of disturbance (Warwick and Clarke 1993a).

Agard *et. al* (1993) tested the technique in a tropical estuary in Trinidad, West Indies, where the area was subjected to natural oil seepage and spillage from oil production activities (Agard *et. al.* 1993). The MDS showed that the Trinidad samples were compatible with the NE Atlantic data in terms of their locations along the principal axis of disturbance; however, the samples were separated out along the upper edge of the meta-analysis 'wedge', which was attributed to the higher relative proportion of Crustacea relative to Echinodermata and Mollusca.

The abundance and biomass data collected off the west coast of southern Africa were entered into a production matrix along with the original 50 samples from the NE Atlantic shelf. The multidimensional scaling program was then re-run using the amended production matrix. The MDS program in PRIMER is restricted to a 125x125 (dis)similarity matrix. Unfortunately, therefore, we could not use the combined cruise data which, when merged with the original 50 samples, totals 147 samples. So four separate analyses were performed using different combinations of the samples collected off the west coast of southern Africa:

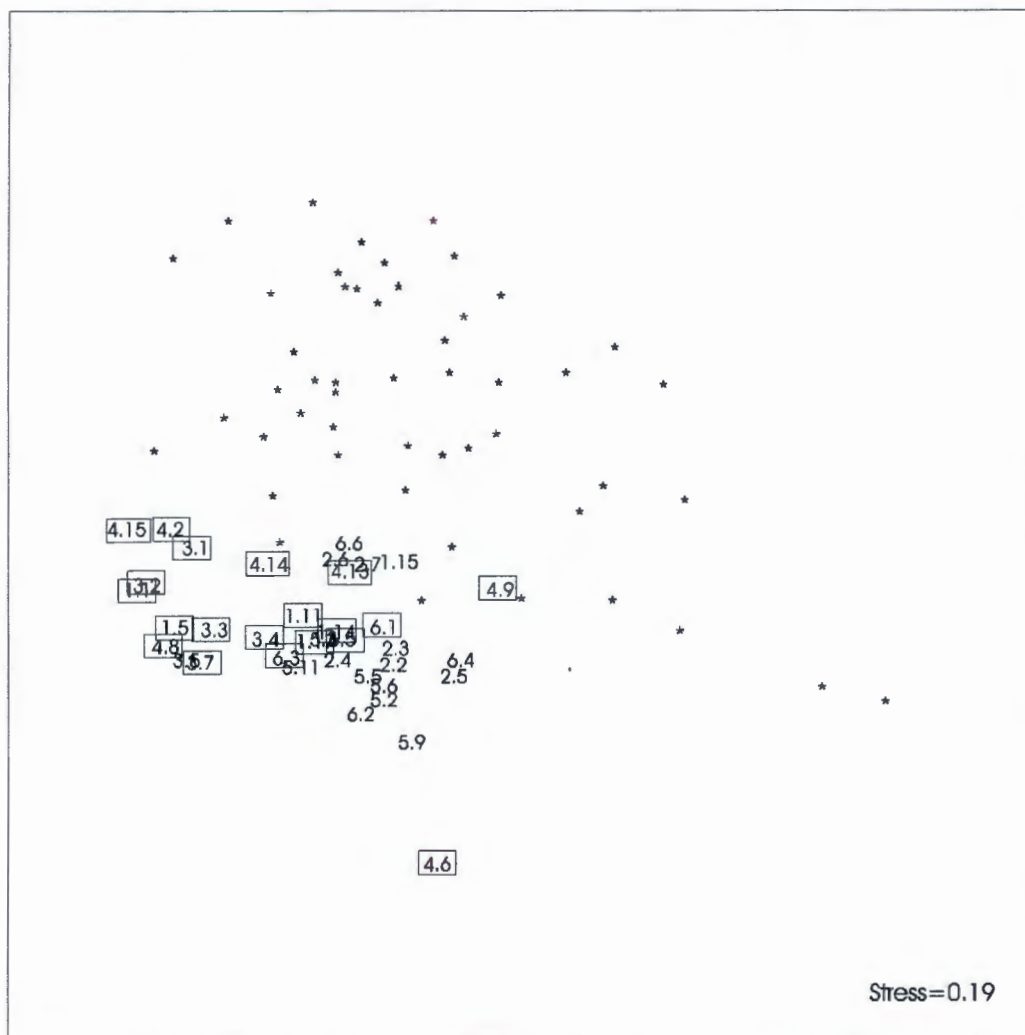
- The NE Atlantic Shelf samples and all the unmined samples from both cruises;
 - The NE Atlantic Shelf samples and the mined and unmined samples from (a) the *Rockfish* cruise and (b) the *Pentow Salvor* cruise;
 - The NE Atlantic Shelf samples and the mined samples from both cruises.
-

7.3.1 Meta-analysis comparing the severity of disturbance of NE Atlantic Shelf samples with unmined samples collected off the west coast of Southern Africa

The unmined samples represent the undisturbed condition of macrobenthic communities off the west coast of Southern Africa. Therefore, an MDS of these samples with Warwick and Clarke's (1993a) original data set should detect any differences due to natural variability between the two groups of studies. A non-metric MDS was performed on the 4th root-transformed production values using the Bray-Curtis coefficient of similarity. The Namibian samples are identified by their sample numbers and the N.E. Atlantic Shelf samples are represented by an asterisk so that the relative positions of the Namibian samples can be clearly seen (Refer to Figure 7.3).

Predictably, most of the unmined samples are concentrated to the left of the disturbance 'wedge'. R3.7, however, is located to the extreme right of the ordination, suggesting that it exhibits gross disturbance. The reasons for this anomaly are unclear and may be due to misclassification of the sample. The unmined samples form a distinct group from the original data set (Global $R = 0.565$; $p < 0.001\%$). This result suggests that there are inherent differences between the N.E. Atlantic Shelf samples and the macrobenthos off the Namibian coast. Possible reasons for this distinction are discussed in Section 7.3.3.

Figure 7.5. MDS ordination comparing the N.E. Atlantic Shelf samples to the *Pentow Salvor* mined and unmined samples. The N.E. Atlantic Shelf samples are represented by * and the Namibian samples are identified. Mined replicates are denoted by a border and the unframed replicates are unmined. Stress = 0.19.



The group of Namibian samples are significantly different from the N.E. Atlantic shelf samples (*Rockfish*: Global $R = 0.536$, $P < 0.001\%$; *Pentow Salvor*: Global $R = 0.473$, $P < 0.001\%$).

The mined samples from the *Pentow Salvor* cruise are generally positioned below the N.E. Atlantic Shelf samples and separate out approximately half-way across the “wedge” of disturbance. The unmined samples are generally clustered in a group below the mined Namibian samples. The pattern is not as clear-cut for the *Rockfish* data set, where the mined and unmined samples exhibit some overlap in their distribution on the MDS plot. The

samples exhibiting the most severe effects of disturbance are predominantly from station 3 in the *Rockfish* data set and station 4 in the *Pentow Salvor* data set, namely R3.7, R3.6, S4.9 and S4.6. None are as grossly disturbed as the benthic communities at the centre of the Garroch Head sewage-sludge dump-ground in Clyde, which are situated to the extreme right of the disturbance 'wedge'. Sample 3.7 from the *Rockfish* cruise is consistently grouped with the mined samples in the cluster analysis in Chapter 4 and in the MDS results above. It would appear that it was originally misclassified as unmined. This anomaly may, however, be due to a sampling error as the sample contained very few benthic organisms.

7.3.3. Meta-analysis comparing the severity of disturbance of N.E. Atlantic Shelf Samples with mined samples collected off the west coast of Southern Africa

Thirty-two samples were obtained from 6 areas subjected to offshore diamond mining. The samples were collected over 2 consecutive years and represented various stages of post-mining recovery (Table 7.2).

Table 7.2. Temporal states of post-mining recovery at time of sampling. R denotes samples collected on the *Rockfish* (May 1994) cruise and S denotes samples collected on the *Pentow Salvor* (February 1995) cruise.

Recovery status at time of sampling	Sample number
Just mined (1 month prior to sampling)	R3.2, R3.4, S1.1, S1.11, S1.14, S1.17, S3.1, S3.2
Mined 7-9 months previously	R4.2, R4.6, R4.7, R4.8, R4.9, R4.10, S1.5, S3.3, S3.4, S3.7
Mined 12-24 months previously	S4.2, S4.6, S4.8, S4.9, S4.13, S4.14, S4.15, R5.3
Mined 36+ months previously	R6.8, R6.9, R6.10, S6.1, S6.3, S6.5

in determining between-sample relationships. A one-way analysis of similarities test demonstrates a highly significant difference between the N.E. Atlantic group of samples and the Namibian group of samples (Global R = 0.757, $P < 0.001\%$).

The Namibian samples span halfway across the disturbance axis, suggesting that on a global scale some of the samples are severely disturbed. Samples S4.6, R6.9 and R3.4 show the most severe effects of disturbance, however, no samples are as grossly disturbed as those at the centre of the Clyde sewage-sludge dump-ground, C6 and C7.

Within the mined group, there was no pattern in terms of temporal states. The samples represented a range of temporal states of post-mining recovery and one might predict that the samples with the longest recovery period would be positioned to the left of the plot with the relatively undisturbed stations, however, no temporal trends were evident.

The relatively low stress value (stress = 0.18) indicates that the 2-D plot is a good representation of between-sample relationships. We can, therefore, confidently display the groups in two-dimensions.

Possible factors which are responsible for the principal axis are summarised below:

- The principal axis could be reflecting the distinction in benthic community structure between northern and southern hemispheres; or
 - the axis could be reflecting differences between organic pollution studies and physical disturbance studies. The N.E. Atlantic samples were obtained from areas subjected to organic enrichment and the changes in macrobenthos communities after an organic pollution event may be different to those after physical disturbance. The effects of organic
-

pollution are likely to have residual effects where contaminating chemicals remain in the sediment for prolonged periods, affecting the benthos that recolonise the area. Conversely, physical disturbance will cause defaunation, however, there will not be a release of chemicals into the sediment. However, the distinction between the unmined samples collected off Namibia and the N.E. Atlantic Shelf samples seem to suggest that disturbance *per se* is not responsible for the difference between the two study areas on a global scale; or

- the distinction of the Namibian samples may be due to the characteristic oxygen-deficient Shelf-water. The west coast of Southern Africa, and in particular, the continental shelf off the Namibian coast, experiences a seasonal period of very low oxygen concentrations annually (Chapman and Shannon 1985). The benthos residing in the Namibian waters may therefore be a distinct community which is able to survive oxygen-deficient conditions.

