A STUDY OF BENTHIC INVERTEBRATE COMMUNITY STRUCTURE IN SELECTED AREAS ON THE CONTINENTAL SHELF OFF KWAZULU/NATAL, SOUTH AFRICA.

by

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Thesis submitted in fulfillment of the requirements of the degree of

MASTER OF SCIENCE

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DECLARATION

This thesis reports the results of research that I carried out under the auspices of the Marine Biology Research Institute, University of Cape Town. It has not been submitted for any other degree or examination at any other university. Unless indicated otherwise, most of the data that are presented were obtained from the Council for Scientific and Industrial Research (CSIR). All assistance that I received has been fully acknowledged.

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Date

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ABSTRACT. Gumede, SV. 2001. *A study of benthic invertebrate community structure in selected areas on the continental shelf off KwaZulu/Natal.* M.Sc thesis. University of Cape Town.

The primary aim of this study was to investigate changes in benthic community structure and to assess how they relate to environmental factors using multivariate and distributional techniques. Multivariate statistical testing using analysis of similarity (ANOSIM) revealed highly significant differences between shallow and deeper stations, and among the three transects. Statistical testing also revealed highly significant differences among samples grouped by sediment grain size and by Chemical Oxygen Demand (COD). Multivariate analyses were performed using data identified to taxonomic level lower than family for the macrofauna, and higher taxonomic levels for the meiofauna. Cluster analysis of macrofaunal abundance and biomass data revealed four major groups of samples, two shallow water groups, one deeper and the other group consisting of mixed shallow and deeper samples. Cluster analyses of the meiofauna abundance data revealed three major groups, each grouped according to the site at which they were taken. Multidimensional scaling ordination confirmed the groupings detected by cluster analysis. The use of the data aggregated to higher taxonomic levels for the macrofauna showed different patterns than those at the species level. This suggested that higher taxonomic levels might be inadequate when assessing natural variability at a local scale. A comparison of the community structure of the macrofauna and meiofauna at three transects showed that the two components are affected differently by natural variability. Multivariate analyses indicated that differences in faunal composition among stations for both macrofauna and meiofauna are related to sediment grain size. Pooling replicates at each station revealed differences between the two components. The multivariate analyses for macrofauna formed three groups based on mean water depths, which are 25, 35 and 45 m. On the other hand, meiofauna did not show the effect of depth but the results revealed three groups based on the position along the coast (transect), closer stations relatively grouped together. This anomaly might have been due to the difference in data aggregation of the two components of the biota. Macrofaunal species which were more abundant in finer sediments included the pelecypod; *Lasaea sp.,* amphipods; *Ampelisca brevicornis, Ampelisca diadema and Urothoe sp.* Sandy samples were characterized by an unidentified gastropod and an amphipod, *Photis sp.* For the meiofauna, the ostracods and harpacticoids were characteristic of those groups with coarser sediments and the annelids characterized the group with finer sediments. The ABC curves were not useful in showing natural variability at the scale of 5-20 km. There were no significant correlations found between the W-statistic and the environmental variables (% mud, % coarse sand and % gravel). The ABC curves have proved to be less sensitive measures of natural variability in benthic community studies. They are designed to indicate stress due to pollution.

KEYWORDS: Macrofauna
Meiofauna
Sediments
Community structure
Continental shelf
Environmental

TABLE OF CONTENTS

CHAPTER ONE

GENERAL INTRODUCTION

CHAPTER 1: GENERAL INTRODUCTION

Methods that assess benthic community structure have several advantages over experimental methods for the detection of anthropogenic disturbance. The benthos can integrate conditions over a period of time rather than reflecting conditions just at the time of sampling. Benthic animals have advantages over pelagic organisms in that they are relatively immobile and are therefore more useful in assessing local effects (Warwick *et al.* 1990). Despite this, benthic communities are extremely complex comprising a wide size range of organisms and usually a large number of species that make their analysis time consuming and labour intensive (Warwick *et al.* 1990).

Studies of biological effects at the community level have involved either the macrofauna (>1000*u*m) or the meiofauna (100-1000*u*m). Theoretical considerations suggest that their community structures may be determined by different mechanisms, so a differential response may indicate the cause of disturbance (Warwick 1988b). Austen *et al.* (1989) suggested that responses of communities are non-specific to particular types of disturbances, although different types of disturbances may cause responses at different levels of organization. Consideration of the relationship of organisms to sediments is complex, since sediment characters influence a number of subsidiary parameters and the subsidiary factors may in fact be the limiting ones (Gray, 1974).

Studies of marine benthic organisms have revealed the existence of relationships between properties of marine sediments and the distribution of benthic organisms. The macrofauna in general, is more sensitive to low oxygen concentrations than meiofauna (Josefson and Widbom 1988). Abundance Biomass Comparison (ABC) plots have been used to give a

theoretical basis to measuring biological stress imposed on benthic communities (Warwick *et al.* 1987), based on r- and k- selection. Recently disturbed communities are likely to be dominated by smaller, r- selected species.

Flemming and Hay (1988) found a general trend from "terrigenous domination in the nearshore to carbonate domination in the offshore" for most of the KwaZulu Natal continental shelf. They found that mud patches are common in this section of the coast and are derived from local rivers. Mud patches are naturally rich in organic material, not only because they may contain detritus, but also because they offer large surface areas per unit volume for adsorption. It was noted by McClurg *et al.* (2000a) that there had been broad increases in the diversity and abundance of benthic macrofauna along the KwaZulu/Natal coast in 1999 compared to previous years. This appeared to be related to the prevalence of a naturally settled period of oceanographic conditions prior to 1999.

The City of Durban in KwaZulu/Natal has been discharging sewage and selected industrial wastes through its two deep-sea submarine outfalls since about 1970 (McClurg *et al.* 2000a). Sappi Saiccor in the south coast discharges its effluent at 6.5 km offshore via a 740 m diffuser, at a water depth of 42m (McClurg *et al.* 2000b). To ensure that the ecological integrity of the region is not being compromised, stringent and comprehensive monitoring programmes have been applied by the CSIR (Council for Scientific and Industrial Research). It was therefore considered to be of particular interest to study benthic communities at sites between the outfalls, which were remote from their influence. The CSIR surveys use a synoptic approach and therefore have no control sites, which are remote from the outfalls. The samples were collected as part of the CSIR contracts and the supervisor had little control over number of samples or location of sampling.

Numerical analysis

A wide variety of numerical and statistical techniques has been developed for handling community data. The choice of a method of analysis ultimately depends on the aims of the study, and also on the nature and the validity of the statistical assumptions (Heip *et al.* 1988). The available methods have been summarized by Clarke and Warwick (1994) as:

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 summarize the relative abundance and/or biomass in each sample by a curve or histogram, for example an abundance-biomass comparison curves (ABC curves).

This second approach extracts universal features of community structure, which are not a function of the specific taxa present, and may therefore be related to levels of biological "stress" (Clarke and Warwick 1994).

3. Multivariate methods, which take account of the varying sensitivity of each taxon in the community, thereby preserving taxon-specific information. The primary objective of multivariate methods 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.

This study utilizes distributional and multivariate statistical techniques as tools to assess the benthic community structure. Univariate and distributional techniques are considered less sensitive than multivariate techniques; this is because they are species-independent. However, multivariate methods are species-dependent and exploit the fact that various organisms

respond differently to disturbance, hence they are much more sensitive than univariate or distributional methods (Gray *et al.*1990, Warwick *et al.* 1990, Warwick & Clarke 1991).

Aims

The main aims of this study were thus:

1. To test the null hypothesis that there is no difference in community composition between transects, different depths and different stations.

2. To ascertain macrobenthic community patterns in the three transects using graphical and multivariate methods and to investigate links with the sedimentology. To determine which macrofaunal species are primarily responsible for the dissimilarities.

3. To ascertain meiobenthic community patterns and compare them with those of the macrofauna.

4. To measure stress levels in benthic communities by interpreting ABC curves and W-statistics.

Dissertation structure

In order to reflect the main elements of the research, the dissertation is structured as follows. Chapter 1 is the contextual introduction to the research describing objectives and background of the study. Chapter 2 (methods) describes in detail the methods that were used for fieldwork, laboratory work and statistical analysis.

Chapter 3 attempts to explain within-site versus between-site variability. One-way ANOSIM (analysis of similarity) tests are performed.

Chapter 4 is the descriptive stage of 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 easily interpreted. The SIMPER (similarity percentages) program assesses the relative importance of each macrofaunal species to the overall multivariate analysis

Chapter 5 compares patterns of response by meiofauna to that of macrofauna. Multivariate measures included the Bray-Curtis classification and ordination through multidimensional scaling (MDS). In order to assess the relative importance of each meiofaunal species to the overall multivariate analysis, SIMPER is used.

Chapter 6 attempts to measure natural stress levels in the benthic community by interpretation of the W-statistic (a summary statistic of the ABC curves).

Chapter 7 summarizes the overall conclusions of the study.

CHAPTER TWO

METHODS

LIST OF FIGURES

LIST OF TABLES

CHAPTER 2: METHODS

2.1 STUDY AREA

This study was carried out on the KwaZulu/Natal coast off the east coast of southern Africa. Sampling was limited to the continental shelf at depths of between 25 – 45 m and a distance of between 2 and 3.8 km offshore. Three transects were selected, viz. off Brighton Beach, off Mbokodweni and off the Lovu River mouth. The positions of sampling sites are shown in Fig 2.1. Transect 1 is located off Brighton Beach and stations are indicated as B1, B2 and B3 with mean water depths of 25, 35 and 45 m, and distances offshore of about 2, 2.5 and 3.5 kilometres respectively. The two stations off Mbokodweni River mouth (M2 and M3) were at water depths of 35 and 45 m and at a distance of 3 and 3.5 kilometres offshore. There was a reef at a water depth of 25 m, so no inshore sample was obtained. The three stations off Lovu river mouth (L1 to L3) were at depths of 25, 35 and 45 m and were situated about 1.8, 2.3 and 3.8 km offshore respectively.

A number and a letter represent each transect. The first number represents the station number and the second letter represents the replicate sample taken out of three, for example M2c means the third replicate taken at second station off Mbokodweni. Transect names are denoted by their initials e.g. B, M and L for Brighton Beach, Mbokodweni and Lovu Rivers, respectively.

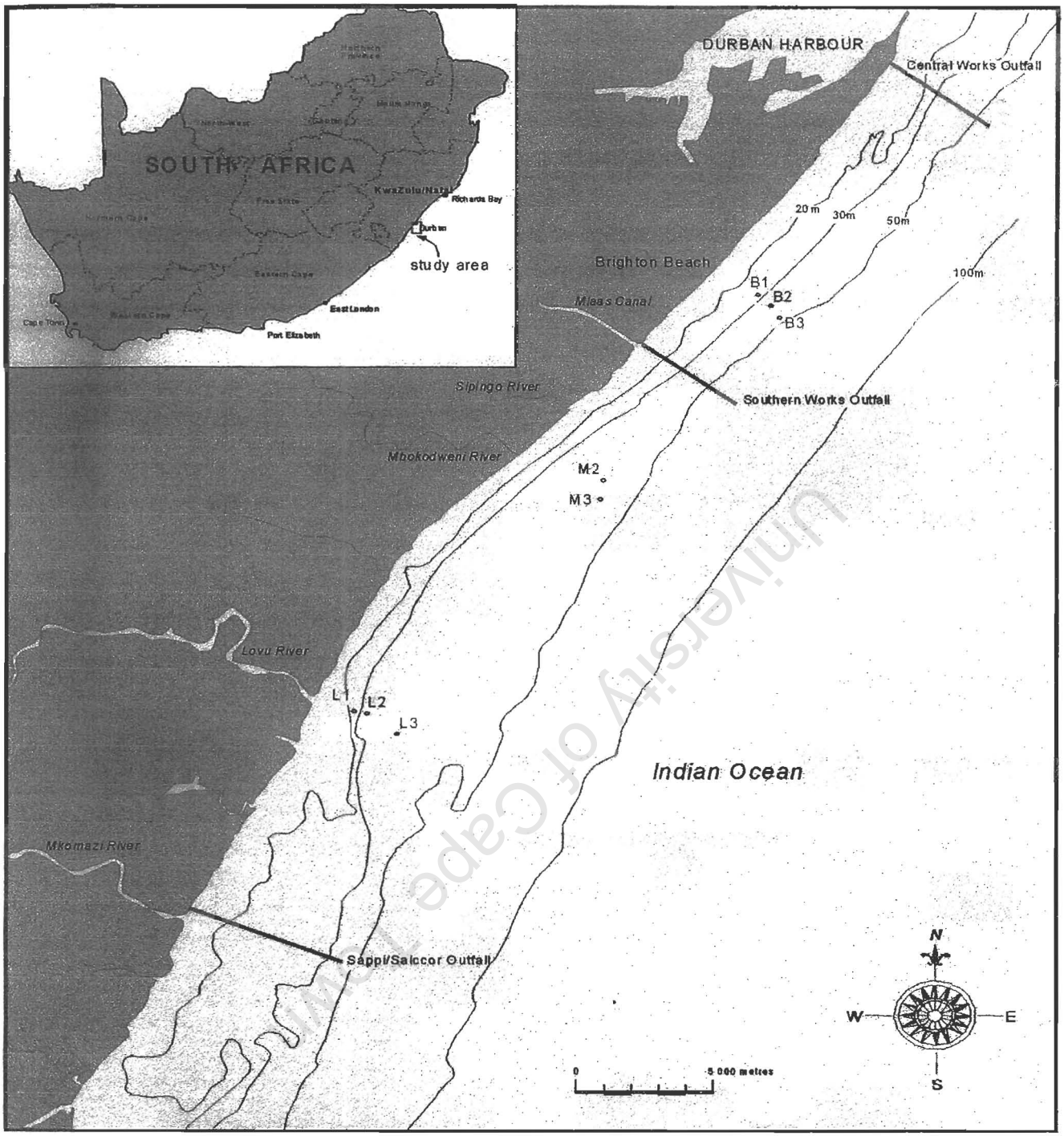

Figure 2.1 Locality of the sea sampling stations off the KwaZulu/Natal coast, South Africa

2.2 FIELD WORK

Sampling took place between 17 and 28 May 1999 from the supply vessel *Ocean Mariner.* Stations were located using GPS. Using a Day grab (0.25 m^2 "bite" area) eight stations were sampled with three replicates at each. On board the sampling vessel, sediment from each grab was sub-sampled and preserved in 5% formaldehyde for later laboratory meiofaunal analysis. Three 200 cc sand core samples were taken to a depth of 20 cm at different places in each grab for the meiofauna. The three cores were combined before the analysis. Another portion of sediment was cored as in the meiofauna and mixed thoroughly in a bigger bottle and retained for physical and chemical analysis. The remainder was washed through a 1 mm sieve on board and preserved in 5% formaldehyde pending later macrofaunal analysis in the laboratory.

2.3 LABORATORY WORK

2.3.1 Macrofaunal analysis

All macrofauna samples were washed three times with freshwater through a 1 mm sieve to remove formaldehyde since it dissolves the calcium carbonate in mollusc shells, which makes them difficult to identify. Using both dissecting and compound microscopes, the fauna was identified to the lowest possible taxon and counted for later numerical analysis. The dry biomass of each constituent taxon was measured with shells to three decimal places using a Mettler PM 200 analytical balance.

2.3.2 Meiofaunal analysis

The meiofauna were extracted using a modified Oostenbrink separator (Fricke, 1979) and a 45-micron sieve. Counts were made of each meiofaunal group distinguishable at 63 X magnification.

2.3.3 Sediment particle size analysis

Gibbs (1972) described an accurate method of particle size analysis using settling tubes. This procedure was carried out in three steps:

Step 1. Wet sieving the sample

Representative sub-sample of each sample was wet sieved using a 63 *um* sieve to separate the mud fraction from the sand and gravel. The sand and gravel fractions remained in the sieve and the mud fraction was collected after passing through the sieve. The gravel and sand were transferred to a pre-weighed beaker and the mud fraction funneled into another pre-weighed beaker. The two beakers with sediments were placed under infrared lamps and dried at 50 ^{o}C to obtain their dry weights.

Step 2. Dry sieving

The sand and gravel fractions were then sieved through a 2 mm sieve overnight at constant temperature (~50 ^{0}C) to separate the gravel from the sand, and the two separated fractions (sand and gravel) were then weighed.

Step 3. Settling tube

The size distribution of the sand fraction (from dry sieving) was measured using a computer-linked settling tube. A riffled (remains representative of the original) sand sample was placed into the settling tube and using a computer programme (Tube 96), the size distribution of the

sand fraction was determined. Sediment particle size were categorized as percent gravel (>2 mm); very coarse sand (1-2mm); coarse sand (0.5 – 1 mm); medium sand (0.25 – 0.5 mm); fine sand (0.125 – 0.25 mm); very fine sand (0.063 – 0.125 mm) and mud (0<0.063 mm).

2.3.4 Organic nitrogen and ammonia nitrogen

All samples were analyzed for the total nitrogen content by the CSIR in Durban. Each sample was digested by 0.5 ml of the hydrogen peroxide (H_2O_2) at 380 °C. Digested samples were analyzed using a Technicon Autoanalyser II. The result was calculated by measuring each peak using a ruler. The average of the two reagent blanks was subtracted from each sample peak. The concentration of the standard was divided by the average peak height of the three standards to give a conversion factor. This factor was then multiplied by each net sample peak height to give the concentration in *u*g/l.

2.3.5 Chemical oxygen demand

All samples were analyzed for the amount of oxygen needed to oxidize organic and inorganic material contained in each of them. About 100 ml of sample was added to a 250 ml conical flask. About 10 ml of $KMnO_4$, was added to each flask and 0.5 ml (33%) NaOH added and heated for about 30 minutes at 100 °C on a water bath in a fume cupboard. About 25 ml MnO_4 solution was added and cooled rapidly. One scoop (about 20 ml) potassium iodide crystals were added to the solution. This was titrated against 0.01N sodium triosulphate using 1% starch as an indicator. The results were therefore achieved in mg O_2 g^{-1}. This method is in accordance with the standard method proposed by Watling (1981) for use in South African marine pollution surveys.

abundant species sothat the less dominant, and even the rare, species play some role in determining similarity of two samples.

This study uses 4th root transformation:

$$Y_{ij} = \sqrt{\sqrt{X_{ij}}} = X_{ij}\,¼ \qquad \text{(Field } et\ al. \text{1982)}$$

Y_{ij} = corresponding transformed score and X_{ij} = sum of i^{th} taxon in j^{th} sample

2.4.3 Analysis of similarity (ANOSIM)

The ANOSIM test is built on a simple non-parametric permutation procedure applied to the similarity matrix underlying the ordination or classification of samples.

In order to examine the null hypothesis that there are no differences in community composition of the eight stations, a test statistic was computed, reflecting "between site" and "within site" variability.

If $\bar{r}_w$ is defined as the average of all rank similarities among replicates within groups, and $\bar{r}_b$ is the average of rank similarities arising from differences of replicates between different groups, then the suitable test statistic is

$$\mathbf{R = (\bar{r}_b - \bar{r}_w)/(M/2)} \text{ (Clarke and Green, 1988)}$$

The R statistic is a useful comparative measure of the degree of separation of groups, though the main interest usually centers on whether it is significantly different from zero. The denominator of equation, $R = (\bar{r}_b - \bar{r}_w)/M/2$ (section 2.4.3) has been chosen so that R can

Field *et al.* (1982) presented a strategy for analyzing marine biological survey data and relating the biotic patterns to environmental data. The inherent flexibility of the multivariate method is shown 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.

2.4.2 Transformations

There are two distinct roles for transformation in community analyses:

(1) To meet statistical assumptions for parametric techniques.

(2) To weight the contributions of common and rare species in the (non-parametric) multivariate representations (Clarke and Green 1988).

The choice of transformation in a multivariate analysis may have more effect than choice of similarity coefficient or ordination method. Statistical considerations do enter, however, particularly in relation to the reliability of sampling. With untransformed data, a single chance capture of a very large-bodied species can totally distort a biomass MDS; similar effects will results from sampling small-bodied species with a strong degree of spatial clustering (Clarke and Green 1988).

At the other extreme, an analysis which places a lot of weight on species which are typically only ever found as single individuals in one sample is highly susceptible to the "noise" introduced by the chance capture of rarer species. The practical choice is therefore often between a moderate "root" and fairly severe "root-root" or 4^{th} root transformations, which retains the hard-won quantitative information but downplays the species dominance (Clarke and Warwick, 1994). Fourth root transformation down-weighs the importance of the very

2.4 STATISTICAL AND NUMERICAL ANALYSIS

2.4.1 Background

It is convenient to categorize possible analyses broadly into four main stages.

- Representing communities by graphical description of the relationships between the biota in the various samples.
- Discriminating sites / conditions on the basis of their biotic composition.
- Assessing levels of "stress" or disturbance, by attempting to construct biological measures from the community data which are indicative of disturbed conditions
- Relating biotic patterns to environmental variables.

never technically lie outside the range (-1,1). R=0, if all "replicates" within groups are more similar to each other than any "replicates" from different sites. R is approximately zero if the null hypothesis is true, so that similarities between and within groups will be the same on average (Clarke and Green, 1988).

2.4.4 Measurement of similarity

Clarke and Warwick (1994) described several possibilities for modifying species counts in data matrices:

- The absolute numbers (or biomass), i.e. the fully quantitative data observed for each species, are most commonly used.
- Two samples are considered perfectly similar only if they contain the same species in exactly the same abundances.
- The relative numbers (or biomasses) are sometimes used, i.e. the data are standardized to give the percentage of total abundance or biomass that is accounted for by each species.
- A reduction to simple presence or absence of each species may be all that is justifiable.

Most matrices in benthic invertebrate survey data have more than half of the data entries as zeros. Transformation of the data should not alter this. Field *et al.* (1982) adopted a measure which is not affected by joint absences and sufficiently robust for marine data, yet giving more weight to abundant species (in comparing samples) than to rare ones. This is the Bray-Curtis coefficient and has the form

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

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

Y_{ij} represents score for the *ith* species in the *jth* sample; Y_{ik} represents score for the i^{th} species in the k^{th} sample; δ_{jk} represents dissimilarity between the j^{th} and k^{th} samples summed over all species.

δ_{jk} ranges from 0 (identical scores for all species) to 1 (no species in common) and is the complement of the similarity, S_{jk}.

2.4.5 Classification

Cluster analysis (or classification) aims to find the "natural grouping" of samples such that samples within a group are more similar to each other, generally, than samples in different groups. This study uses hierarchical agglomerative methods. These take a similarity matrix as their starting point and successively fuse 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 process ends with a single cluster containing all samples. The end result is a tree diagram (or dendrogram).

There are four main disadvantages to dendrograms:

- The hierarchy is irreversible, i.e. once a sample has been placed in a group its identity is lost.
- Dendrograms only show inter-group relationships; the level of similarity indicated is the average inter-group value.

- The sequencing of samples is arbitrary, so unrelated samples may be placed next to each other.
- Dendrograms tend to over-emphasize discontinuities and may force a graded series into discrete classes.

Considering the above disadvantages, it is important to employ an additional method of presentation, such as an ordination technique, to show individual relationships. If the two methods tell the same story then discontinuities can be accepted as real, if not, distinct classes shown by the dendrogram must be examined closely (Field *et al.* 1982).

2.4.6 Ordinations

The main purpose of non-metric multidimensional scaling (MDS) is to construct a "map" or configuration of the samples, in a specified number of dimensions. The distance between points on the plot is a measure of their relative degree of similarity or dissimilarity, e.g. if sample A has higher degree of similarity to sample B than it does to sample C, then sample A will be placed closer to sample B than it is to sample C in the ordination plot (Gray *et al.* 1988).

The accuracy of a 2-dimensional (2-D) MDS can be measured by comparing its stress value with that of higher dimensions. In theory, stress increases with reducing dimensionality of the ordination, and the lower the stress value the more accurate the representation of samples in the MDS. The current studies use 2-dimensions (2-D) with 6 repetitions of the analysis to ensure that results converge to an optimal configuration

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

2.4.7 Relationships between biotic and environmental data

Here biological observations are compared to environmental observations of the same sample. The abiotic and environmental data are determined separately and superimposed at the end. The BIOENV, procedure of determining the best combination match was not employed in this study. An ordination based on abiotic information should group sites in the same way as for the biotic plot. Chemical Oxygen Demand (COD), total Kjeldahl Nitrogen and percentage composition of mud, sand and gravel fractions of the sediment were used as environmental variables in the current study.

2.4.8 Abundance/biomass comparison (ABC) plots or *k*-dominance curves

Distributional techniques are graphical methods for assessing community responses to stress. The species are ranked in order of importance in terms of abundance or biomass on the x-axis (log scale) with percentage dominance on the y-axis (cumulative scale). According to the theory, in undisturbed communities the biomass is dominated by a few large (k-selected) species, each represented by rather few individuals. Thus, the curve for biomass lies above the curve for abundance for its entire length.

In moderately disturbed sites, the large longer-lived species may be eliminated and the inequality between the abundance and biomass dominance is reduced so that the two curves are closely coincident and may cross each other one or more times. In severely disturbed

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sites, benthic communities become increasingly numerically dominated by one or a few very small, short-lived; opportunistic (r-selected) species and the abundance curve lies above the biomass curve throughout its length. These three conditions should be recognizable in a community without reference to control samples in time or space, the two curves acting as an "internal control" against each other. Reference to control samples is, however, still desirable. Replication is important because large biomass dominance are represented by few individuals which are which are liable to larger sampling error than numerical dominance (Clarke and Warwick, 1994).