An analysis of the contribution of each phylum to the average Bray-Curtis dissimilarity between all the mined Namibian samples and all the N.E. Atlantic samples was performed using the SIMPER program in PRIMER. The results are tabulated in Table 7.3.

Table 7.3. Results of the SIMPER program showing the relative contribution of each phylum to the average dissimilarity between the N.E. Atlantic samples and the mined Namibian samples. The dominant group for each phylum is highlighted in bold type. Average dissimilarity between the two groups = 53.17%.

PHYLUM	N.E. ATLANTIC SAMPLES - AVE. PRODUCTION	NAMIBIAN SAMPLES - AVE. PRODUCTION	PERCENT CONTRIBUTION	CUMULATIVE PERCENT
Annelida	54.08	32.11	24.27	24.47
Echinodermata	10.22	0.25	18.63	43.10
Mollusca	29.20	49.47	15.38	58.48
Crustacea	3.58	16.71	12.72	71.20
Nemertea	1.15	0.33	10.70	81.90
Cnidaria	0.35	1.15	5.18	87.08
Sipunculida	0.31	0.14	5.00	92.08
Nematoda	0.98	0.00	4.62	96.70
Hemichordata	0.05	0.00	1.32	98.02
Platyhelminthes	0.02	0.00	0.64	98.66
Priapulida	0.03	0.00	0.49	99.15
Chordata	0.01	0.00	0.41	99.56
Chelicerata	0.00	0.00	0.27	99.83

The Annelida were responsible for approximately 25% of the average dissimilarity between the two groups and although they formed a major component of the Namibian samples, their abundance was still relatively less than their abundance in the N.E. Atlantic samples. Annelids are typically regarded as 'weedy' species which are found in large numbers in organically enriched areas (Pearson and Rosenberg 1978). Organically polluted areas characteristically show a shift in community structure towards a greater predominance of opportunistic species, particularly in the Annelida phylum, because of the organically enriched environment. Conversely, mining is an unselective process which denudes all fauna present and the organisms that recolonise an area are most likely those exhibiting superior invasive abilities coupled with the ability to survive in sediment exhibiting a polymodal particle-size distribution.

Echinodermata were abundant in the N.E. Atlantic samples and were virtually absent from the current study. Mollusca were a major contributing phylum being approximately twice as abundant in the Namibian samples compared to the N.E. Atlantic samples. Their predominance in mined areas has already been discussed in the “similarity percentages” chapter where a marked increase in both Bivalves and Gastropods was recorded following disturbance by marine mining. Several phyla were present in the original data set but entirely absent from the mined Namibian samples. These phyla include the Nematoda (which did occur in the unmined samples), the Hemichordata, Chordata, Platyhelminthes (also occurred in unmined samples), Priapulida and Chordata. Chelicerata were absent from both groups.

This multivariate approach to comparative studies of benthic communities seems to be a lot more sensitive than species independent methods. The mined samples show patterns of disturbance which are comparable on a global scale and separate out approximately half-way across the axis of disturbance. There appears to be a second factor which is responsible for distinguishing between the Namibian samples (both mined and unmined) and the samples collected on the N.E. Atlantic Shelf. The phyla having the greatest contribution to this dissimilarity between the two groups are the Annelida, Echinodermata and Mollusca. The reasons for the distinction between the two groups of studies and their distribution along the vertical axis are unclear but most likely reflect a difference in community structure due to the characteristically oxygen-deficient Shelf-water off the west coast of Southern Africa.

CHAPTER 8

CONCLUSION

CONCLUSION

Field *et. al.* (1982) outlined a strategy for analysing multivariate community data which has proven to be particularly sensitive in elucidating changes in benthic community structure following organic pollution events. The technique is based on a biologically-motivated definition of similarity between two communities and is therefore sensitive to the fact that various species respond differently to disturbance. The current study uses samples from a physically disturbed area with no putative organic pollution to test whether multivariate methods are also sensitive to shifts in community structure as a consequence of physical disturbance. The five main aims of the study were treated as separate chapters and the main findings discussed in the following five paragraphs.

A priori statistical testing was used to test the null hypothesis that there is no difference between mined and unmined samples. Analysis of similarities statistical testing rejected the null hypothesis and showed a highly significant difference between mined and unmined samples in terms of their faunistic attributes. Statistical testing also revealed inherent variability among study sites, and it was concluded that both natural fluctuations and induced disturbance effects act together to produce the observed community structure.

Graphical multivariate methods were used as a tool to discern the most salient patterns in the macrobenthic community. Aggregation of the data to higher taxonomic levels did not result in the loss of information, and in fact, improved the resolution of inter-sample relationships. Analysis of the biomass data closely resembled the results of the abundance data and it was hence concluded that either component of the biotic data can be used to represent the benthic

community structure. Cluster analysis revealed two major groups with the mined samples forming a distinct group from the unmined samples in terms of their faunistic attributes. Within these two broad groups, cluster and MDS analyses distinguished between sites 1 and 2, sites 3 and 4, and sites 5 and 6 in the *Rockfish* data. The *Pentow Salvor* data showed similar trends in terms of natural variability among the study areas, however, area 1 which was subsequently mined, now grouped with the mined samples from areas 3 and 4. The mining therefore appears to have a dominant effect in terms of influencing the groupings of samples. Several samples (R3.5, R3.7, S4.6, S4.9) are consistently distinguished as outliers in both the cluster and the MDS analyses. Possible reasons for this anomaly are explored by relating the community patterns to the environmental data.

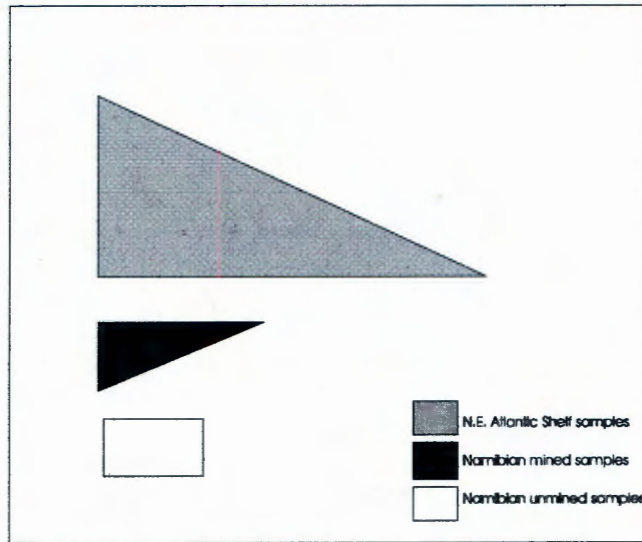
The dissimilarity between mined and unmined samples was related back to the component species in each group of samples. The general pattern that emerges is that the Amphipoda *Ampelisca anomala* and *Hippomedon longimanus* and the Polychaeta *Prinospio pinnata*, *Haploscoloplus kerguelensis* and the *Lumbrineris* genus, are sensitive to the effects of marine mining and are reduced in abundance. The mined areas exhibited a relative increase in the abundance of Gastropoda and Bivalvia such as *Macoma crawfordi*, *Nassarius vinctus* and *Tricolia capensis*. The “opportunistic” polychaete, *Terebellides stroemi*, also increased in abundance in disturbed areas.

The biological composition of an area is largely affected by the prevalent environmental conditions. Therefore, one of the aims of the study was to assess the degree of concordance between environmental factors and the biotic patterns. Sediment particle-size appears to play a key role in influencing benthic community patterns and was particularly important in distinguishing the outliers. Average percentage organic carbon and nitrogen showed a marked

decrease in mined areas and this is also likely to affect community patterns. The sediment particle-size is, in turn, affected by the mining process. Mining essentially removes the fine sand component of the sediment, leaving larger proportions of gravel and mud and this altered stratigraphy presumably affects the composition of benthic communities.

The severity of the disturbance caused by offshore marine mining was estimated using a meta-analysis of phylum-level data. A comparative study of the samples off the west coast of Southern Africa and samples from the N.E. Atlantic Shelf revealed two very distinct groups which separated out along the vertical axis on the MDS. The N.E. Atlantic Shelf samples separated out along a “wedge” of disturbance. Several samples from this study stretched approximately halfway across the axis of disturbance, however, none showed signs of stress as severe as those noted for the benthos near the centre of the Firth-of-Clyde sewage-sludge dump-ground. The meta-analysis appears to be applicable to studies of both organic and physical disturbance, although there seems to be a second factor causing the separation along the vertical axis. It was hypothesized that this distinction may be due to the characteristic oxygen-deficient water on the continental shelf off the west coast of Southern Africa. A highly schematic diagram illustrating the most salient patterns of the meta-analysis is depicted in Figure 8.1.

Figure 8.1 Schematic diagram showing the relationship of the Namibian samples to the N.E. Atlantic Shelf samples in terms of their production values. Patterns are as determined by the *Pentow Salvor* cruise data.