In order to link biological information to environmental variables the current study uses a summary statistic, W, which summarizes the difference in area under the biomass and abundance curves (Clarke, 1990).

$$W = \sum_{i=1} (B_i - A_i)/ [50(S-1)] \quad \text{(Clarke, 1990)}$$

W takes values in the range (-1,1), with W→ +1 for even abundance across species but with biomass dominated by a single large species (undisturbed state), and W→ -1 in the converse disturbed state, when the abundance curve is well above the biomass curve throughout its length (though neither limit is likely to be attained in practice).

In correlations, the Y's at each X are assumed to be normal and also the X values at each Y are assumed to have come at random from a normal population. This is referred to as sampling from a "bivariate normal distribution". The effect of deviations from the assumption of bivariate normality appears unimportant when there is only slight correlation (in this case between W-statistic and %mud, %coarse sand and % gravel), but if there is

substantial correlation, then there may be a marked adverse effect of such non-normality, this effect not being diminished by increasing sample size (Norris and Hjelm, 1961: as cited by Zar, 1994). In this case W-statistic is tested for correlations with percentage coarse sand, percentage mud and percentage gravel.

CHAPTER THREE

STATISTICAL TESTING

CHAPTER 3: STATISTICAL TESTING - MACROFAUNA AND MEIOFAUNA.

3.1 BACKGROUND

One approach to the analysis of ecological data is to separate the biotic data into groups, based on environmental criteria and then to test for significant differences amongst the biotic groups (Field *et al.* 1982). The simple structure of groups, and replicates within groups, is referred to as one-way layout. Clarke and Green (1988) proposed a statistical test, which is built on a simple non-parametric permutation procedure, applied to the rank similarity matrix underlying the ordination or classification of samples called ANOSIM (analysis of similarity). The ANOSIM test is presented before the results of the multivariate analysis in order to emphasize that the tests are not based on groups formed by cluster analysis.

3.2 ANOSIM FOR THE ONE-WAY LAYOUT

Methods are given in section 2.4.3. This analysis is based on four factors, i.e. transect (site), depth, % coarse sand and Chemical Oxygen Demand (COD). The null hypothesis, (H_o), to be tested is that there are no differences in community composition between groups of samples. In order to examine this hypothesis, a test statistic needs to be constructed which reflects observed differences between groups, constructed with differences among "replicates" within groups (Clarke and Ainsworth, 1993). This method involves computing the average distance between every pair of 'replicates' within a group and contrasting this with the average distance apart of all pairs of samples corresponding to replicates from different groups.

The test is based not on distances between samples in multi-dimensional scaling (MDS) but on the corresponding (rank) similarities between samples grouped by one factor at a time (Clarke and Green, 1988)

3.2.1 Transects/ sites

Lovu River and Brighton Beach. The abundance data of nine samples from Lovu River and nine samples from Brighton Beach were 4^{th} root transformed and the Bray-Curtis similarities calculated. The test statistic R was calculated using ANOSIM and is computed under 5000 permutations. For the macrofauna, the Global R statistic value was found to be 0.583 and an associated significance level of 0.1% (Table 3.1). This rejects the null hypothesis, (H_o), and therefore there is highly significant difference between these two transects. The meiofauna results have a Global R statistic value of 0.767 and an associated significance level of 0.1%, which also rejects the null hypothesis and indicates that there is a highly significant difference between Lovu and Brighton Beach samples.

Table 3.1 The results of the one-way ANOSIM tests for inter-site difference for samples taken from off Lovu and Mbokodweni River mouths and Brighton Beach, n= number of samples, NS indicates non- significant results.

No of samples used (n_1)	No of samples used (n_2)	Transect/ Site	Null Hypothesis (H_0)	Global R (macrofauna)	Global R (meiofauna)	Significance level (macrofauna)	Significance level (meiofauna)
9	9	Lovu, Brighton	There is no difference across transects	0.583	0.720	0.1%	0.1%
9	6	Lovu, Mbokodweni	There is no difference across transects	0.642	0.441	0.7	0.1%
9	6	Brighton Mbokodweni	There is no difference across transects	0.192 (NS)	0.898	6.4% (NS)	0.1%

Lovu and Mbokodweni River. The abundance data of nine benthic samples from Lovu and six samples from Mbokodweni were selected and 4th root transformed and the Bray-Curtis similarity calculated. There was a reef at one station at Mbokodweni, hence the three missing samples. 5000 permutations were used to calculate the test statistic. For the macrofauna, the Global R statistic value was found to be 0.642 and an associated significance level of 0.1%, which leads to the rejection of the null hypothesis (H_0). The meiofauna results show a Global R value of 0.441 and a significance level of 0.7%. From both cases it was then concluded therefore that Lovu and Mbokodweni samples were significantly different.

Brighton Beach and Mbokodweni River. Nine samples and six samples were selected from Brighton beach and Mbokodweni River respectively. The biotic abundance data were 4th root transformed and the Bray-Curtis similarity calculated. For the macrofauna, the Global R value was found to be 0.192 at 6.4% significance level. This result shows that there is no significant difference between the two transects, and the null hypothesis is accepted (P>0.05).

However, the meiofaunal result shows a Global R value of 0.898 at a significance level, P= 0.1%. This allows rejection of the null hypothesis and indicates that Brighton and Mbokodweni meiofaunal samples are distinct.

Except for the macrofauna of Brighton Beach and Mbokodweni River, the null hypotheses are rejected indicating that there are significant differences among the benthos of different transects. Even though macrofaunal and meiofaunal results for Brighton Beach and Mbokodweni samples differes, the high Global R value of 0.898, for the meiofauna indicates that the two sites are well separated. The samples taken from the three transects contains different sets of organisms.

3.2.2 Depth

The 25 and 35 m depth samples at all three transects were 4^{th} root transformed and the Bray-Curtis similarity calculated. For the macrofauna, the Global R value was found to be 0.306 and an associated significance level of 1.3% (Table 3.2). This allows the rejection of the null hypothesis and it is inferred that macrofaunal communities at 25 and 35 m depth are significantly different. Meiofaunal results show Global R of -0.017 at 47.2% significance level. The null hypothesis is then accepted in that there is no difference between the meiofauna samples of pooled transects at 25 and 35 m mean water depth.

Table 3.2 The results of the one-way ANOSIM tests for inshore-offshore variability for samples taken from off Lovu and Mbokodweni River mouths and Brighton beach, n=number of samples, NS indicate non-significant results.

No of samples used (n_1)	No of samples used (n_2)	Depth (m)	Null Hypothesis (H_0)	Global R (macrofauna)	Global R (meiofauna)	Significance level (macrofauna)	Significance level (meiofauna)
6	9	25,35	There are no differences between "inshore" and deeper stations.	0.306	-0.017	1.3%	47.2% (NS)
6	9	25,45	There are no differences between "inshore" and deeper stations.	0.53	0.307	0.1%	1.9%
9	9	35,45	There are no differences between "inshore" and deeper stations.	-0.018	0.148	50.7% (NS)	4.5%

Six and nine samples were used for the ANOSIM test at 25 and 45 m mean water depths respectively. These were tested for significant differences using 5000 permutations. The macrofauna produced Global R= 0.53 at significance level P= 0.1%. The null hypothesis was rejected and it was concluded that the shallow and deeper macrofaunal samples were significantly different. The same was tested for the meiofauna, Global R was found to be 0.307 at a significance level of 1.9%. Since these samples were taken not only at different depths but also at different distances offshore it is likely that the cleaner and coarser sediments from deeper waters and the muddier inshore samples would naturally support distinctive communities (McClurg, 1996).

Nine inshore samples and nine offshore samples at 35 and 45 m mean water depths were tested for significant differences using 5000 permutations. The macrofauna produced a Global R value of –0.018 at an associated significance level of 50.7%. Thus the null

hypothesis is accepted and there is no significant difference between the 35 and 45 m deep samples. However, meiofaunal results show a Global R of 0.148 and a significance level of 4.5%, which just allows the rejection of the null hypothesis, and indicates that there are differences between samples at 35 and 45 m mean water depth. It is, however, important to note that even though depths differ, the 35 and 45 m samples were closer to each other in terms of distance than the 25 and 35 m samples.

3.2.3 Percentage coarse sand

Coarse sand in the current study is classified as having sediment particle sizes of between 0.5 and 1 mm (Table 3.3). Percentage coarse sand was classified into three groups, A, B and C. Group A consist of samples with less than 2% coarse sand, i.e. samples L1a; L1b; L1c; L2a; L2b; L2c; L3a; L3b and L3c. Group B consists of samples of between 2 and 5% coarse sand, i.e. samples B1a; B1b and B1c. Group C consists of samples with more than 5% coarse sand, i.e. samples, B2a; B2b; B2c; B3a; B3b; B3c; M2a; M2b; M2c; M3a; M3b; and M3c. The null hypothesis to test here is that there are no differences among these three groups, based on percentage coarse sand.

Table 3.3 Physical and chemical characteristics of sediment samples showing coarse sand groupings.

Station No.	CODmn (mg O_2 g^{-1})	COD groupings	% Coarse Sand (0.5 to1 mm)	% Coarse sand groupings
L1a	0.245	C	0.5	A
L1b	0.323	C	0.2	A
L1c	0.222	C	0.2	A
L2a	0.922	C	0	A
L2b	1.799	C	0	A
L2c	3.499	C	0.5	A
L3a	0.657	C	0.6	A
L3b	0.849	C	0.2	A
L3c	0.339	C	0	A
B1a	<0.00	A	2.1	B
B1b	<0.01	A	3.1	B
B1c	<0.00	A	3.1	B
B2a	0.197	B	12.4	C
B2b	0.111	B	10.2	C
B2c	0.239	C	6.9	C
B3a	0.152	B	39.2	C
B3b	<0.01	A	33.3	C
B3c	0.054	A	38.1	C
M2a	0.150	B	18.6	C
M2b	0.084	A	12.4	C
M2c	0.089	A	17.7	C
M3a	0.187	B	8.7	C
M3b	0.138	B	10.7	C
M3c	0.101	A	7	C

The biotic abundance data of the three groups of samples was 4th root transformed and the Bray-Curtis similarities calculated for both the macrofauna and meiofauna. For the macrofauna data the Global R value for groups A-B, A-C and B-C was found to be 0.983, 0.69 and 0.872 at 0.5%, 0.1% and 0.2% significance levels respectively (Table 3.4). This allows the rejection of the null hypothesis and indicates that there are differences among these groups. The meiofauna allows the rejection of the null hypothesis for groups A-B and A-C; R= 0.613 and 0.606 at 0.5 % and 0.1% significance levels respectively. However, comparing groups B-C allows the acceptance of the null hypothesis, having Global R= 0.085

at 26.2% significance level. It is clear that group B is more similar to group C than to group A because all other six remaining group B replicates are found in group C (Table 3.3).

Table 3. 4 The results of the one-way ANOSIM test of the biota, based on samples grouped by % coarse sand from off the KwaZulu/Natal coast in May 1999. A (<2%), B (2-5%) and C (>5%) percentage coarse sand, NS indicate the non-significant results. See Table 3.3.

No of samples used, n_1	No of samples used, n_2	Groups	Null Hypothesis (H_0)	Global R (macrofauna	Global R (meiofauna)	Significance level macrofauna	Significance level meiofauna
9	3	A- B	There are no differences between groups of samples.	0.983	0.613	0.5%	0.5%
9	12	A-C	There are no differences between groups of samples.	0.69	0.606	0.1%	0.1%
3	12	B- C	There are no differences between groups of samples.	0.872	0.085	0.2%	26.2% (NS)

It is important to note that since the three transects were taken from different environments (that is, Lovu and Mbokodweni were taken from off river mouths and Brighton samples from off the beach) some natural or anthropogenic disturbances may have taken place prior to our sampling.

3.2.4 Chemical oxygen demand (COD)

This is defined as the amount of oxygen needed to oxidize organic and inorganic material. The COD was classified into three different groups A, B and C. Group A consists of those samples with COD value less than 0.1 $mg0_2g^{-1}$, i.e. B1a; B1b; B1c; B3b; B3c; M2b; M2c; and M3c. Group B contains the samples with COD value of between 0.1 $mg0_2g^{-1}$ and 0.2 $mg0_2g^{-1}$ (B2a; B2b; B3a; M3a; M3b and M2a) while Group C includes the samples with COD

value of more than $0.2mg0_2g^{-1}$, notably L1a; L1b; L1c; L2a; L2b; L2c; L3a; L3b; L3c and B2c (See Table 3.3).