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APPENDICES

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APPENDIX A

Abundance and Biomass Data

APPENDIX A

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Macrofauna biomass data for the *Pentow Salvor* cruise:
Area 3 and 4
Macrofauna biomass data for the *Pentow Salvor* cruise:
Area 5 and 6

APPENDIX A

SECTION I

Abundance data for Rockfish cruise

SPECIES	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	1.10	1.11
CLASS CRUSTACEA											
Sub-Class Copepoda											
Copepod A											
Sub-Class Ostracoda											
Myodocopa											
ISOPODA											
Isopod A											
Arcturidae											
Arcturidae A			1								2
Arcturid B						1					
Arcturid C											
Arcturid D							1				
<i>Cirolina imposita</i>											
<i>Cirolana sulcata</i>											
<i>Microarcturus quadriconus</i>											
AMPHIPODA											
New amphipod											
Ampeliscidae											
<i>Ampelisca anisuropa</i>						2	2				
<i>Ampelisca anomala</i>	3	3	6	1	7	5	2	5	3	3	3
<i>Ampelisca brachycerus</i>											
<i>Ampelisca brevicornis</i>		4	1			3	1	8		2	
<i>Ampelisca natalensis</i>											1
<i>Ampelisca palmata</i>								2		1	
<i>Ampelisca spinimana</i>											
Coropiidae											
<i>Aora kerguelene</i>											
<i>Aorcho delgadus</i>		2				1					
Corophiid A (Gammaropsis)				1			1				
Corophiid Q											
Dexaminidae											
<i>Atylus swammerdamei</i>											
<i>Guernea rhomba</i>											
Eusiridae											
<i>Paramoera capensis</i>											
<i>Rhachotropis spp.</i>											
Gammaridae											
<i>Elasmopus affinis</i>											
<i>Elasmopoides chevreux</i>											
<i>Maera spp.</i>											
Haustoriidae											
<i>Urothoe grimaldi</i>	1						1		1		
<i>Urothoe pinnata</i>		1									
<i>Urothoe elegans</i>										3	1
<i>Urothoe coxalis</i>											
Leucothoidae											
<i>Leucothoe spinicarpa</i>											
<i>Leucothoe richiardi</i>			1								1
Liljeborgiidae											
<i>Listriella lindae</i>											
Lysianassidae											
<i>Acidostoma obesum</i>					2						

SPECIES	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	3.10
PHYLUM ARTHROPODA										
CLASS CRUSTACEA										
Sub-Class Copepoda										
Copepod A									1	
Sub-Class Ostracoda										
Myodocopa										
ISOPODA										
Isopod A										
Arcturidae						2				
Arcturidae A										
Arcturid B										
Arcturid C										
Arcturid D										
<i>Cirolina imposita</i>										
<i>Cirolana sulcata</i>			2	3						
<i>Microarcturus quadriconus</i>										
AMPHIPODA										
New amphipod	1									
Ampeliscidae										
<i>Ampelisca anisuropa</i>										
<i>Ampelisca anomala</i>	3	0	6	0	0	71	0	20	25	21
<i>Ampelisca brachycerus</i>						1				
<i>Ampelisca brevicornis</i>				5		1		2		3
<i>Ampelisca natalensis</i>										
<i>Ampelisca palmata</i>	2		3			4			1	3
<i>Ampelisca spinimana</i>										
Coropiidae										
<i>Aora kerguelene</i>										
<i>Aorcho delgadus</i>			1			8				
Corophiid A (Gammaropsis)										
Corophiid Q										
Dexaminidae										
<i>Atylus swammerdamei</i>										
<i>Guerneia rhomba</i>										
Eusiridae										
<i>Paramoera capensis</i>										
<i>Rhachotropis spp.</i>										
Gammaridae										
<i>Elasmopus affinis</i>										
<i>Elasmopoides chevreaux</i>										
<i>Maera spp.</i>										
Haustoriidae										
<i>Urothoe grimaldi</i>										
<i>Urothoe pinnata</i>										
<i>Urothoe elegans</i>										
<i>Urothoe coxalis</i>										
Leucothoidae										
<i>Leucothoe spinicarpa</i>										
<i>Leucothoe richiardi</i>	2					8		1		1
Liljeborgiidae										
<i>Listriella lindae</i>										
Lysianassidae										
<i>Acidostoma obesum</i>				146				1	1	

SPECIES	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	4.10
PHYLUM ARTHROPODA										
CLASS CRUSTACEA										
Sub-Class Copepoda										
Copepod A										
Sub-Class Ostracoda										
Myodocopa										
ISOPODA										
Isopod A			1							
Arcturidae										
Arcturidae A										
Arcturid B										
Arcturid C										
Arcturid D										
<i>Cirolina imposita</i>								1		
<i>Cirolana sulcata</i>										
<i>Microarcturus quadriconus</i>	2							2		
AMPHIPODA										
New amphipod										
Ampeliscidae										
<i>Ampelisca anisuropa</i>								2		
<i>Ampelisca anomala</i>	27	0	29	3	1	2	2	5	0	0
<i>Ampelisca brachycerus</i>										
<i>Ampelisca brevicornis</i>	1		3				1	1		
<i>Ampelisca natalensis</i>										
<i>Ampelisca palmata</i>			2				1			
<i>Ampelisca spinimana</i>										
Coropiidae										
<i>Aora kerguelene</i>										
<i>Aorcho delgadus</i>						1		1		
Corophiid A (Gammaropsis)										
Corophiid Q										
Dexaminidae										
<i>Atylus swammerdamei</i>	1			3						
<i>Guernea rhomba</i>	1									
Eusiridae										
<i>Paramoera capensis</i>										
<i>Rhachotropis spp.</i>										
Gammaridae										
<i>Elasmopus affinis</i>										
<i>Elasmopoides chevreux</i>										
<i>Maera spp.</i>										
Haustoriidae										
<i>Urothoe grimaldi</i>										
<i>Urothoe pinnata</i>										
<i>Urothoe elegans</i>										
<i>Urothoe coxalis</i>										
Leucothoidae										
<i>Leucothoe spinicarpa</i>										
<i>Leucothoe richiardi</i>					3		1	3		
Liljeborgiidae										
<i>Listriella lindae</i>										
Lysianassidae										
<i>Acidostoma obesum</i>		3				1		1		

SPECIES	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	4.10
Anomura A										
<i>Anomura (Paguristes barnardi)</i>					1		2	2		
<i>Callianassa kraussii</i>										
Brachyura										
<i>Gonoplax angulata juveniles</i>	1	6	13	6	1	6	4	17	2	
<i>Goneplax angulata</i>			2		4		1	1		
<i>Mursia cristimanus</i>				1				2		
Brachyura A										
Brachyura C										
PHYLUM BRACHIOPODA										
<i>Terebratulina meridionalis</i>										
PHYLUM MOLLUSCA										
AMPHINEURA										
<i>Ischnochiton bergoti</i>										1
CLASS PELECYPODA										
BIVALVIA										
<i>Macoma spp.</i>	27	57	38	71	18	123	32	153	8	11
<i>Macoma C (Tellina alfredensis)</i>								7		
<i>Dosinia spp.</i>			2	2	1	2		8		
<i>Nucula nucleus</i>	7		3		5				2	1
Bivalve F					1					
<i>Tellina spp.</i>								3		
<i>Dosinia lupinus orbigny</i>										
Bivalve L										
CLASS GASTROPODA										
<i>Alvania fenestrata</i>								3	1	
<i>Epitonium kraussi</i>								6		
<i>Heliacus variegata</i>										
<i>Marginella capensis</i>	7		1	1	14	2		4	3	
<i>Marginella kerochuta</i>										
<i>Marginella musica</i>										
<i>Nassarius analogica</i>								73		
<i>Nassarius plicatellus</i>								28		
<i>Nassarius plicatellus form scopularcus</i>										
<i>Nassarius pyramidalis</i>										
<i>Nassarius speciosus</i>										
<i>Nassarius vidalensis</i>								1	1	
<i>Nassarius vinctus</i>		14	41		4	11	2			
<i>Natica tecta</i>										
<i>Ocenebra scrobiculata</i>								5		
<i>Pyramidella spp.</i>								2		
<i>Solariella agulhasensis</i>								42		
<i>Tricolia capensis</i>						1		31	4	
<i>Triphora africana</i>										
<i>Turris spp.</i>										
<i>Turris flavidula</i>										
<i>Turritella sanguinea</i>										
<i>Volutocorbis abyssicola</i>										
PHYLUM ECHINODERMATA										
<i>Ophionereis porrecta</i>								3		
<i>Henricia spp.</i>								1		

**MACROFAUNA ABUNDANCE DATA FOR THE FIRST SAMPLING CRUISE
(ROCKFISH: JUNE 1994)**

AREA 5

SPECIES	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	5.10
PHYLUM PORIFERA										
Porifera A										
PHYLUM CNIDARIA										
Class Scyphozoa										
Scyphozoa A										
Class Anthozoa										
Anthozoa A										
Anthozoa B										
Anthozoa C										
Anthozoa D										
PHYLUM NEMERTEA										
<i>Cerebratulus spp.</i>	1	1		1				1	1	1
<i>Cerebratulus fascus</i>	1				1					
<i>Lineus spp.</i>										
Nemertea A	3	1			2					
Nemertea B										
Nemertea C										
Nemertea D										
Nemertea E										
SIPUNCULIDAE										
Siphunculid A										
Siphunculid B										
PHYLUM ANNELIDA										
POLYCHAETA										
Eunicidae										
<i>Lumbrineris spp.</i>	15			4	13	9				
<i>Lumbrineris heteropoda difficilis</i>	2	13	1	2		3	4	6	5	2
<i>Lumbrineris P (cavifrons)</i>										
<i>Lumbrineris R (albidenta)</i>		5	3						14	
Lumbrinerinae F										
<i>Lumbrineris tetraura</i>							2			2
Lumbrineris B										
<i>Lumbrineris magalhaensis</i>								2		
<i>Lumbrineris latreilli</i>										
<i>Lumbrineris meteorana</i>										
<i>Arabella spp.</i>										
<i>Arabella iricolor caerulea</i>					1		2		1	
<i>Arabella L</i>										
<i>Diopatra spp.</i>	70			7	2	25			9	
<i>Diopatra cuprea</i>	1									
<i>Diopatra monroi</i>			26		1		2			26
Glyceridae										
Nereidae										
<i>Nereis spp.</i>			5		1					
<i>Micronereides capensis</i>					1					
Nephtyidae	4	3		2				9		