Table 3. 5 The results of the one-way ANOSIM test for samples taken from off the KwaZulu/Natal coast in May 1999. A ($< 0.1mg0_2g^{-1}$); B ($0.1\text{-}0.2mg0_2g^{-1}$); C ($>0.2\ mg0_2g^{-1}$). N.S indicate non-significant results. See Table 3.3.

No of samples used, n_1	No of samples used, n_2	Groups	Null Hypothesis (H_o)	Global R macrofauna	Global R meiofauna	Significance level macrofauna	Significance level meiofauna
10	8	C-A	There are no differences between groups of samples	0.764	0.578	0.1%	0.1%
10	6	C-B	There are no differences between groups of samples	0.622	0.514	0.1%	0.1%
8	6	A-B	There are no differences between groups of samples	0.264	-0.049 NS	1.8%	61% NS

The biotic abundance data of the three groups was 4th root transformed and the Bray-Curtis similarities calculated for both macrofauna and meiofauna. Table 3.5 shows the results of one-way ANOSIM, with 5000 permutations. The following pairs of groups showed significant differences at P<0.001% significance level:

C-A (macrofauna)

C-B (macrofauna)

C-A (meiofauna)

C-B (meiofauna)

A-B (macrofauna)

The null hypothesis is thus rejected, showing that there are differences among these groups. However, the result of group A and B allow the acceptance of the null hypothesis for the

meiofauna. This may be because these two groups share samples of similar transect between themselves with the exception of sample B2a that is found in group C (See Table 3.3).

3.3 CONCLUSION

The results show that the macrofauna differ significantly between all three transects except Brighton Beach and Mbokodweni River. It also differs between depths 25/35 m and 25/45 m, but not between 35/45 m depths. The macrofauna differs between all three categories of coarse sand abundance and between all three categories of COD. The macrofauna component thus seems to be more sensitive to the type of sediment as measured by percentage coarse sand and COD.

The meiofauna on the other hand showed a different pattern. The meiofauna differed between all pairs of transects, and between 25/45 m and 35/45 m depth, but not between 25/35 m. The meiofauna also differed between A-B and A-C but not between B-C, the larger categories of coarse sand. The meiofauna also differed between C-A and C-B, but not between A-B the lower categories of COD. Thus, the meiofauna showed different sensitivity to transect, depth, type of sediment and COD to the macrofauna, but some sensitivity to all four variables used.

CHAPTER FOUR

MACROFAUNAL COMMUNITY PATTERNS

CHAPTER 4: MACROFAUNAL COMMUNITY PATTERNS

4.1 BACKGROUND

Species dependent (multivariate) methods are much more sensitive than species independent (univariate and distributional) methods in discriminating between sites and times (Warwick *et al.* 1990). Various taxa of marine organisms differ in their sensitivity to disturbance, and it is desirable that measures of disturbance should in some way capture and utilizes that information. Multivariate methods simply demonstrate change with no indication as to whether this can be regarded as deleterious. Multivariate analyses based on higher taxa may adequately reflect anthropogenic disturbance on a local scale, whereas those based on species data, may be sensitive to fine scale natural environmental variation, thus confusing the picture (Warwick, 1988a). The macrofauna analysis is performed using data identified to genus and species level. Methods are given in section 2.4.

4.1.1 Abundance data

The dendrogram showing station affinities based on 4^{th} root transformation is depicted in Figure 4.1, using the Bray-Curtis measure of similarity and group average sorting. Cluster analysis reveals four major groups (A, B, C and D) of stations at 38% similarity level. Group A consists of inshore samples from Brighton Beach (i.e. B1a, B1b and B1c). Group B consist of inshore and middle samples from Lovu River mouth (i.e. L1a, L1b, L1c, L2a, L2b and L2c). Group C consists of middle samples from Mbokodweni River mouth (i.e. M2a, M2b and M2c) and middle and offshore samples from Brighton Beach, (i.e. B2a, B2b, B2c, B3a, B3b, and B3c). Group D consists of samples from offshore stations for both Lovu and Mbokodweni River mouths (i.e. L3a, L3b, L3c, M3a, M3b and M3c). Apart from sample B2a, all replicates group together. Group C divides in two homogenous subgroups, which are

designated as C1 and C2. Group C1 comprises of stations from off Brighton beach and Group C2 comprises of middle stations from off Mbokodweni river mouth site. Group C1 and C2 cluster together at approximately the 40% similarity level. Group D divides into two subgroups, which are designated as D1 and D2 at the 38% similarity level. Group D1 and D2 comprises of deeper stations from off both Lovu and Mbokodweni river months. Group B divides into subgroups B1 and B2 at the 55% similarity level. Group B1 and B2 consist of inshore and middle stations of the Lovu river mouth transect. Group A consist of inshore stations from off Brighton beach. These groupings seem to be related to depth and sediment type, which is discussed in section 4.3.

MDS (multi-dimensional scaling) was performed in 2-dimensions and 6 repetitions were carried out with a resulting minimum stress of 0.19. The relationships observed in the cluster analysis are substantiated by the MDS (Figure 4.2). Samples M2a, M2b, M2c and samples B2a, B2b, B2c, B3a, B3b, B3c are clustered in Group C and conform to groupings defined in the dendrogram. Group A, B and D stations also conform to groupings defined in the dendrogram.

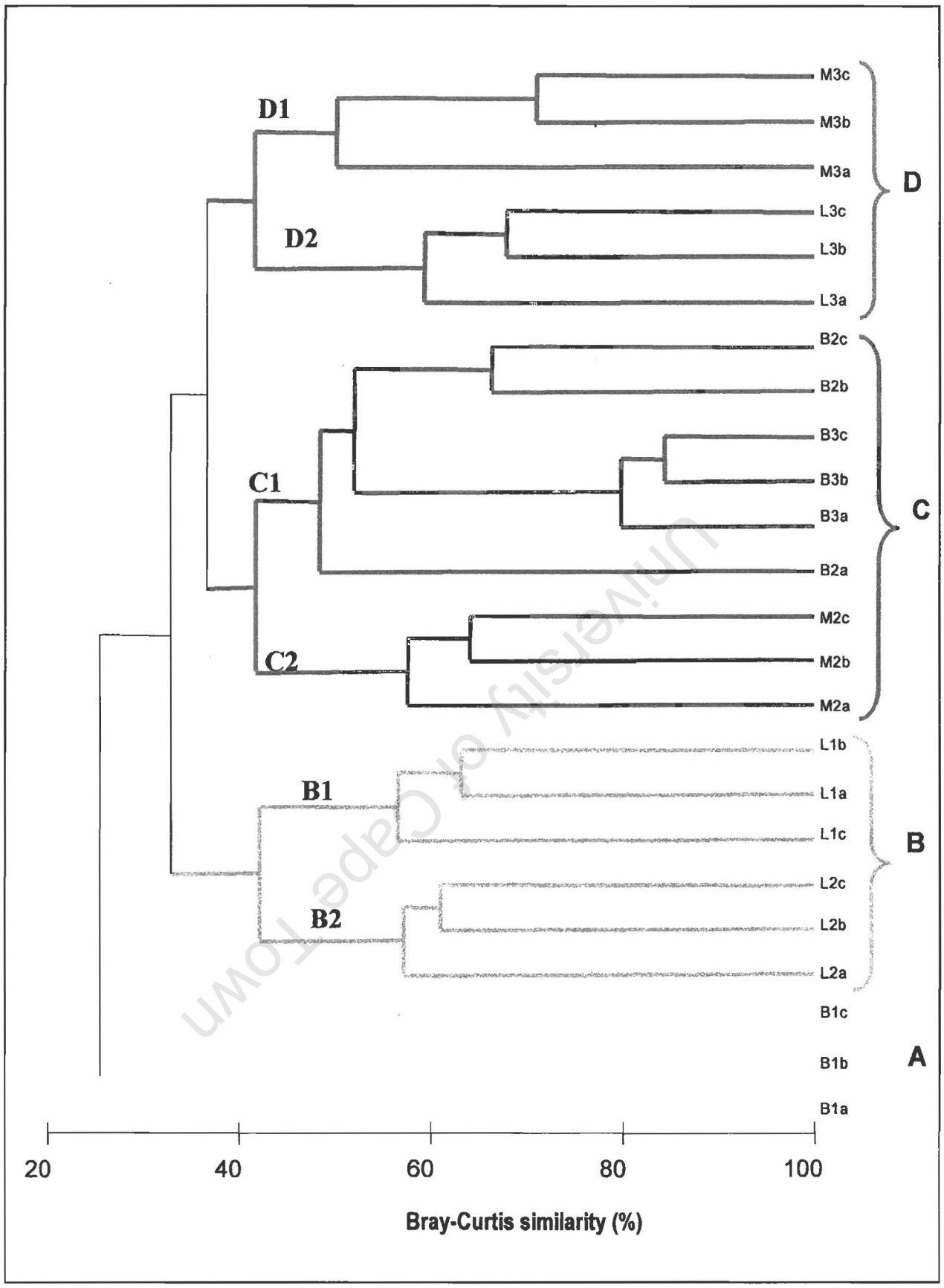


Figure 4.1. Dendrogram showing affinities between the macrobenthic samples using abundance data. Samples were taken by a Day grab off the KwaZulu/Natal coast in May 1999.L, M and B denote Lovu, Mbokodweni and Brighton Beach; a, b and c indicate the samples from 25, 35 and 45 m mean water depth respectively. Numbers denot replicates at same site and date.

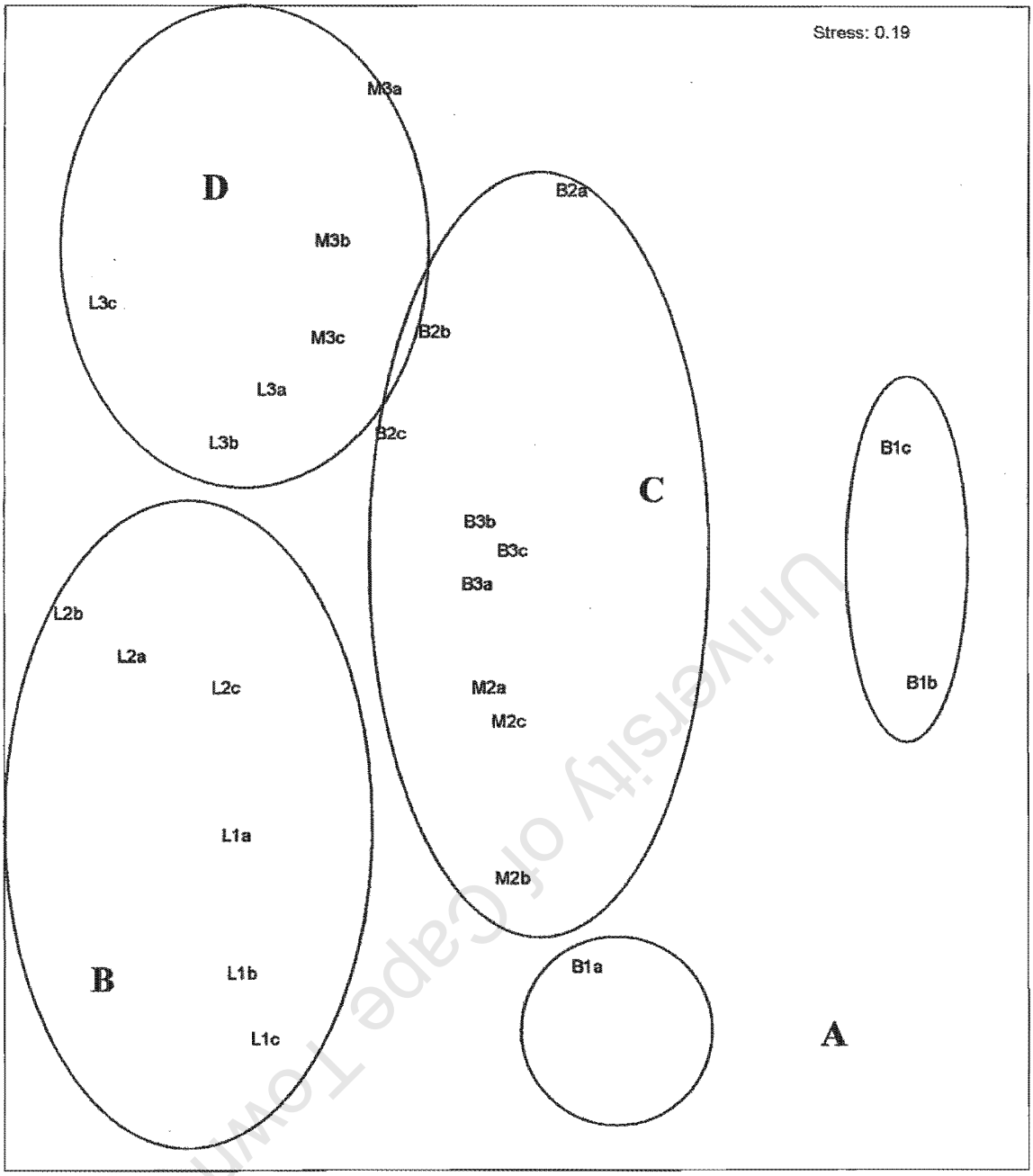


Figure 4.2 MDS plot for the macrobenthos abundance data.