SPECIES	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	5.10
PHYLUM ARTHROPODA										
CLASS CRUSTACEA										
Sub-Class Copepoda										
Copepod A		1					1	7		
Sub-Class Ostracoda										
Myodocopa										
ISOPODA										
Isopod A										
Arcturidae										
Arcturidae A										
Arcturid B										
Arcturid C										
Arcturid D										
<i>Cirolina imposita</i>										
<i>Cirolana sulcata</i>										
<i>Microarcturus quadriconus</i>										
AMPHIPODA										
New amphipod										
Ampeliscidae										
<i>Ampelisca anisuropa</i>										
<i>Ampelisca anomala</i>	0	14	0	1	1	13	17	23	41	3
<i>Ampelisca brachycerus</i>										
<i>Ampelisca brevicornis</i>						1		1		
<i>Ampelisca natalensis</i>										
<i>Ampelisca palmata</i>										
<i>Ampelisca spinimana</i>										
Coropiidae										
<i>Aora kerguelene</i>										
<i>Aorcho delgadus</i>			1							
Corophiid A (Gammaropsis)										
Corophiid Q									1	
Dexaminidae										
<i>Atylus swammerdamei</i>										
<i>Guernea rhomba</i>										
Eusiridae										
<i>Paramoera capensis</i>										
<i>Rhachotropis spp.</i>							1			
Gammaridae										
<i>Elasmopus affinis</i>				2						
<i>Elasmopoides chevreux</i>										
<i>Maera spp.</i>						1				
Haustoriidae										
<i>Urothoe grimaldi</i>										
<i>Urothoe pinnata</i>										
<i>Urothoe elegans</i>										
<i>Urothoe coxalis</i>										
Leucothoidae										
<i>Leucothoe spinicarpa</i>										
<i>Leucothoe richiardi</i>					5					
Liljeborgiidae										
<i>Listriella lindae</i>		1	2			3		1		
Lysianassidae										
<i>Acidostoma obesum</i>			1		2					

SPECIES	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	6.10
<i>Hippomedon longimanus</i>							1			
Oedicerotidae										
<i>Monoculodopsis longimana</i>										
<i>Oediceroides cinderella</i>										
<i>Perioculodes longimanus</i>										
<i>Perioculodes pallidus</i>										
<i>Westwoodilla manta</i>			1		4		1			6
Phoxocephalidae										
Phoxocephalid B										
<i>Heterophoxus cephalodens</i>										
<i>Paraphoxus oculatus</i>		2		3	1	1	1			
<i>Platyischnopus herdmani</i>										
Podoceridae										
<i>Podocerus brasiliensis</i>										
<i>Podoceropsis sophiae</i>										
Aeginellidae										
<i>Eupariambus fallax</i>										
Phtisicidae										
<i>Phtisica marina</i>										
Hyperiididae					1		4	1		1
Ingolfiellidae										
Ingolfiellid A										
Ingolfiellid B										
Ingolfiellid C										
Suborder Cumacea										
Cumacea A										
ORDER LEPTOSTRACA										
Leptostraca A										
ORDER STOMATOPODA										
<i>Pterosquilla armata</i>	1		1	1			3			2
Stomatopoda B										
Stomatopod juvenile		1					1			
<i>Meiosquilla desmarestii</i>							1			
ORDER MYSIDACEA										
<i>Gastrosaccus psammodytes</i>										
DECAPODA										
Macrura										
Penaeid A										
Penaeid B										
Carida A							1			
Carida B					1					3
Carida C (Mysidacea)										
Carida D										
EUPHAUSIACEA							8	3	1	2
Carida F										
Anomura										
<i>Calocaris barnardi</i>	5		1	5			4			5
<i>Calocaris barnardi juvenile</i>	1			2	2			2		2
<i>Callianassa rotundicaudata</i>				1	2		3			
<i>Callianassa rotundicaudata juvenile</i>		2								
<i>Callianassa catocaris barnardi</i>										
Callianassa B (long hair)		1							1	
<i>Callianassa adamas</i>							2			

APPENDIX A

SECTION II

Biomass data for *Rockfish* cruise

SPECIES	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	1.10	1.11
PHYLUM ARTHROPODA											
CLASS CRUSTACEA											
Sub-class Copepoda											
Copepoda A											
Sub-class Ostracoda											
Myodocopa											
ISOPODA											
Isopod A											
Arcturidae											
Arcturidae A			0.01								0.01
Arcturid B						0.01					
Arcturid C											
Arcturid D							0.01				
<i>Cirolana imposita</i>											
<i>Cirolana sulcata</i>											
<i>Microarcturus quadriconus</i>											
AMPHIPODA											
New amphipod											
Ampeliscidae											
<i>Ampelisca anisuropa</i>						0.01	0.01				
<i>Ampelisca anomala</i>	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
<i>Ampelisca brachycerus</i>											
<i>Ampelisca brevicornis</i>		0.02	0.01			0.03	0.01	0.01		0.01	
<i>Ampelisca natalensis</i>											0.01
<i>Ampelisca palmata</i>								0.01		0.01	
<i>Ampelisca spinimana</i>											
Coropiidae											
<i>Aoro kergeuleni</i>											
<i>Aorcho delgadus</i>		0.01				0.01					
Corophiid A (Gammaropsis)				0.01			0.01				
Corophiid Q											
Dexaminidae											
<i>Atylus swammerdamei</i>											
<i>Guernea rhomba</i>											
Eusiridae											
<i>Paramoera capensis</i>											
<i>Rhachotropis spp.</i>											
Gammaridae											
<i>Elasmopus affinis</i>											
<i>Elasmopoides chevreux</i>											
<i>Maera spp.</i>											
Haustoriidae											
<i>Urothoe grimaldi</i>	0.01						0.01		0.01		
<i>Urothoe pinnata</i>		0.01									
<i>Urothoe elegans</i>										0.01	0.01
<i>Urothoe coxalis</i>											
Leucothoidae											
<i>Leucothoe spinicarpa</i>											
<i>Leucothoe richiardi</i>			0.01								0.01
Liljeborgiidae											
<i>Listriella lindae</i>											
Lysianassidae											
<i>Acidostoma obesum</i>					0.01						

SPECIES	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	2.10
<i>Nephtys sphaericirrata</i>										
<i>Nephtys hombergi</i>	0.06		0.08			0.2	0.08	0.05		
<i>Nephtys capensis / macroura</i>								0.03		
<i>Nephtys spp.</i>		0.04								
<i>Nephtys spp. C</i>										
Spionidae										
<i>Prionospio pinnata</i>	0.43	0.44	0.19	0.75	0.43	1.73	0.51	0.5	0.02	0.36
<i>Spio spp.</i>										
<i>Spio filicornis</i>								0.01		
<i>Spiophanes spp.</i>										
<i>Spiophanes soederstroemii</i>							0.01			
<i>Laonice cirrata</i>	0.09					0.08	0.06			0.02
Spionid O			0.01		0.05					
Spionid P							0.01			
<i>Polydora spp.</i>										
<i>Malacoceros indicus</i>										
Orbiniidae	0.13	0.22		0.05			0.01			0.07
<i>Haploscoloplos kerguelensis</i>						0.09	0.07	0.03	0.02	
<i>Haploscoloplos spp.</i>			0.03							
<i>Scoloplos spp.</i>				0.01			0.01			
<i>Phylo capensis</i>						0.39				
<i>Phylo foetida ligustica</i>										
<i>Phylo capusu</i>										
Orbiniidae B					0.08					
<i>Orbinia angrapaquensis</i>										
Poly BB			0.21							
Poly WW										
Paraonidae							0.01			
<i>Cirrophorus branchiatus</i>										
Opheliidae										
<i>Ophelia spp.</i>										
Capitellidae										
<i>Notomastus spp.</i>							0.02	0.34		
<i>Notomastus latericeus</i>		0.12								
Maldanidae	0.01	0.01		0.3						
Maldaninae A										
Maldaninae B										
<i>Euclymene luderitziana</i>							0.01			
<i>Petaloproctus terricola</i>										
<i>Petaloproctus spp.</i>										
Sabellidae										
<i>Sabellides spp.</i>										
Ampharetidae										
<i>Amphicteis gunneri</i>										
Terebellidae		0.23		0.12						
<i>Terebellides stroemi</i>	0.26		0.39	0.44			0.05	0.03		1.22
<i>Amaeana trilobata/Polycirrus</i>						0.05		1.57		
Pilgaridae										
<i>Ancistrosyllis parva</i>										
Flabelligeridae										
<i>Flabelligera spp.</i>					0.18					
Pectinariidae										
Poly UU							0.01			

SPECIES	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	2.10
PHYLUM ARTHROPODA										
CLASS CRUSTACEA										
Sub-class Copepoda										
Copepoda A										
Sub-class Ostracoda										
Myodocopa									0.01	
ISOPODA										
Isopod A										
Arcturidae										
Arcturidae A							0.01	0.01		
Arcturid B										
Arcturid C								0.01		
Arcturid D										
<i>Cirolana imposita</i>										
<i>Cirolana sulcata</i>								0.02		
<i>Microarcturus quadriconus</i>										
AMPHIPODA										
New amphipod										
Ampeliscidae										
<i>Ampelisca anisuropa</i>										
<i>Ampelisca anomala</i>	0.03	0.01	0.01	0.01	0.04	0.01	0.05	0.03		0.02
<i>Ampelisca brachycerus</i>										
<i>Ampelisca brevicornis</i>	0.02	0.01	0.01	0.05	0.01	0.05	0.01	0.01		0.01
<i>Ampelisca natalensis</i>									0.01	0.01
<i>Ampelisca palmata</i>	0.06	0.01		0.01	0.02	0.01	0.01	0.01	0.01	0.02
<i>Ampelisca spinimana</i>										
Coropiidae										
<i>Aoro kergeuleni</i>							0.01			
<i>Aorcho delgadus</i>								0.01	0.01	
Corophiid A (Gammaropsis)		0.01			0.01					
Corophiid Q							0.01			
Dexaminidae										
<i>Atylus swammerdamei</i>										
<i>Guernea rhomba</i>										
Eusiridae										
<i>Paramoera capensis</i>					0.01					
<i>Rhachotropis spp.</i>										
Gammaridae										
<i>Elasmopus affinis</i>										
<i>Elasmopoides chevreux</i>										
<i>Maera spp.</i>	0.01	0.01								
Haustoriidae										
<i>Urothoe grimaldi</i>						0.01				
<i>Urothoe pinnata</i>										
<i>Urothoe elegans</i>								0.01		
<i>Urothoe coxalis</i>		0.01								
Leucothoidae										
<i>Leucothoe spinicarpa</i>					0.01					0.01
<i>Leucothoe richiardi</i>						0.01		0.01		
Liljeborgiidae										
<i>Listriella lindae</i>										
Lysianassidae										
<i>Acidostoma obesum</i>		0.01						0.01	0.01	