4.1.2 Indicator species

Sections 4.1.1 described the benthic community patterns using two complementary techniques. This section aims to determine which species are primarily responsible for influencing the sample groupings based on the cluster and MDS groupings. The dendrogram and ordination plots for the abundance data divided the samples into four different groups.

Six separate analyses were performed using the 4^{th} root abundance data. The SIMPER analyses are based on the groups found in the dendrogram and the MDS ordination (Figure 4.1 and 4.2). Group B&D (Table 4.1), B&A (Table 4.2), D&A (Table 4.3), B&C (Table 4.4), D&C (Table 4.5) and A&C (Table 4.6), respectively. The tables list the average abundance of each species in one group and the average abundance in the other group. The arbitrary cut-off percentage of 25% was chosen to limit the species list. Species beyond 25% cumulative percentage contributed less than 2% to the sample groupings and were ignored in this interpretation.

Table 4.1 The percentage contribution of each species to the separation of groups B&D based on classification and ordination results, abundance data. An arbitrary cut-off percentage of 25% dissimilarity was chosen. The more abundant groups are highlighted in bold type. Average dissimilarity between group B and D = 65.64%. N is the number of samples in each group.

IDENTITY	TAXONOMIC GROUP	GROUP B Av Abundance N=6	GROUP D Av Abundance N=6	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Lasaea sp.	Pelecypoda	**96.83**	8.13	2.65	2.65
Scoloplos sp.	Polychaeta	1.83	**51.63**	2.54	5.18
Byblis gaimardi	Amphipoda	0.50	**16.88**	2.17	7.35
Timoclea sp.	Pelecypoda	**52.33**	18.63	1.92	9.27
Urothoe sp.	Amphipoda	25.33	1.50	1.89	11.16
Siliqua fasciata	Pelecypoda	0.00	**19.00**	1.86	13.82
Ampelisca brevicornis	Amphipoda	**12.50**	**54.88**	1.82	14.84
Ampelisca diadema	Amphipoda	5.50	1.75	1.82	16.66
Capitellidae	Polychaeta	**19.50**	0.75	1.82	18.48
Gastropoda	Gastropoda	1.83	9.38	1.76	20.24
Ophiuroidea	Ophiuroidea	**33.33**	0.25	1.74	21.98
Gammaropsis sp..	Amphipoda	1.00	**20.63**	1.72	23.71

These groups represent shallow and middle samples of Lovu River (Group B) and deeper samples of both Lovu and Mbokodweni River sites (Group D). In order to limit the species list to manageable size, an arbitrary cut-off percentage of 25% was chosen for macrofauna abundance data. The main contributor was the pelecypod, *Lasaea sp.*, which was ten times more abundant in group B and contributed 2.65% to the separation between group B and D. Other species which were more abundant in group B were the polychaete, capitellid; the amphipods, *Urothoe sp.* and *Ampelisca brevicornis*; the pelecypod, *Timoclea arakana* and the unidentified ophiuroid species. Indicator species which were characteristic of group D were the polychaete, *Scoloplos sp.*; and the amphipods, *Byblis gaimardi;*, *Ampelisca brevicornis* and *Gammaropsis sp,* and the pelecypod *Siliqua fasciata.*

Table 4.2 The percentage contribution of each species to the separation of groups B&A based on classification and ordination results, abundance data. An arbitrary cut-off percentage of 25% dissimilarity was chosen. The more abundant groups are highlighted in bold type. Average dissimilarity between group B and A = 76.6%. N is the number of samples in a group.

IDENTITY	TAXONOMIC GROUP	GROUP B Av Abundance N=6	GROUP A Av Abundance N=3	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Lasaea sp.	Pelecypoda	**96.83**	0.00	5.06	5.06
Ampelisa brevicornis	Amphipoda	**12.50**	0.00	2.56	7.62
Urothoe sp.	Amphipoda	**25.33**	0.00	2.53	10.15
Ampelisca diadema	Amphipoda	**5.50**	0.00	2.49	12.64
Urothoe coxalis	Amphipoda	**52.33**	1.00	2.29	14.93
Crinoidea	Crinoidea	**12.17**	0.67	2.21	17.15
Marphysa depressa	Polychaeta	**10.17**	1.33	2.10	19.25
Ophiuroidea	Ophiuroidea	**33.33**	0.00	2.10	21.35
Xanthidae	Brachyura	0.33	**4.33**	1.98	23.33
Capitellidae	Polychaeta	**19.50**	1.00	1.86	25.19

These groups represent shallow and middle samples of Lovu River mouth (Group B and shallow samples of Brighton Beach (Group A). As with the previous grouping, *Lasaea sp., Ampelisca brevicornis, Urothoe sp., Ampelisca diadema* and ophiuroidea were characteristic of group B. These species are referred to as perfect indicators because they are not found in group A. They contributed 5.06%, 2.56%, 2.53%, and 2.49 % respectively to the separation between the two groups. This pattern may be caused by the fact that group A consists of only three samples with low abundances compared to group B which consists of six samples. The most prominent taxon characteristic of group A is an unidentified xanthid crab.

Table 4. 3 The percentage contribution of each species to the separation of groups D&A based on classification and ordination results, abundance data. An arbitrary cut-off percentage of 25% dissimilarity was chosen. The most abundant groups are highlighted in bold type. Average dissimilarity between group D and A = 75.14. N is the number of samples in a group.

IDENTITY	TAXONOMIC GROUP	GROUP D Av. Abundance N=6	GROUPA Av. Abundance N=3	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Ampelisca brevicornis	Amphipoda	**54.88**	0.00	2.98	2.98
Scoloplos sp.	Polychaeta	**51.63**	0.67	2.97	5.95
Crinoidea	Crinoidea	**40.88**	0.67	2.60	8.55
Byblis gaimardi	Amphipoda	**16.88**	0.00	2.58	11.13
Corophium sp.	Amphipoda	**9.25**	0.00	2.11	13.24
Gastropoda	Gastropoda	**9.38**	0.00	2.06	15.30
Marphysa depressa	Polychaeta	**18.88**	1.33	1.99	17.29
Siliqua fasciata	Pelecypoda	**19.00**	0.00	1.97	19.26
Gammaropsis	Amphipoda	**20.63**	0.00	1.96	21.23
Eunice sp.	Polychaeta	5.63	0.00	1.81	23.04
Onuphis eremita	Polychaeta	**10.00**	0.67	1.75	24.79
Phyllodoce sp.	Polychaeta	8.38	0.00	1.71	26.50

These groups represent inshore samples from Brighton Beach (Group A) and offshore samples from both Mbokodweni and Lovu River (Group D). The perfect indicators for group D were the amphipods, *Ampelisca brevicornis, Byblis gaimardi* and *Gammaropsis sp.*; and the pelecypod, *Siliqua fasciata.* An unidentified gastropod and *Corophium spp.* were also perfect indicators for group D relative to group A. These contributed 2.98%, 2.58%, 1.96% and 1.97% respectively to the separation between group D and A. Group A did not reveal any significant indicator species. This was due to the fact that this group contained very few organisms.

Table 4.4 The percentage contribution of each species to the separation of groups B&C based on classification and ordination results, abundance data. An arbitrary cut-off percentage of 25% dissimilarity was chosen. The most abundant groups are highlighted in bold type. Average dissimilarity between group B and C = 68.59%. N is the number of samples in a group.

IDENTITY	TAXONOMIC GROUP	GROUP B Av. Abundance N=6	GROUP C Av. Abundance N=9	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Lasaea sp.	Pelecypoda	**96.83**	2.29	3.28	3.28
Timoclea arakana	Pelecypoda	**52.33**	0.00	2.24	5.52
Ampelisca brevicornis	Amphipoda	**12.50**	0.00	2.16	7.69
Ampelisca diadema	Amphipoda	**5.50**	0.00	2.11	9.80
Xanthidae	Brachyura	0.33	**10.14**	2.07	11.87
Urothoe sp.	Amphipoda	**25.33**	0.71	2.06	13.93
Anthuridae	Isopoda	**3.83**	0.00	1.85	15.78
Ophiuroidea	Ophiuroidea	**33.33**	1.00	1.83	17.61
Dromiidae	Brachyura	1.83	**6.14**	1.77	19.38
Sthenalais boa	Polychaeta	0.00	**18.86**	1.69	21.07
Photis sp.	Amphipoda	1.67	**3.71**	1.65	22.72
Onuphis sp.	Polychaeta	0.00	**7.14**	1.62	24.33
Nereis sp.	Polychaeta	2.33	**21.29**	1.61	25.95

These groups consist of middle samples from Mbokodweni and middle and offshore samples from Brighton Beach (Group C), and inshore and middle samples from Lovu (Group B). The principal contributor was the pelecypod, *Lasaea sp.*, which was approximately fifty times more abundant in group B than it is in group C and contributed 3.28% to the separation between samples of the two groups. The pelecypod, *Timoclea arakana* and amphipod, *Ampelisca brevicornis* were found to be perfect indicators for group B and the polychaete, *Sthenelais boa* emerged as the perfect indicator for group C. Other indicators that were characteristic of differences are brachyuran, xanthidae and the polychaete, *Nereis sp.*

Table 4.5 The percentage contribution of each species to the separation of groups D&C based on classification and ordination results, abundance data. An arbitrary cut-off percentage of 25% dissimilarity was chosen. The most abundant groups are highlighted in bold type. Average dissimilarity between group D and C = 62.69%. N is the number of samples in each group.

IDENTITY	TAXONOMIC GROUP	GROUP D Av Abundance N=6	GROUP C Av Abundance N=9	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Ampelisca brevicornis	Amphipoda	**54.88**	0.00	2.83	2.83
Anthuridae	Isopoda	5.50	0.00	1.94	4.77
Timoclea arakana	Pelecypoda	**18.63**	0.00	1.90	6.67
Photis sp.	Amphipoda	0.00	3.71	1.79	8.46
Sthenelais boa	Polychaeta	**17.38**	18.86	1.75	10.21
Siliqua fasciata	Pelecypoda	**19.00**	2.43	1.74	11.95
Onuphis eremita	Polychaeta	**10.00**	1.57	1.63	13.58
Marphysa depressa	Polychaeta	**18.88**	2.14	1.60	15.18
Phyllodoce sp.	Polychaeta	**8.38**	2.29	1.56	16.74
Gammaropsis sp.	Amphipoda	**20.63**	7.00	1.55	18.29
Nephtys dibranchus	Polychaeta	3.50	21.29	1.54	19.83
Osteichthyesa	Osteichthyesa	0.00	3.14	1.50	21.34
Xanthidae	Brachyura	**11.50**	10.14	1.46	22.79
Spiophanes soederstromi	Polychaeta	3.50	9.71	1.44	24.23

Group D consist of offshore samples from Mbokodweni and Lovu River and Group C consist of middle samples from Mbokodweni and middle and offshore samples from Brighton Beach. The two perfect indicators were the amphipod, *Ampelisca brevicornis*; the pelecypod, *Timoclea arakana* which contributed 2.83% and 1.9% to the separation of the groups. *Sthenalais boa* is now more common in group C than in group D which was not the case with the other groups. The difference in average abundance between group C and group D for *Sthenelais boa* is negligible (18.86 and 17.38), its importance is mainly due to high densities. Other indicators that were characteristic of the differences between groups are the polychaete, *Nephtys dibranchus* and a brachyuran, xanthidae.

Table 4. 6 The percentage contribution of each species to the separation of groups A&C based on classification and ordination results, abundance data. An arbitrary cut-off percentage of 25% dissimilarity was chosen. The most abundant groups are highlighted in bold type. Average dissimilarity between group A and C = 71.74%. N is the number of samples in each group.