SPECIES	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	3.10
PHYLUM ARTHROPODA										
CLASS CRUSTACEA										
Sub-class Copepoda										
Copepoda A									0.01	
Sub-class Ostracoda										
Myodocopa										
ISOPODA										
Isopod A										
Arcturidae						0.01				
Arcturidae A										
Arcturid B										
Arcturid C										
Arcturid D										
<i>Cirolana imposita</i>										
<i>Cirolana sulcata</i>			0.03	0.03						
<i>Microarcturus quadriconus</i>										
AMPHIPODA										
New amphipod	0.01									
Ampeliscidae										
<i>Ampelisca anisuropa</i>										
<i>Ampelisca anomala</i>	0.01		0.02			0.1		0.01	0.02	0.01
<i>Ampelisca brachycerus</i>						0.01				
<i>Ampelisca brevicornis</i>				0.01		0.01		0.01		0.01
<i>Ampelisca natalensis</i>										
<i>Ampelisca palmata</i>	0.01		0.01			0.01			0.01	0.01
<i>Ampelisca spinimana</i>										
Coropiidae										
<i>Aoro kergeuleni</i>										
<i>Aorcho delgadus</i>			0.01			0.01				
Corophiid A (Gammaropsis)										
Corophiid Q										
Dexaminidae										
<i>Atylus swammerdamei</i>										
<i>Guernea rhomba</i>										
Eusiridae										
<i>Paramoera capensis</i>										
<i>Rhachotropis spp.</i>										
Gammaridae										
<i>Elasmopus affinis</i>										
<i>Elasmopoides chevreaux</i>										
<i>Maera spp.</i>										
Haustoriidae										
<i>Urothoe grimaldi</i>										
<i>Urothoe pinnata</i>										
<i>Urothoe elegans</i>										
<i>Urothoe coxalis</i>										
Leucothoidae										
<i>Leucothoe spinicarpa</i>										
<i>Leucothoe richiardi</i>	0.01					0.01		0.01		0.01
Liljeborgiidae										
<i>Listriella lindae</i>										
Lysianassidae										
<i>Acidostoma obesum</i>				1.2				0.01	0.01	

SPECIES	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	4.10
PHYLUM ARTHROPODA										
CLASS CRUSTACEA										
Sub-class Copepoda										
Copepoda A										
Sub-class Ostracoda										
Myodocopa										
ISOPODA										
Isopod A			0.01							
Arcturidae										
Arcturidae A										
Arcturid B										
Arcturid C										
Arcturid D										
<i>Cirolana imposita</i>								0.02		
<i>Cirolana sulcata</i>										
<i>Microarcturus quadriconus</i>	0.01							0.01		
AMPHIPODA										
New amphipod										
Ampeliscidae										
<i>Ampelisca anisuroopa</i>								0.01		
<i>Ampelisca anomala</i>	0.03		0.02	0.01	0.01	0.01	0.01	0.01		
<i>Ampelisca brachycerus</i>										
<i>Ampelisca brevicornis</i>	0.01		0.01				0.01	0.01		
<i>Ampelisca natalensis</i>										
<i>Ampelisca palmata</i>			0.01				0.01			
<i>Ampelisca spinimana</i>										
Coropiidae										
<i>Aoro kergeuleni</i>										
<i>Aorcho delgadus</i>						0.01		0.01		
Corophiid A (Gammaropsis)										
Corophiid Q										
Dexaminidae										
<i>Atylus swammerdamei</i>	0.01			0.01						
<i>Guerneia rhomba</i>	0.01									
Eusiridae										
<i>Paramoera capensis</i>										
<i>Rhachotropis spp.</i>										
Gammaridae										
<i>Elasmopus affinis</i>										
<i>Elasmopoides chevreux</i>										
<i>Maera spp.</i>										
Haustoriidae										
<i>Urothoe grimaldi</i>										
<i>Urothoe pinnata</i>										
<i>Urothoe elegans</i>										
<i>Urothoe coxalis</i>										
Leucothoidae										
<i>Leucothoe spinicarpa</i>										
<i>Leucothoe richiardi</i>					0.01		0.01	0.01		
Liljeborgiidae										
<i>Listriella lindae</i>										
Lysianassidae										
<i>Acidostoma obesum</i>		0.01				0.01		0.01		

SPECIES	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	4.10
Anomura A										
<i>Anomura (Paguristes barnardi)</i>					0.01		0.01	0.01		
<i>Callianassa kraussii</i>										
Brachyura										
<i>Gonoplax angulata juveniles</i>	0.01	0.05	0.04	0.07	0.01	0.17	0.03	0.08	0.01	
<i>Goneplax angulata</i>			1.59		0.61		0.53	0.26		
<i>Mursia cristimanus</i>				10.83				5.31		
Brachyura A										
Brachyura C										
PHYLUM BRACHIOPODA										
<i>Terebratulina meridionalis</i>										
PHYLUM MOLLUSCA										
AMPHINEURA										
<i>Ischnochiton bergoti</i>										0.27
CLASS PELECYPODA										
BIVALVIA										
<i>Macoma spp.</i>	0.1	0.53	0.08	0.49	0.07	0.82	0.44	1.08	0.04	0.06
<i>Macoma C (Tellina alfredensis)</i>								0.17		
<i>Dosinia spp.</i>			0.02	0.01	0.01	0.02		0.09		
<i>Nucula nucleus</i>	2.01		0.68		1.1				0.42	0.56
Bivalve F					0.01					
<i>Tellina spp.</i>								0.01		
<i>Dosinia lupinus orbigny</i>										
Bivalve L										
CLASS GASTROPODA										
<i>Alvania fenestrata</i>								0.01	0.01	
<i>Epitonium kraussi</i>								0.02		
<i>Heliacus variegata</i>										
<i>Marginella capensis</i>	0.06		0.01	0.01	0.11	0.01		0.01	0.03	
<i>Marginella kerochuta</i>										
<i>Marginella musica</i>										
<i>Nassarius analogica</i>								0.31		
<i>Nassarius plicatellus</i>								0.12		
<i>Nassarius plicatellus form scopularcus</i>										
<i>Nassarius pyramidalis</i>										
<i>Nassarius speciosus</i>										
<i>Nassarius vidalensis</i>								0.01		
<i>Nassarius vinctus</i>		3.08	6.03		0.42	0.8	0.01			
<i>Natica tecta</i>										
<i>Ocenebra scrobiculata</i>								0.02		
<i>Pyramidella spp.</i>								0.02		
<i>Solariella agulhasensis</i>								0.22		
<i>Tricolia capensis</i>						0.01		0.13	0.02	
<i>Triphora africana</i>										
<i>Turris spp.</i>										
<i>Turris flavidula</i>										
<i>Turritella sanguinea</i>										
<i>Volutocorbis abyssicola</i>										
PHYLUM ECHINODERMATA										
<i>Ophonereis porrecta</i>								0.01		
<i>Henricia spp.</i>								0.53		

**MACROFAUNA BIOMASS DATA FROM THE FIRST SAMPLING CRUISE
(ROCKFISH: JUNE 1994)**

AREA 5

SPECIES	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	5.10
PHYLUM PORIFERA										
Porifera A										
PHYLUM CNIDARIA										
Class Scyphozoa										
Scyphozoa A										
Class Anthozoa										
Anthozoa A										
Anthozoa B										
Anthozoa C										
Anthozoa D										
PHYLUM NEMERTEA										
<i>Cerebratulus spp.</i>	0.05	0.42		0.16				0.64	0.03	0.85
<i>Cerebratulus fascus</i>	0.6				0.01					
<i>Lineus spp.</i>										
Nemertea A	0.05	0.01			0.06					
Nemertea B										
Nemertea C										
Nemertea D										
Nemertea E										
SIPUNCULIDAE										
Siphunculid A										
Siphunculid B										
PHYLUM ANNELIDA										
POLYCHAETA										
Eunicidae										
<i>Lumbrineris spp.</i>	2.56			0.1	3.96	0.05				
<i>Lumbrineris heteropoda difficilis</i>	1.13	1.9	0.57	0.97		1.88	1.23	2.09	0.8	0.53
<i>Lumbrineris P (cavifrons)</i>										
<i>Lumbrineris R (albidenta)</i>		0.03	0.01						0.05	
Lumbrinerinae F										
<i>Lumbrineris tetraura</i>							0.01			0.01
Lumbrineris B										
<i>Lumbrineris magalhaensis</i>								0.01		
<i>Lumbrineris latreilli</i>										
<i>Lumbrineris meteorana</i>										
<i>Arabella spp.</i>										
<i>Arabella iricolor caerulea</i>					1.01		0.69		0.34	
Arabella L										
<i>Diopatra spp.</i>	5.3			0.2	0.05	2.74			0.8	
<i>Diopatra cuprea</i>	0.93									
<i>Diopatra monroi</i>			2.09		0.14		1.65			1.8
Glyceridae										
Nereidae										
<i>Nereis spp.</i>			0.34		0.24					
<i>Micronereides capensis</i>					0.01					
Nephtyidae	0.04	0.06		0.01				0.48		

SPECIES	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	5.10
PHYLUM ARTHROPODA										
CLASS CRUSTACEA										
Sub-class Copepoda										
Copepoda A		0.01					0.01	0.01		
Sub-class Ostracoda										
Myodocopa										
ISOPODA										
Isopod A										
Arcturidae										
Arcturidae A										
Arcturid B										
Arcturid C										
Arcturid D										
<i>Cirolana imposita</i>										
<i>Cirolana sulcata</i>										
<i>Microarcturus quadricornis</i>										
AMPHIPODA										
New amphipod										
Ampeliscidae										
<i>Ampelisca anisuropa</i>										
<i>Ampelisca anomala</i>		0.02		0.01	0.01	0.02	0.02	0.02	0.07	0.01
<i>Ampelisca brachycerus</i>										
<i>Ampelisca brevicornis</i>						0.01		0.01		
<i>Ampelisca natalensis</i>										
<i>Ampelisca palmata</i>										
<i>Ampelisca spinimana</i>										
Coropiidae										
<i>Aoro kergeuleni</i>										
<i>Aorcho delgadus</i>			0.01							
Corophiid A (Gammaropsis)										
Corophiid Q									0.01	
Dexaminidae										
<i>Atylus swammerdamei</i>										
<i>Guernea rhomba</i>										
Eusiridae										
<i>Paramoera capensis</i>										
<i>Rhachotropis spp.</i>							0.01			
Gammaridae										
<i>Elasmopus affinis</i>				0.01						
<i>Elasmopoides chevreur</i>										
<i>Maera spp.</i>						0.01				
Haustoriidae										
<i>Urothoe grimaldi</i>										
<i>Urothoe pinnata</i>										
<i>Urothoe elegans</i>										
<i>Urothoe coxalis</i>										
Leucothoidae										
<i>Leucothoe spinicarpa</i>										
<i>Leucothoe richiardi</i>					0.04					
Liljeborgiidae										
<i>Listriella lindae</i>		0.01	0.01			0.03		0.01		
Lysianassidae										
<i>Acidostoma obesum</i>			0.01		0.01					

SPECIES	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	6.10
<i>Hippomedon longimanus</i>							0.01			
Oedicerotidae										
<i>Monoculodopsis longimana</i>										
<i>Oediceroides cinderella</i>										
<i>Perioculodes longimanus</i>										
<i>Perioculodes pallidus</i>										
<i>Westwoodilla manta</i>			0.01		0.01		0.01			0.01
Phoxocephalidae										
Phoxocephalid B										
<i>Heterophoxus cephalodens</i>										
<i>Paraphoxus oculus</i>		0.01		0.01	0.01	0.01	0.01			
<i>Platyischnopus herdmani</i>										
Podoceridae										
<i>Podocerus brasiliensis</i>										
<i>Podoceroopsis sophiae</i>										
Aeginellidae										
<i>Eupariambus fallax</i>										
Phtisicidae										
<i>Phtisca marina</i>										
Hyperiididae					0.01		0.01	0.01		0.01
Ingolfiellidae										
Ingolfiellid A										
Ingolfiellid B										
Ingolfiellid C										
Suborder Cumacea										
Cumacea A										
ORDER LEPTOSTRACA										
Leptostraca A										
ORDER STOMATOPODA										
<i>Pterosquilla armata</i>	0.36		0.91	0.2			5.02			0.36
Stomatopoda B										
Stomatopod juvenile		0.01					0.01			
<i>Meiosquilla desmarestii</i>							0.04			
ORDER MYSIDACEA										
<i>Gastrosaccus psammodytes</i>										
DECAPODA										
Macrura										
Penaeid A										
Penaeid B										
Carida A							0.22			
Carida B					0.01					0.02
Carida C (Mysidaea)										
Carida D										
EUPHAUSIACEA							0.01	0.01	0.01	0.01
Carida F										
Anomura										
<i>Calocaris barnardi</i>	1.44		0.19	0.22			0.2			0.29
<i>Calocaris barnardi</i> juvenile	0.01			0.01	0.01			0.01		0.01
<i>Callianassa rotundicaudata</i>				0.01	0.01		1.8			
<i>Callianassa rotundicaudata</i> juvenile		0.01								
<i>Callianassa catocaris barnardi</i>										
Callianassa B (long hair)		0.03							0.06	
<i>Callianassa adamas</i>							0.01			

APPENDIX A

SECTION III

Abundance data for Pentow Salvor cruise

SPECIES	1.1	1.5	1.11	1.14	1.15	1.17	2.2	2.3	2.4	2.5	2.6	2.7
Maldanidae			1	4	1	1						
<i>Maldanella capensis</i>												
<i>Petaloproctus spp.</i>												
<i>Rhodine gracilior</i>			1		2							
Ampharetidae												
<i>Amphicteis gunneri</i>					1							1
Ampharete spp. A												
Terebellidae												
<i>Trichobranchus glacialis</i>												
<i>Terebellides spp. A</i>												
<i>Terrebellides stroemi</i>			5				5		2			
<i>Amaeana trilobata/Polycirrus</i>										1		
Flabelligeridae												
<i>Flabelligera spp.</i>												
<i>Flabelligera affinis</i>												
PHYLUM												
ARTHROPODA												
CLASS CRUSTACEA												
Tanaid A												
Sub-Class Copepoda												
Copepod A	1								1		1	
Sub-Class Ostracoda												
ISOPODA												
Isopod A												
Arcturidae				1	1							
Arcturid B												1
<i>Cirolana sulcata</i>												
AMPHIPODA												
Ampeliscidae												
<i>Ampelisca anomala</i>			1	3		1	5	3	3	4	7	3
<i>Ampelisca brevicornis</i>				1				1	13		3	4
<i>Ampelisca palmata</i>									3		1	2
Coropiidae												
<i>Aora kerguelene</i>												
<i>Aorcho delgadus</i>					1						1	
Corophiid Q												
Dexaminidae												
<i>Guernea rhomba</i>												
Gammaridae												
<i>Ceradocus natalensis</i>												
<i>Maera spp.</i>												
<i>Maera inaequipipes</i>												
<i>Maera hironellei</i>												
<i>Maera komma</i>												
<i>Maera serrata</i>												
<i>Maera vagans</i>												
Leucothoidae												
<i>Leucothoe dentitelson</i>												
<i>Leucothoe spinicarpa</i>			1									
<i>Leucothoe richiardi</i>				2	2	1			3	1	4	2
Lysianassidae												
<i>Acidostoma obesum</i>				1	6							
<i>Hippomedon longimanus</i>	10	5	11	27		39	1		14			6
<i>Euonyx biscayensis</i>										3		
<i>Socarnopsis crenulata</i>												
Oedicerotidae												
<i>Periculodes pallidus</i>						1						

SPECIES	5.2	5.3	5.5	5.6	5.9	5.11	6.1	6.2	6.3	6.4	6.5	6.6
<i>Periocolodes pallidus</i>												
<i>Westwoodilla manta</i>	1		1	1		4				10		
Phoxocephalidae												
<i>Paraphoxus oculatus</i>							1		2	1	1	
<i>Platyischnopus herdmani</i>												
Podoceridae												
<i>Podocerus brasiliensis</i>										1		
Aeginellidae												
<i>Eupariambus fallax</i>			1									
Phtisicidae												
<i>Phtisica marina</i>												
Hyperiididae		1			1					3		1
Hyperiid B						2	1					
Ingolfiellidae												
Ingolfiellid A												
Suborder Cumacea												
Cumacea A												
Cumacea B										1		
Cumacea C												
ORDER LEPTOSTRACA												
Leptostraca A												
ORDER STOMATOPODA												
<i>Pterosquilla armata</i>	2	1	1		3		2	1	3			
Stomatopod juvenile		1						1		1		
ORDER MYSIDACEA												
<i>Mysidacea sp.</i>												
DECAPODA												
Macrura												
Penaeid A												
Penaeid C												
Carida A						1						
Carida B	1											
Carida C										23		
EUPHAUSIACEA	1	1				3				2	1	
Anomura												
<i>Calocaris barnardi</i>	4	11	3	16	5		8	25	6		5	3
<i>Calocaris juvenile</i>	12	4								3		
<i>Callianassa rotundicaudata</i>		7		4	4	4		2				
<i>Callianssa juvenile</i>	6				2	1		3			1	
Anomura A												
Brachyura												
<i>Goneplax angulata juvenile</i>						1					1	
<i>Goneplax angulata</i>			2	1		4	3					2
Brachyura B												
<i>Mursia cristimanus</i>												1
PHYLUM												
BRACHIOPODA												
<i>Terebratulina meridionalis</i>												
PHYLUM MOLLUSCA												
AMPHINEURA												
<i>Ischnochiton bergoti</i>												
CLASS PELECYPODA												
BIVALVIA												
<i>Macoma crawfordi</i>	17	85	23	24	12	6	10	11	50	6	10	1
<i>Macoma C</i>		2					1					
<i>Nucula nucleus</i>		1				3	1	1	1			
<i>Dosinia spp.</i>			1						1			
Bivalve F		2	1				1		1			1

APPENDIX A

SECTION IV

Biomass data for *Pentow Salvor* cruise

SPECIES	1.1	1.5	1.11	1.14	1.15	1.17	2.2	2.3	2.4	2.5	2.6	2.7
<i>Petaloproctus spp.</i>												
<i>Rhodine gracilior</i>			0.01		0.01							
Ampharetidae												
<i>Amphicteis gunneri</i>					0.02							0.02
<i>Ampharete spp. A</i>												
Terebellidae												
<i>Trichobranchus glacialis</i>												
<i>Terebellides spp. A</i>												
<i>Terrebellides stroemi</i>			0.08				0.6		0.39			
<i>Amaeana trilobata/Polycirrus</i>										0.12		
Flabelligeridae												
<i>Flabelligera spp.</i>												
<i>Flabelligera affinis</i>												
PHYLUM ARTHROPODA												
CLASS CRUSTACEA												
Tanaid A												
Sub-Class Copepoda												
Copepod A	0.01								0.01		0.01	
Sub-Class Ostracoda												
ISOPODA												
Isopod A												
Arcturidae				0.01	0.01							
Arcturid B												0.01
<i>Cirolana sulcata</i>												
AMPHIPODA												
Ampeliscidae												
<i>Ampelisca anomala</i>			0.01	0.01		0.01	0.01	0.01	0.01	0.01	0.01	0.01
<i>Ampelisca brevicornis</i>				0.01				0.01	0.04		0.02	0.02
<i>Ampelisca palmata</i>									0.01		0.01	0.01
Coropiidae												
<i>Aora kerguelene</i>												
<i>Aorcho delgadus</i>					0.01						0.01	
Corophiid Q												
Dexaminidae												
<i>Guernea rhomba</i>												
Gammaridae												
<i>Ceradocus natalensis</i>												
<i>Maera sp.</i>												
<i>Maera inaequipes</i>												
<i>Maera hironellei?</i>												
<i>Maera komma</i>												
<i>Maera serrata</i>												
<i>Maera vagans</i>												
Leucothoidae												
<i>Leucothoe dentitelson</i>												
<i>Leucothoe spinicarpa</i>			0.01									
<i>Leucothoe richiardi</i>				0.01	0.01	0.01			0.01	0.01	0.01	0.01
Lysianassidae												
<i>Acidostoma obesum</i>				0.01	0.01							
<i>Hippomedon longimanus</i>	0.03	0.02	0.03	0.1		0.18	0.01		0.02			0.01
<i>Euonyx biscayensis</i>										0.02		
<i>Socarnopsis crenulata</i>												
Oedicerotidae												
<i>Periculodes pallidus</i>						0.01						
<i>Westwoodilla manta</i>								0.01		0.01		
Phoxocephalidae												
<i>Paraphoxus oculatus</i>			0.01									
<i>Platyischnopus herdmani</i>							0.01					