IDENTITY	TAXONOMIC GROUP	GROUP A Av Abundance N=3	GROUP C Av Abundance N=9	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Mandibulophoxus stimpsoni	Amphipoda	0.33	**21.29**	2.63	2.63
Gastropoda	Gastropoda	0.00	**6.14**	2.34	4.97
Photis sp.	Amphipoda	0.00	**3.71**	2.24	7.21
Urothoe coxalis	Amphipoda	0.00	**3.57**	2.03	9.24
Scoloplos sp.	Polychaeta	0.67	**12.86**	2.01	11.25
Sthenelais boa	Polychaeta	0.00	**18.86**	1.96	13.21
Crinoidea	Crinoidea	0.67	**6.86**	1.95	15.15
Onuphis sp.	Polychaeta	0.00	**7.14**	1.88	17.04
Gammaropsis sp.	Amphipoda	0.00	**7.00**	1.88	18.92
Osteichthyes	Osteichthyes	0.00	**3.14**	1.88	20.80
Byblis gaimardi	Amphipoda	0.00	**4.71**	1.85	22.65
Urothoe sp.	Amphipoda	3.00	**0.14**	1.84	24.49

Group A consist of inshore samples from Brighton Beach and Group C consist of middle Mbokodweni samples and middle and offshore samples from Brighton Beach. The principal contributors were the amphipod, *Mandibulophoxus stimpsoni* and polychaete, *Scoloplos* that contributed 2.63% and 2.01%, respectively to the separation of the groups. The polychate, *Sthenelais boa*, is a perfect indicator for group C. while others prominent indicators include the polychaete, *Onuphis*; the amphipods, *Photis, Urothoe coxalis, Gammaropsis* and an unidentified gastropod.

4.2 BIOMASS DATA

The biomass data of the macrofauna was 4th root transformed and the resulting dendrogram is depicted in Figure 4.3. The dendrogram reveals 4 main groups according to transect at the 35% similarity level. Apart from samples B2a and B2b, which separated from group C in the abundance data, the biomass and abundance dendrograms show similar patterns. Group A is loosely associated at about 30% and consists of inshore Brighton beach samples. As in the abundance data, group B divides into two subgroups B1 and B2 at 50% similarity level. These are inshore and middle samples from the Lovu river mouth transect. Group D divides into D1 and D2 at 58% similarity level. Group D1 and D2 contains deeper samples from off the Lovu and Mbokodweni River mouth with the exception of samples B2b and B2c. Group C consist of deeper and middle stations from off Brighton Beach and Mbokodweni. Group A is separated from the others at 25% similarity level.

The non-metric multi-dimensional scaling ordination of the biomass data is similar to the ordination of the abundance data (Figure 4.4). Groups A, B, C and D form clusters in two-dimensional plots. Group A is split into three outlying samples (B1a, B1b, and B1c). Groups B, C and D are more tightly clustered in accord with the dendrogram (Figure 4.3). The stress value of 0.2 indicates some distortion in representing the results in 2 dimensions. Species responsible for the dissimilarities are discussed in section 4.1.2.

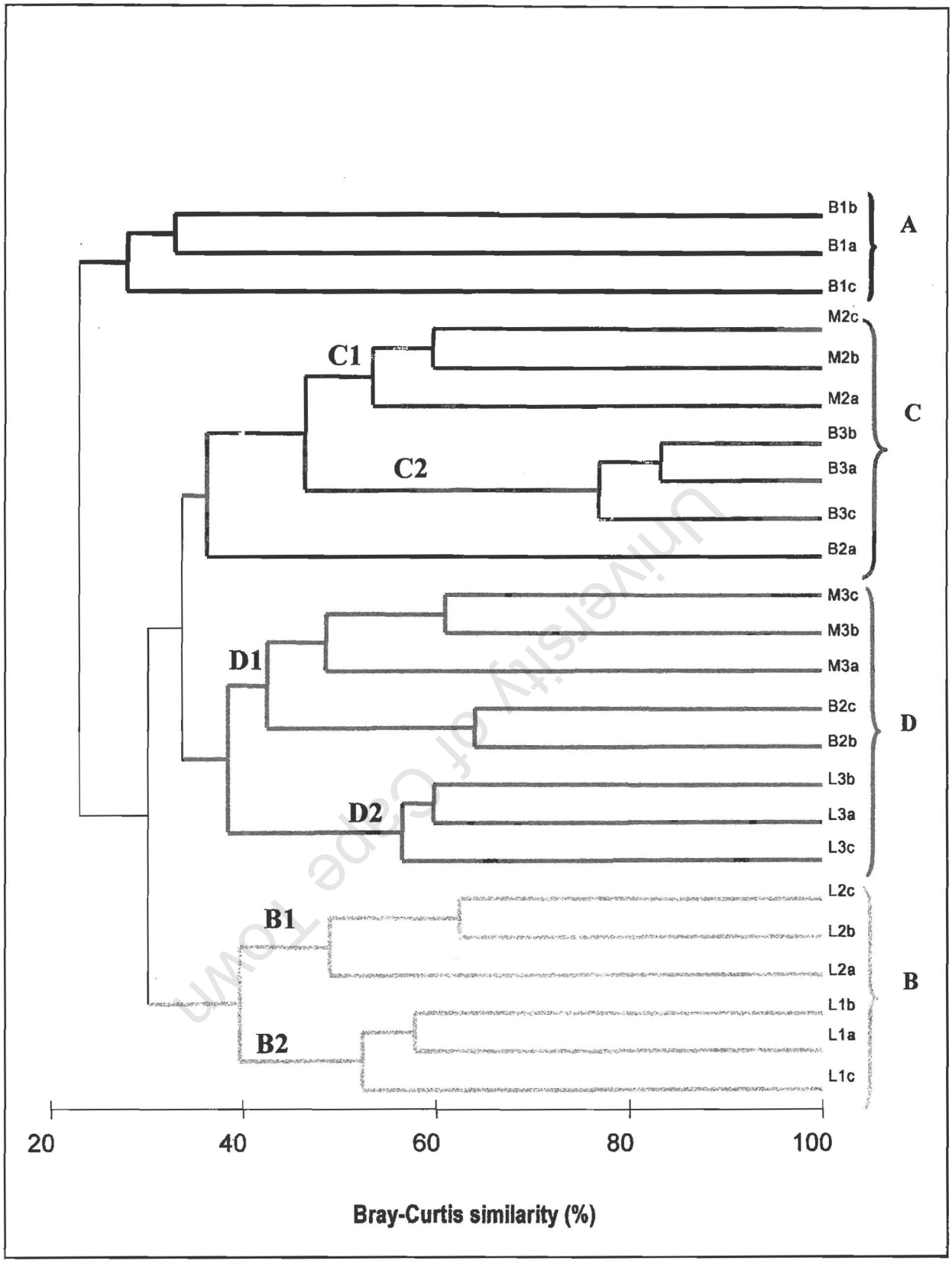


Figure 4.3. Dendrogram showing affinities between the macrobenthic samples using biomass data.

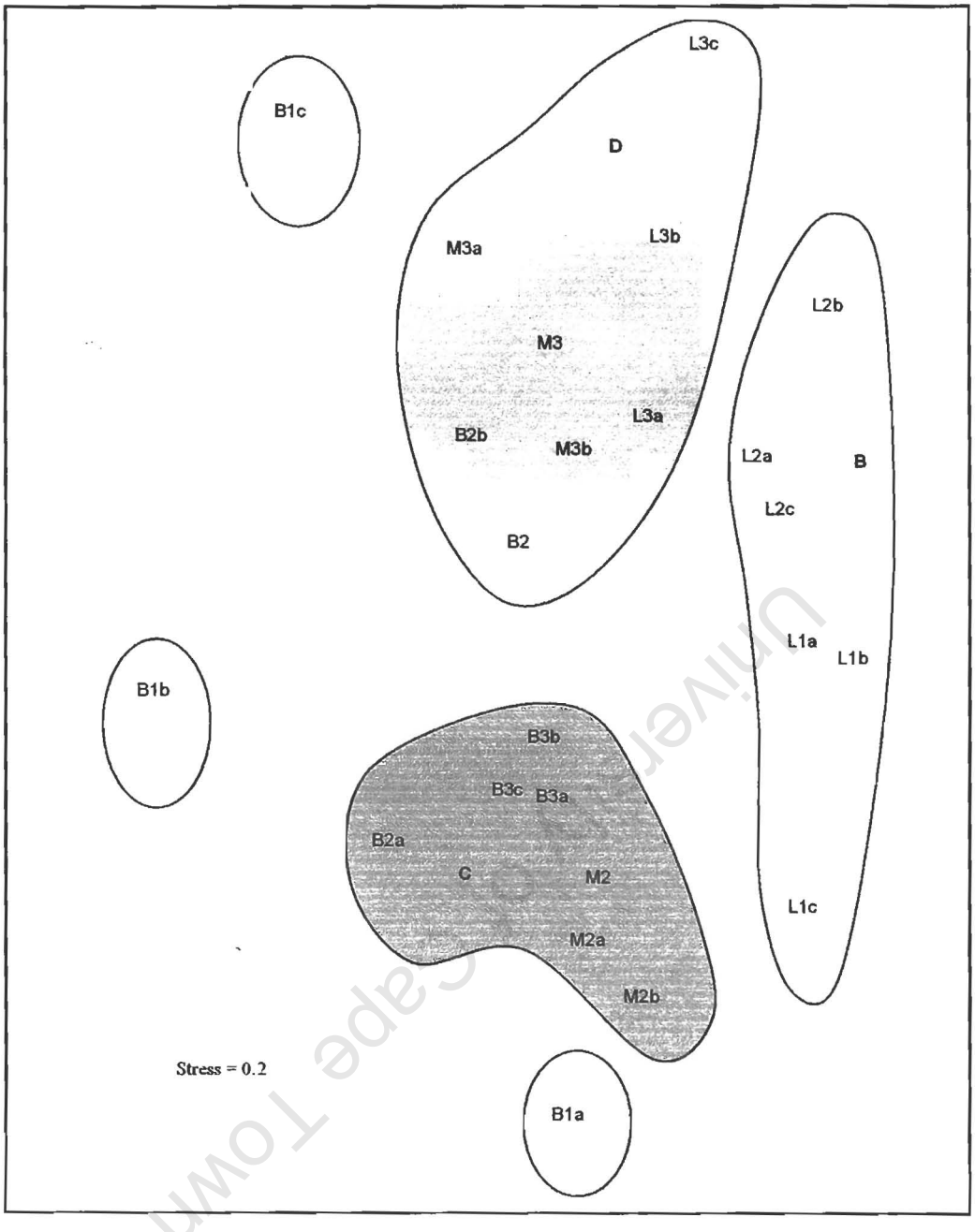


Figure 4.4 MDS plot for the macrobenthos biomass data.

4.3 LINKING BIOTIC PATTERNS TO ENVIRONMENTAL FACTORS – MACROFAUNA.

4.3.1 Background

The sensitivity and generality of multivariate methods make them particularly valuable tools in the assessment of community change, however, it is important to relate this community change to measured environmental parameters (Warwick and Clarke 1991). Field *et al.* (1982) presented a strategy for analyzing marine biological survey data and relating the biotic patterns to environmental data. This approach analyses the biological data first and then the environmental data is tested for concordance. By superimposing environmental parameters (e.g. sediment grain size) on the 2-D ordination from the faunistic data, the extent of co-variation of the variables is illustrated. Some of the measured environmental variables at each sampling station are summarized in Table 4.7.

4.3.1.1 Grain size

The abundance data for macrofauna was 4^{th} root transformed and subjected to non-metric MDS, employing Bray-Curtis similarities. The results were presented in Figure 4.2. The resulting ordination is shown in Figure 4.5. Clarke (1993) showed that sediment grain size may be an important factor influencing benthic communities in an area. To assess what part sediment grain size may have played in the current study, the ordination was replotted with the sediment type ('muddy" and "sandy") shown in place of station names. The "muddy" stations were defined as those, which yielded a percentage mud in excess of 2% in combination with a COD value greater than 0.1 mg O_2 g^{-1} (Table 4.8). The ordinations show the clear predominance of "muddy" sediments in groups B and D and "sandy" sediments in

groups A and C (Figure 4.5). Groups A and C consists of samples from areas with coarser sediments from off Brighton Beach and three middle stations from off Mbokodweni River mouth. Group B and D are samples from areas with muddy sediments from off Lovu and Mbokodweni River mouths.

Table 4.7 Physical and chemical characteristics of sediment samples M and S for the "muddy" and "sandy" sediments respectively. Classification is based on % mud and COD (See text).