SPECIES	1.1	1.5	1.11	1.14	1.15	1.17	2.2	2.3	2.4	2.5	2.6	2.7
Podoceridae												
<i>Podocerus brasiliensis</i>												
Aeginellidae												
<i>Eupariambus fallax</i>												
Phtisicidae												
<i>Phtisica marina</i>					0.01							
Hyperiididae				0.01	0.01		0.01			0.01		
Hyperiid B					0.01						0.01	
Ingolfiellidae												
Ingolfiellid A					0.01							
Suborder Cumacea												
Cumacea A		0.01		0.01			0.01					
Cumacea B												
Cumacea C												
ORDER LEPTOSTRACA												
Leptostraca A									0.01			
ORDER STOMATOPODA												
<i>Pterosquilla armata</i>												
Stomatopod juvenile					0.01							
ORDER MYSIDACEA												
<i>Mysidacea spp.</i>												
DECAPODA												
Macrura												
Penaeid A								0.06	0.03			
Penaeid C				0.03			0.12					
Caridae A												
Caridae B											0.01	
Caridae C		0.01					0.01			0.01		
EUPHAUSIACEA						0.01			0.02			0.01
Anomura										0.01		
<i>Calocaris barnardi</i>												
<i>Calocaris juvenile</i>												
<i>Callinassa rotundicaudata</i>									1.29			
<i>Callinassa juvenile</i>												
Anomura A												
Brachyura												
<i>Goneplax angulata juvenile</i>									0.2			
<i>Goneplax angulata</i>								0.21		1.61		0.07
Brachyura B									0.1			
<i>Mursia cristimanus</i>												
PHYLUM BRACHIOPODA												
<i>Terebratulina meridionalis</i>									0.09		0.01	0.01
PHYLUM MOLLUSCA												
AMPHINEURA												
<i>Ischnochiton bergoti</i>												
CLASS PELECYPODA												
BIVALVIA												
<i>Macoma crawfordi</i>	0.02	0.03	0.07	0.21		0.21	0.01		0.02	0.01	0.01	0.02
<i>Macoma C</i>				0.22	0.01							
<i>Nucula nucleus</i>												
<i>Dosinia spp.</i>	0.01	0.05			0.04						0.01	0.01
Bivalve F			0.01	0.01		0.01	0.14			0.04		
<i>Tellina sp.</i>	0	0	0.01	0	0	0	0	0	0	0	0	0
Bivalve I												
<i>Dosinia lupinus orbigny</i>												
Bivalve M												
CLASS GASTROPODA												
<i>Alvania fenestrata</i>			0.01	0.01	0.01							

SPECIES	3.1	3.2	3.3	3.4	3.5	3.7	4.2	4.6	4.8	4.9	4.13	4.14	4.15
<i>Socarnopsis crenulata</i>			0.01										
Oedicerotidae													
<i>Perioculodes pallidus</i>													
<i>Westwoodilla manta</i>							0.01						
Phoxocephalidae													
<i>Paraphoxus oculatus</i>													
<i>Platyschnopus herdmani</i>													
Podoceridae													
<i>Podocerus brasiliensis</i>													
Aeginellidae													
<i>Eupariambus fallax</i>													
Phtisicidae													
<i>Phtisica marina</i>													
Hyperiididae			0.01	0.01	0.01								
Hyperiid B		0.01				0.01							
Ingolfiellidae													
Ingolfiellid A													
Suborder Cumacea													
Cumacea A													
Cumacea B													
Cumacea C		0.01					0.01						
ORDER LEPTOSTRACA													
Leptostraca A													
ORDER STOMATOPODA													
<i>Pterosquilla armata</i>													
Stomatopod juvenile					0.01								
ORDER MYSIDACEA													
<i>Mysidacea spp.</i>									0.01				
DECAPODA													
Macrura													
Penaeid A													
Penaeid C			0.07	0.05		0.08	0.11		0.18				
Caridae A													
Caridae B					0.02								
Caridae C													
EUPHAUSIACEA			0.02										
Anomura		0.02	0.03	0.03	0.01								
<i>Calocaris barnardi</i>													
<i>Calocaris juvenile</i>													
<i>Callianassa rotundicaudata</i>													
<i>Callianssa juvenile</i>				0.01									
Anomura A						0.01							
Brachyura													
<i>Goneplax angulata juvenile</i>													
<i>Goneplax angulata</i>			0.29	0.06		0.38			0.23			1.05	
Brachyura B													
<i>Mursia cristimanus</i>													
PHYLUM BRACHIOPODA													
<i>Terebratulina meridionalis</i>													
PHYLUM MOLLUSCA													
AMPHINEURA													
<i>Ischnochiton bergoti</i>		0.69											
CLASS PELECYPODA													
BIVALVIA													
<i>Macoma crawfordi</i>	0.03	0.02	0.09	0.09	0.04	0.03	0.14		0.09		0.13	0.01	0.01
<i>Macoma C</i>		0.03							0.19				
<i>Nucula nucleus</i>	0.28					3			0.18				

APPENDIX B

Tru Basic program for estimating S_{∞}

Tru Basic program to estimate S_{∞} .

Tru Basic v2.0 program written by Ms. Eva Plaganyi to estimate number of replicates necessary to adequately represent macrobenthic community. Program was run using 150 permutations on the presence-absence data for:

- the 59 unmined samples from both cruises;
- the 32 mined samples from both cruises;
- the 10 reference samples from area 2 collected on the *Rockfish* cruise.

During each run, the DATA line and the size of the matrix was altered accordingly. The specifications presented below are for the program run on the 10 reference samples from area 2. A total of 107 species in the 10 samples designate a 10*107 matrix.

```
rem candida problem
randomize
let row = 107
let col = 10
let perms = 150
! Number of samples species present in
dim m(107,10)
for counter = 1 to perms
print "counter = ",counter

restore
mat m = 0
for i = 1 to row
read pres
dim r(11)
mat r = 0
for j = 1 to pres
let r(j) = int(rnd*col)+1
if j > 1 then
for k = 1 to j-1
let chk = r(k)
if r(j) = chk then
do
let r(j) = int(rnd*col)+1
loop until r(j) <> chk
let k = 1
end if
next k
end if
let num = r(j)
let m(i,num) = 1
next j
next i
clear
mat print m;
dim cum(107,10)
mat cum = 0
```

```

for i = 1 to row
  for j = 1 to col
    if m(i,j) = 1 then
      let sum = 0
      for k = 1 to j
        let sum = sum + m(i,k)
      next k
      let cum(i,j) = cum(i,j) + sum
    end if
  next j
next i
mat print cum;
dim cumsum(107,10)
for i = 1 to row
  for j = 1 to col
    let cumsum(i,j) = cumsum(i,j) + cum(i,j)
  next j
next i
print
! mat print cumsum;
print;
if counter = perms then
  for i = 1 to row
    for j = 1 to col
      let cumsum(i,j) = cumsum(i,j) / perms
    next j
  next i
print "cumsum average"
mat print cumsum;
end if

next counter

dim est(10)
for j = 1 to col
  let sum = 0
  for i = 1 to row
    let sum = sum + cumsum(i,j)
  next i
  let est(j) = sum / row
next j
print
Print " Final solution vector... "
for i = 1 to col
  print using "#####.###":est(i)
next i
print "press a letter to continue... "
input bb$

set window 0,120,0,120
for i = 2 to 10
  let j = i - 1
  plot est(j),est(i)
  PRINT #1:EST (J)
  PRINT #1:EST (I)
next i
CLOSE #1

```

PLOT 0,0;120,0
PLOT 0,0;0,120
PLOT 0,0;120,120

DATA 1,3,1,2,2,7,6,6,2,1
DATA 1,2,2,1,1,1,1,3,1,2
DATA 1,1,4,1,1,1,6,1,1
DATA 5,4,3,1,1,1,1,1,1,1
DATA 6,1,1,3,1,1,1,6,1,2
DATA 1,2,1,1,2,1,6,1,2
DATA 2,2,3,1,2,2,1,1,1
DATA 3,7,1,2,2,4,8,6,1,1
DATA 1,9,3,1,2,2,6,5,1,3
DATA 4,2,4,1,1,2,1
DATA 3,4,2,1,2,4,6,2,1,1
DATA 10,10,10

end

APPENDIX C

Geological Results

GEOLOGICAL RESULTS

a) *Rockfish* cruise. The results of the particle-size analysis and the average percentage carbon and nitrogen for the *Rockfish* sampling cruise. The mined samples are underlined and the dominant particle size is highlighted in bold type.