Station No.	Kjeldahl Nitrogen ($\mu g\ g^{-1}$)	CODmn (mg O_2 g-1)	% Mud (<0.063mm	Classification (M/S)
L1a	18.9	0.245	4	M
L1b	34.3	0.323	4.9	M
L1c	51.1	0.222	3.5	M
L2a	57.8	0.922	12	M
L2b	53.1	1.799	29.3	M
L2c	48.7	3.499	21.8	M
L3a	30.9	0.657	3.8	M
L3b	39.9	0.849	8.8	M
L3c	28.8	0.339	4	M
B1a	26.7	<0.00	0	S
B1b	49.5	<0.01	0	S
B1c	21.7	<0.00	0	S
B2a	65.8	0.197	1.5	S
B2b	74.1	0.111	1.6	S
B2c	59.5	0.239	1.6	S
B3a	97.7	0.152	0.5	S
B3b	46.9	<0.01	0	S
B3c	77.9	0.054	0	S
M2a	130.3	0.150	0.6	S
M2b	58.6	0.084	1.7	S
M2c	78.1	0.089	1.5	S
M3a	42.7	0.187	3.8	M
M3b	59.8	0.138	2.1	M
M3c	38.4	0.101	2.6	M

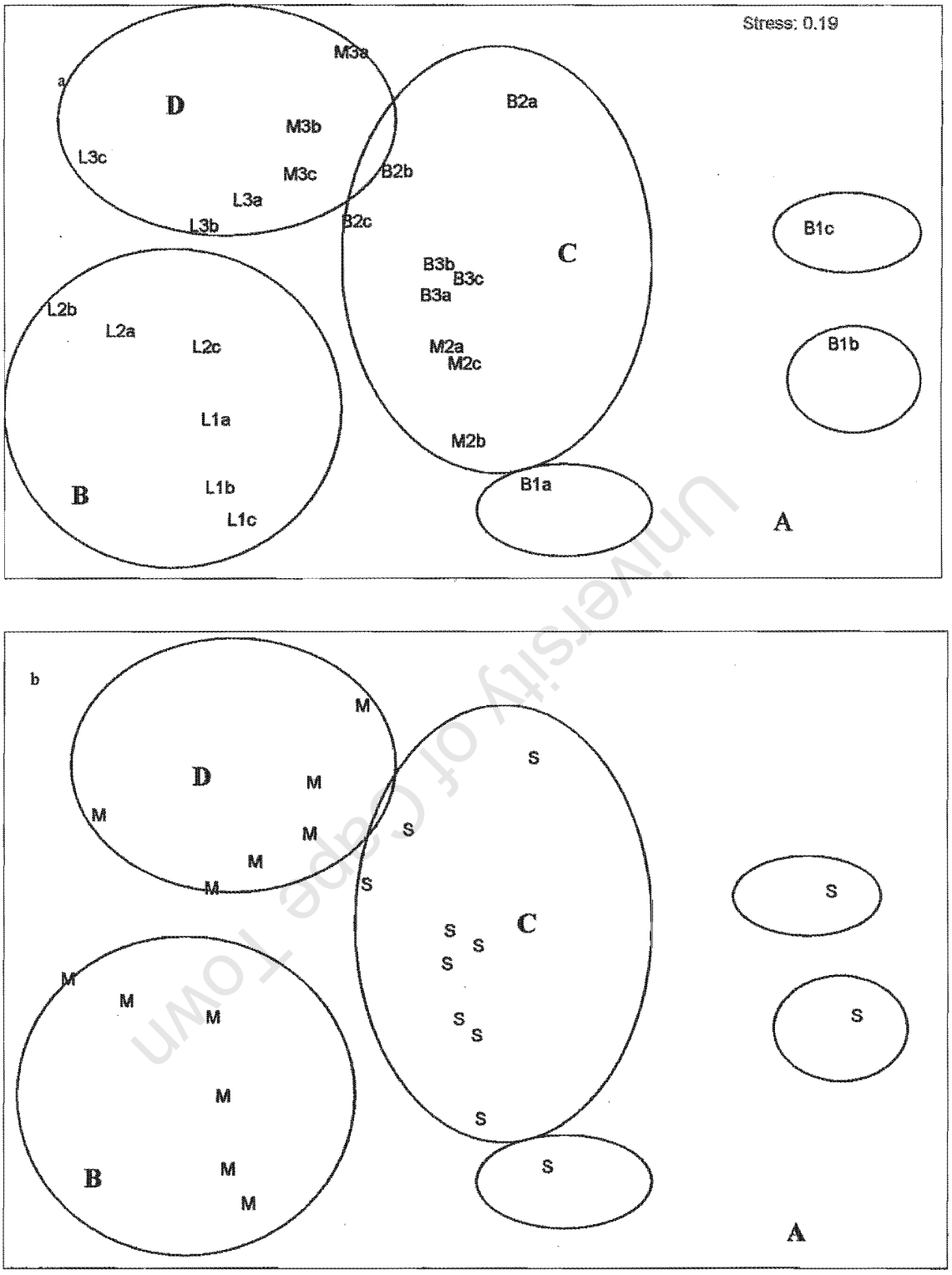


Figure 4.5 MDS plots for the macrofauna abundance. (b) Sediment type (M and S for the "muddy" and "sandy" sediments respectively) is indicated in the plot (stress=0.19)

4.3.1.2 Chemical Oxygen Demand and Kjeldahl Nitrogen.

The percentages COD and Kjeldahl N were superimposed as circles on the biotic MDS plot to assess the degree of concordance (the larger the circle the greater the value of the superimposed variable). The highest COD values are found in Group B, however, some of Group D and all Groups A and C stations have low COD values. The highest Kjeldahl Nitrogen values are found in Group C, with some fairly high values in Group B. It is notable that the three Group B stations with highest Kjeldahl Nitrogen also have high COD values.

Overall, the classification into "muddy" and "sandy" categories gives the best agreement with the biotic groups B and D (muddy) and A and C (sandy). The COD and Kjeldahl Nitrogen results are not as clear-cut, but nevertheless are related to the biotic pattern found.

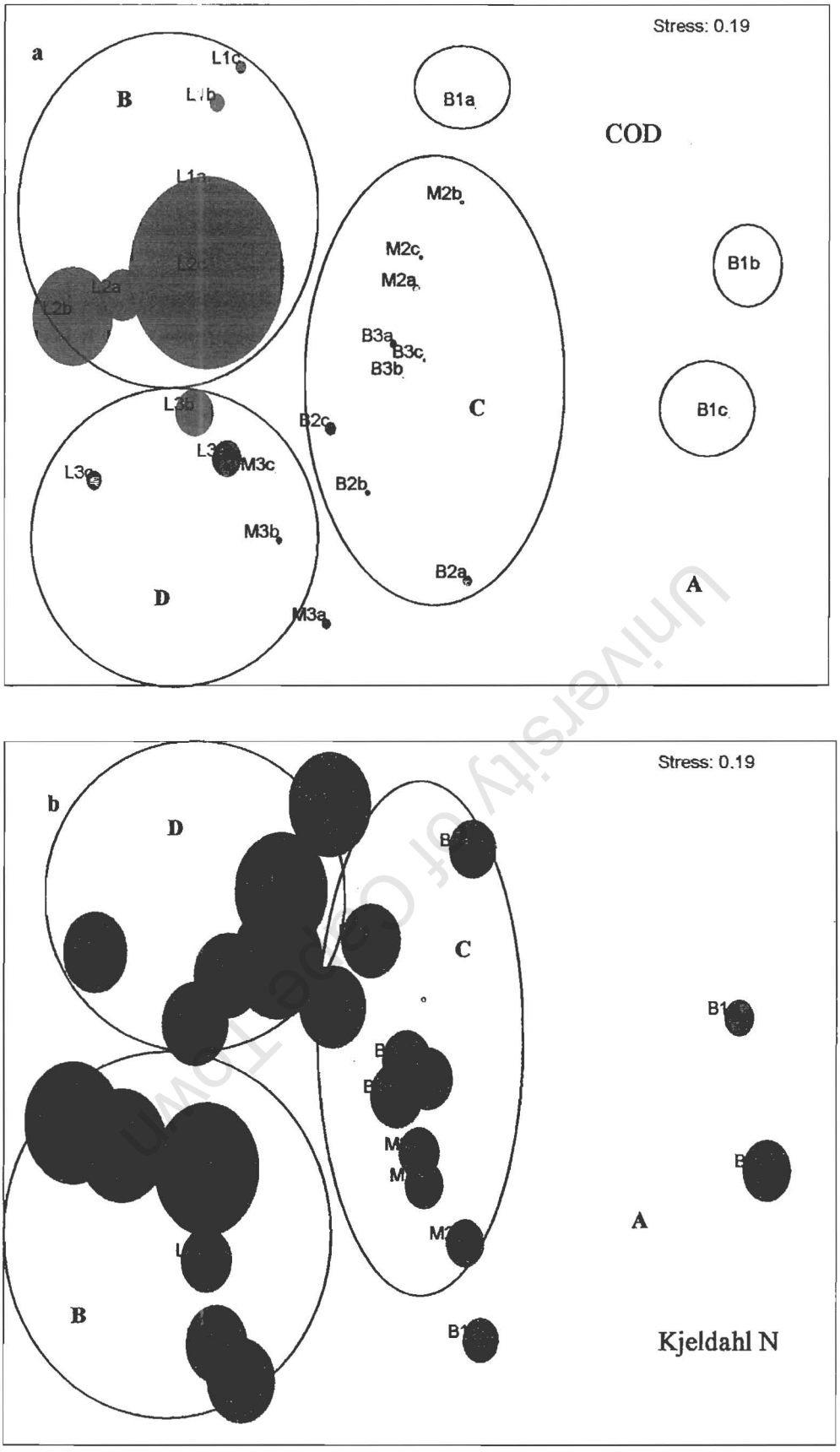


Fig 4.6 (a) The Chemical Oxygen Demand superimposed as circles on the biotic plot, where the size of the circle reflects the value. (b) Kjeldahl Nitrogen superimposed on the biological data.

4.4 CONCLUSION

The results show that there is concordance between the analysis of the biomass and abundance data, both patterns are similar; therefore either measure of the biotic data can be used to study macrofaunal communities. The four groups shown by cluster analysis revealed four groups based on transect and some on depth. A closer look at Group A reveals that the low diversities of these replicates is related to them being species poor "outliers". Apart from sample B2a all replicates group together. Sample B2a seems genuinely different from other B2 replicates in that both numerical and biomass analyses, and both dendrogram and MDS analyses group it apart, in both cases closer to B3. It is suspected that, the ship may have moved from one patch to another during sampling. The shift appears to have affected faunal distribution and not sediment grain size as such, hence COD and Kjeldahl N do not show any changes. The use of higher taxonomic level (Class or Order) may be applicable to large-scale pollution impact studies, but is not sensitive enough to detect natural variability at a local scale.

For each analysis, several species contributed to the overall dissimilarity between each set of groups. The primary contributors came from the Polychaeta, Amphipoda, Pelecypoda and Gastropoda. Based on sediment particle size groupings ("muddy" or "sandy"), there is a general agreement in terms of indicator species between the muddy and sandy groups. Groups B and D are groups of mud and Groups A and C are groups of sand. The perfect indicators are those species, which are abundant in one group and entirely absent to the other. The presence of certain species in one group and not in the other indicates that certain minimal conditions have been met. The superior tolerance of stressful conditions and superior invasion abilities may be of concern in this case. The pelecypod, *Lasaea sp.* amphipod, *Ampelisca brevicornis, Urothoe sp. Ampelisca diadema* were consistently more abundant in

muddy groups. An unidentified gastropod, and an amphipod; *Photis sp*. were more abundant in sandy sediments.

By overlaying sediment type on the ordinations (Figure 4.5a, b), a pattern was discerned which appeared to relate to sediment type. Group B and D are comprised mainly of muddy and deeper samples off Lovu and Mbokodweni. Group C is comprised of coarse, shallower Mbokodweni and deeper Brighton Beach stations. While the three "outliers" (Group A) are defined as sandy, they also show strong affinity with one another in terms of COD and Kjeldahl Nitrogen. The high values of COD and Kjeldahl Nitrogen in muddy samples are expected in that the patches of mud are naturally rich in organic matter and also contain detritus, which therefore, requires large amount of oxygen to oxidize organic and inorganic material. Therefore, high COD provides potential for oxygen depletion in the receiving waters

CHAPTER FIVE

MEIOFAUNAL COMMUNITY PATTERNS

CHAPTER 5: MEIOFAUNAL COMMUNITY PATTERNS

5.1 BACKGROUND

Heip *et al.* (1988) pointed out some potential advantages of using meiofauna in pollution monitoring; e.g. meiofaunal communities are inherently stable (both quantitatively and qualitatively and on a seasonal and year to year basis) because the majority of meiofauna do not have planktonic stages in their life cycles. The meiofauna respond rapidly to pollution due to their fast generation times, and are abundant and diverse in habitats, which are subjected to considerable natural, physical and chemical stress. Meiofauna are considered to be a taxonomically difficult group and analysis to species level is very time consuming (Warwick, 1988a). Ellis (1985) stated that taxonomic sufficiency is required only to level that indicates the community response. There are theoretical advantages to conducting analysis to a level of major groups, the most important being that the two most important natural variables affecting meiofauna distribution offshore (sediment grain size and water depth) usually affect meiofauna more by species replacement than by changes in the proportion of major taxa present (Warwick, 1988b). D'Aubrey-Whitehorn (1986) stated that freshwater influence in KwaZulu/Natal south coast is responsible for the depletion of meiofaunal populations. The meiofauna analysis is performed using data identified to taxonomic levels higher than family. Methods are given in section 2.4.