SAMPLE	%CARBON	%NITROGEN	%GRAVEL	%SAND	%MUD
1.1	1.285	0.16	0.17	77.95	21.88
1.2	1.255	0.15	0.33	94.81	4.85
1.3	0.965	0.12	0	86.47	13.53
1.5	1.125	0.13	0.87	80.98	17.95
1.6	0.865	0.1	0.26	85	14.74
1.10	0.94	0.11	0	85.57	14.43
1.11	0.965	0.115	0.01	81.34	17.99
2.1	1.725	0.2	0.12	69.06	30.82
2.2	1.33	0.155	0	74.42	25.58
2.3	0.855	0.11	0.21	72.28	27.51
2.4	2.09	0.27	0	65.26	34.74
2.5	4.245	0.515	0	24.37	75.63
2.6	2.375	0.28	0.15	54.38	45.47
2.8	1.615	0.195	0.49	68.7	30.81
3.1	0.65	0.065	6.67	44.95	48.38
3.3	1.525	0.18	10.86	40.17	48.98
3.5	1.275	0.13	54.42	25.78	19.8
3.6	2.145	0.28	0.2	30.62	69.18
3.8	0.74	0.085	1.06	49.17	49.77
3.9	1.355	0.145	0.44	32.36	67.2
3.10	0.99	0.115	0.11	43.57	56.32
4.1	2.34	0.22	0.08	28.35	71.57
<u>4.2</u>	4.645	0.175	10.2	36.04	53.76
4.3	0.945	0.11	1.99	42.05	55.96
4.4	0.69	0.07	1.2	40.75	58.05
4.5	1.035	0.1	17.56	28.25	54.19
5.1	0.655	0.07	0.1	72.55	27.35
5.2	0.69	0.08	0.19	64.14	35.67
<u>5.3</u>	0.915	0.1	0.33	67.36	32.31
5.4	0.99	0.11	1.31	70.18	28.51
5.5	1.315	0.155	0	45.97	54.03
5.6	0.99	0.105	0	55.28	44.72
5.7	0.82	0.085	1.07	57.28	41.65
5.8	0.82	0.09	0	59.86	40.14
5.9	1.445	0.16	0.07	40.78	59.15
6.1	2.69	0.15	4.31	48.53	47.16
6.5	1.24	0.16	0.54	47.14	52.32
6.7	0.935	0.12	0.12	53.35	46.53
<u>6.10</u>	2.43	0.27	0	28.73	71.27

- b) *Pentow Salvor* cruise. The results of the particle-size analysis and the average percentage carbon and nitrogen for the *Pentow Salvor* sampling cruise. The mined samples are underlined and the dominant particle size is highlighted in bold type.

SAMPLE	% CARBON	% NITROGEN	%GRAVEL	%SAND	%MUD
1.1	0.215	0.02	5.29	87.82	6.91
<u>1.5</u>	0.2	0.02	35.7	59.72	4.58
<u>1.11</u>	0.23	0.02	1.5	91.56	6.94
<u>1.14</u>	0.26	0.03	0.67	91.27	8.06
1.15	0.325	0.035	21.05	70.89	8.06
<u>1.17</u>	0.26	0.02	1.94	91.07	6.99
2.2	1.6	0.185	3.12	56.54	40.34
2.3	0.89	0.11	0.99	69.32	29.69
2.4	0.985	0.11	0.31	77.32	22.37
2.5	1.02	0.12	1.13	68.73	30.14
2.6	1.345	0.16	0.2	65.65	34.15
2.7	1.26	0.145	0.14	74.62	25.24
<u>3.1</u>	0.88	0.095	8.69	29.85	61.46
<u>3.2</u>	0.495	0.04	28.77	12.26	58.97
<u>3.3</u>	0.92	0.08	41.34	17.82	40.84
<u>3.4</u>	0.67	0.065	16.84	9.93	73.03
3.5	0.475	0.04	39.3	10.73	49.97
<u>3.7</u>	0.675	0.07	16.59	6.44	76.97
<u>4.2</u>	0.845	0.05	17.62	14.12	68.26
<u>4.6</u>	0.54	0.04	14.86	28.79	56.35
<u>4.8</u>	0.82	0.075	24.61	36.16	39.23
<u>4.9</u>	0.665	0.045	38.57	33.94	27.49
<u>4.13</u>	0.85	0.1	33.88	25.33	40.79
<u>4.14</u>	0.675	0.07	13.15	57.92	28.93
<u>4.15</u>	0.57	0.05	28.83	55.59	15.58
5.2	0.995	0.1	0.36	59.99	39.65
5.3	0.515	0.05	0.89	80.4	18.71
5.5	0.97	0.105	1.48	66.39	32.13
5.6	0.945	0.095	0.06	60.08	39.86
5.9	0.585	0.06	0.11	78.55	21.34
5.11	1.53	0.185	0.7	39.34	59.96
<u>6.1</u>	0.99	0.07	8.66	49.22	42.12
6.2	1.08	0.115	0.25	48.43	51.32
<u>6.3</u>	0.725	0.04	8.38	77.13	14.49
6.4	1.27	0.135	0.32	46.99	52.69
<u>6.5</u>	1.04	0.08	7.55	25.57	66.88
6.6	0.39	0.03	55.26	10.76	33.98

APPENDIX D

Production values for Meta-Analysis

PHYLUM	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	6.10
Cnidaria	0	0	1.35	1.28	0	0	0	0	0	0
Platyhelminthes	0	0	0	0	0	0	0	0	0	0
Nemertea	5.16	0	0	0	0	0	0	0	0	0.81
Nematoda	0	0	0	0	0	0	0	0	0	0
Priapulida	0	0	0	0	0	0	0	0	0	0
Sipunculida	0	0	0	0	0	0	0	0	0	0
Annelida	68.15	44.65	75.48	83.30	95.66	94.27	46.82	78.70	17.80	66.55
Chelicerata	0	0	0	0	0	0	0	0	0	0
Crustacea	23.43	9.48	15.92	7.30	3.76	2.01	51.69	14.08	3.90	19.32
Mollusca	3.26	45.59	7.25	7.91	0.58	3.72	1.49	7.22	78.31	13.31
Phoronida	0	0	0	0	0	0	0	0	0	0
Echinodermata	0	0.29	0	0.21	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0	0	0	0	0
Chordata	0	0	0	0	0	0	0	0	0	0

b) *Pentow Salvor* cruise production values.

PHYLUM	1.1	1.5	1.11	1.14	1.15	1.17
Cnidaria	0	0	0	0	0	0
Platyhelminthes	0	0	0	0	0	0
Nemertea	0	0	0	0	1.96	0
Nematoda	0	0	0	0	0	0
Priapulida	0	0	0	0	0	0
Sipunculida	18.86	0	0	0	0	0
Annelida	13.18	5.71	34.92	47.06	62.36	33.49
Chelicerata	0	0	0	0	0	0
Crustacea	3.65	1.57	6.88	13.95	6.06	21.62
Mollusca	64.30	92.72	58.20	38.99	29.62	44.89
Phoronida	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Chordata	0	0	0	0	0	0

PHYLUM	2.2	2.3	2.4	2.5	2.6	2.7
Cnidaria	0	0	0	0	0	0
Platyhelminthes	0	0	0	0	0	0
Nemertea	0	0	0	0	0	0.5
Nematoda	0	0	0	0	0	0
Priapulida	0	0	0	0	0	0
Sipunculida	0	0	0	0	0	0
Annelida	74.45	77.71	39.21	56.94	57.76	59.45
Chelicerata	0	0	0	0	0	0
Crustacea	14.11	7.29	33.39	27.29	11.21	4.64
Mollusca	11.44	15.00	27.41	1.31	30.17	35.41
Phoronida	0	0	0	0	0	0
Hemichordata	0	0	0	14.46	0.86	0
Hemichordata	0	0	0	0	0	0
Chordata	0	0	0	0	0	0

PHYLUM	3.1	3.2	3.3	3.4	3.5	3.7
Cnidaria	0	0	0	0	0	0
Platyhelminthes	0	0	0	0	0	0
Nemertea	0	0	0	0	0	0.5
Nematoda	0	0	0	0	0	0
Priapulida	0	0	0	0	0	0
Sipunculida	0	19.90	0	0	0	0
Annelida	27.88	20.63	12.21	23.32	5.14	6.41
Chelicerata	0	0	0	0	0	0
Crustacea	0	3.00	5.99	17.62	9.54	13.15
Mollusca	72.12	56.46	81.81	59.07	85.32	80.44
Phoronida	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Chordata	0	0	0	0	0	0

PHYLUM	4.2	4.6	4.8	4.9	4.13	4.14	4.15
Cnidaria	0	0	0	0	0	0	0
Platyhelminthes	0	0	0	0	0	0	0
Nemertea	0.87	0	0	0	2.30	1.56	0
Nematoda	0	0	0	0	0	0	0
Priapulida	0	0	0	0	0	0	0
Sipunculida	0	0	0	0	0	0	0
Annelida	5.62	70.00	4.67	72.13	45.64	19.63	12.82
Chelicerata	0	0	0	0	0	0	0
Crustacea	1.46	30.00	4.04	0	12.47	8.96	0
Mollusca	92.05	0	91.29	27.87	39.59	69.85	87.18
Phoronida	0	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0	0
Chordata	0	0	0	0	0	0	0

PHYLUM	5.2	5.3	5.5	5.6	5.9	5.11
Cnidaria	0	0	0	0	1.92	0
Platyhelminthes	0	0	0	0	0	0
Nemertea	0	0	0	0	0	0
Nematoda	0	0	0	0	0	0
Priapulida	0	0	0	0	0	0
Sipunculida	0	0	0	0	0	0
Annelida	62.40	48.12	59.73	68.10	51.50	27.71
Chelicerata	0	0	0	0	0	0
Crustacea	31.04	17.45	28.27	23.93	42.67	41.28
Mollusca	6.56	34.43	12.00	7.98	3.91	31.01
Phoronida	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Chordata	0	0	0	0	0	0

PHYLUM	6.1	6.2	6.3	6.4	6.5	6.6
Cnidaria	0	0	0	0	0	0
Platyhelminthes	0	0	0	0	0	0
Nemertea	0.97	0	0	0.71	0	2.13
Nematoda	0	0	0	0	0	0
Priapulida	0	0	0	0	0	0
Sipunculida	0	0	0	0	0	0
Annelida	39.96	43.58	26.74	84.60	57.54	23.51
Chelicerata	0	0	0	0	0	0
Crustacea	46.91	49.51	33.64	13.15	14.33	62.02
Mollusca	12.15	6.91	39.62	1.54	28.13	11.98
Phoronida	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Hemichordata	0	0	0	0	0	0
Chordata	0	0	0	0	0	0