5.1.1 Abundance data

Figure 5.1 shows a dendrogram depicting station affinities, based on the 4^{th} root transformations of meiofaunal abundance using the Bray-Curtis measure of similarity and group average sorting. Hierarchical agglomerative clustering revealed 3 major groups (A, B and C) at the 70% similarity level. It is notable that most of the Lovu samples group together

in Group A and the Brighton samples form group B. Of the three main Groups, Group C divides into two subgroups at about 73% similarity level, designated as C1 and C2. C1 consists of the Mbokodweni samples and C2 is formed of the remaining Lovu offshore samples. C2 (L3 station) is also separated from other Lovu station in the macrofauna analysis. This may be linked to environmental factors, and is discussed in section 5.3 below.

Figure 5.2 shows the results of multidimensional scaling (MDS) using the similarity matrix as in the classification. The ordination for the same data set shows the same picture and thus complements the dendrogram pattern. This confirms that the three groups are different and the grouping is based on transects.

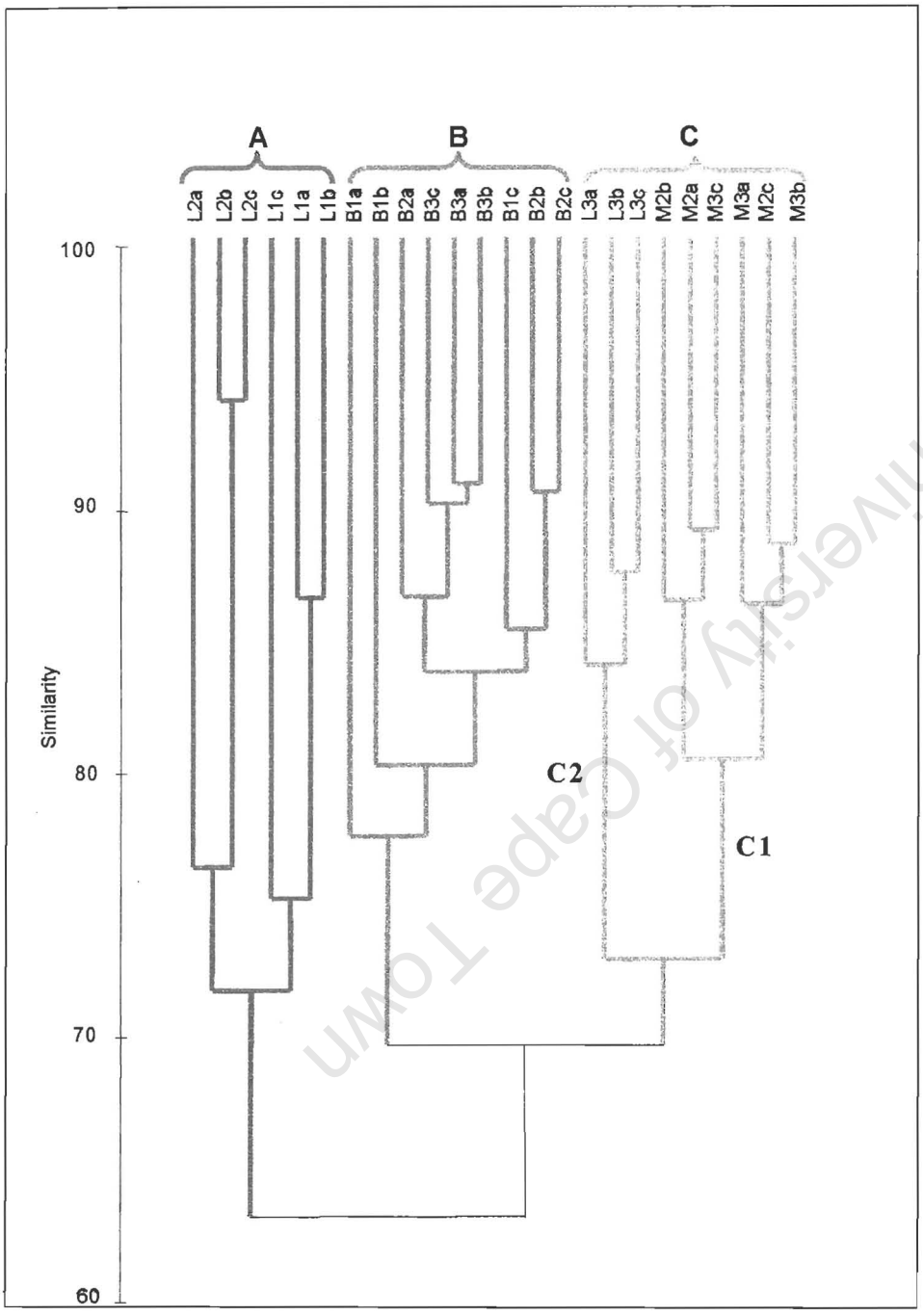


Figure 5.1 MDS plot for meiobenthic samples taken in May 1999 using a Day grab off the KwaZulu Natal coast. L, M and B is for Lovu, Mbokodweni and Brighton beach samples; a, b and c indicate samples from 25, 35 and 45 m mean water depth respectively.

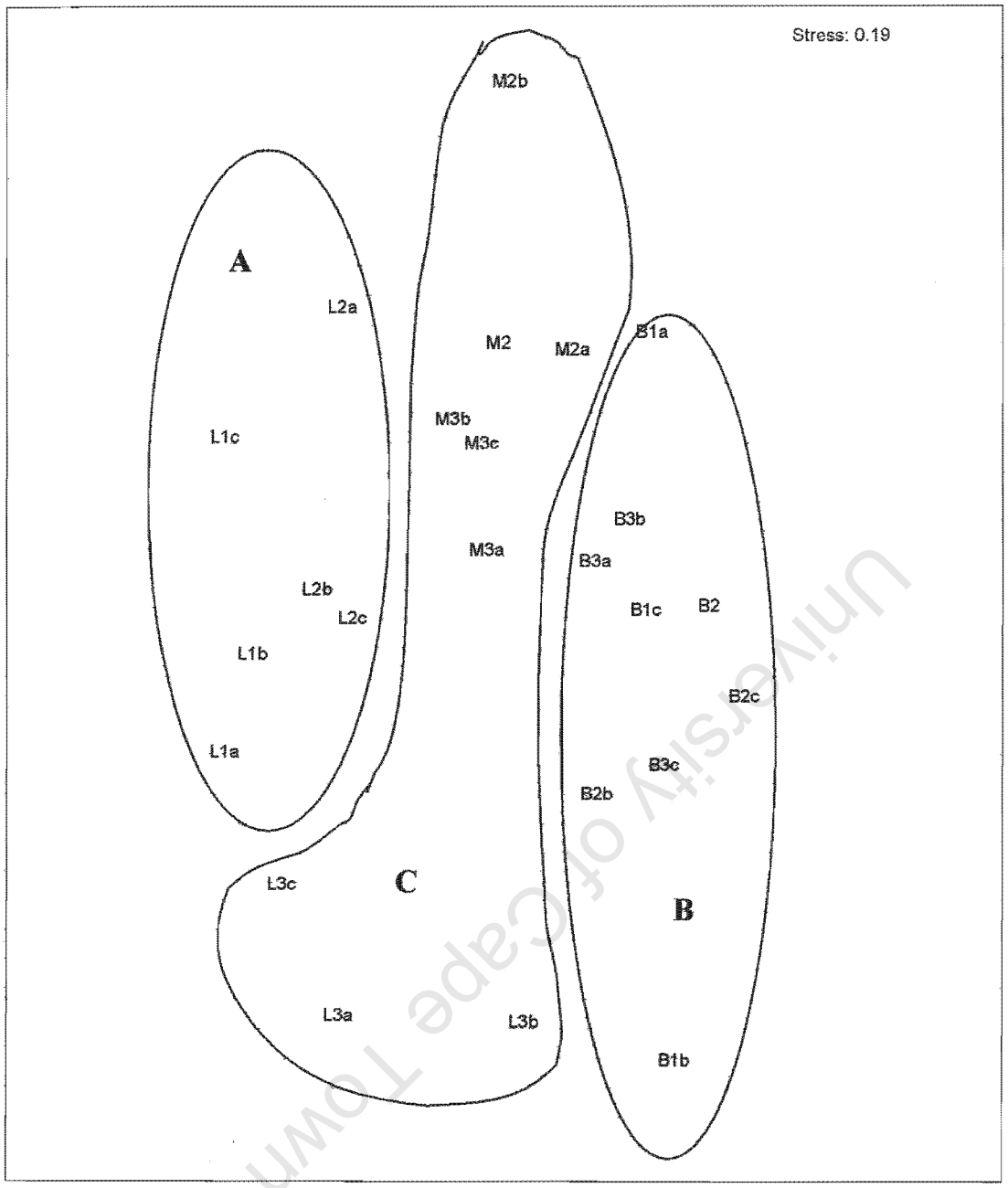


Figure 5.2 MDS plot for the meiobenthic abundance data.

5.2 INDICATOR TAXA

The dendrograms and ordinations produced in section 5.1 above are now tested for taxa primarily responsible for influencing the sample groupings. Samples were divided into three distinct groups which are based on transect. It is important to refer back to the biological data and find which taxa are characteristics of one transect and which taxa are reduced in abundance. The ANOSIM test in chapter 3 revealed that there are major transect to transect differences. The test also indicated that depth; % coarse sand and COD are not major environmental factors for the meiofauna (see section 5.4).

Three separate analyses were performed using the 4^{th} root abundance data. Tables 5.1, 5.2 and 5.3 show the results of SIMPER for treatments, A&C, A&B and C&B. The table lists the average abundance of each meiofaunal taxa in one group and the average abundance in the other group. The arbitrary cut-off percentage of 50% was chosen in order to limit the taxa list to manageable size. Taxa beyond 50% cumulative percentage were contributing less than 8% to the sample groupings and were excluded from the interpretation. (Appendix 3 gives the 90% cut-off percentage results).

Table 5.1 The percentage contribution of each species to the separation of groups A&C, based on classification and ordination results. An arbitrary cut-off percentage of 50% dissimilarity was chosen. The more abundant groups are highlighted in bold type. Average dissimilarity between groups A&C = 30.92. N is the number of samples in each group.

TAXONOMIC GROUP	GROUP A Av Abundance N=6	GROUP C Av Abundance N=9	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Harpacticoida	8.50	**104.44**	14.52	14.52
Gastrotricha	0.00	**11.00**	10.60	25.12
Ostracoda	4.00	**16.56**	8.87	33.99
Annelida	**10.83**	**13.00**	8.80	42.79
Amphipoda	**6.50**	1.89	8.27	51.06

These groups represent shallower samples of Lovu River (Group A) and the combination of Mbokodweni and deeper Lovu samples (Group C). The principal contributor was the Harpacticoida, which was found to be twelve times more abundant in group C than in group A and contributed 14.52% to the separation between group A and group C. Other species which were more abundant in group C were the ostracods and annelids. The gastrotrichans were perfect indicators and are only found in group C. The ANOSIM test for the meiofauna (section 3.2.1) showed that even though these two groups are different the degree of separation is very low. This is because deeper samples of Lovu transect separated from group A and are combined with Mbokodweni samples (Group C).

Table 5.2 The percentage contribution of each species to the separation of groups A&B, based on classification and ordination results. An arbitrary cut-off percentage of 50% dissimilarity was chosen. The most abundant groups are highlighted in bold type. Average dissimilarity between groups A&C = 35.96. N is the number of samples used in each group.

TAXONOMIC GROUP	GROUP A Av Abundance N=6	GROUP B Av abundance N=9	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Harpacticoidea	8.50	**111.11**	12.78	12.78
Gastrotricha	0.00	**3.89**	9.95	22.73
Nemertea	**24.17**	4.89	8.55	31.28
Copepoda	0.50	**4.44**	8.50	39.78
Ostracoda	**4.00**	1.11	8.20	47.98
Amphipoda	**6.50**	0.78	7.73	55.71

Group A consists of shallower Lovu samples and group B is a group of Brighton Beach samples. Harpacticoida were found to be the major contributors for the separation of group A and group B. They are more than ten times abundant in group B then in group A contributing 12.78% to the separation between these two groups. Gastrotricha and Nemertea were found to be other main contributors to the separation of the groups. They contributed 8.55% to the separation. The ANOSIM test in section 3.2.1 revealed that these groups were very different.

Table 5.3 The percentage contribution of each species to the separation of groups C&B, based on classification and ordination results. An arbitrary cut-off percentage of 50% dissimilarity was chosen. The more abundant groups are highlighted in bold type. Average dissimilarity between group A&C = 33.82%. N is the number of samples in each group.

TAXONOMIC GROUP	GROUP C Av Abundance N=9	GROUP B Av Abundance N=9	PERCENT DISSIMILARITY	CUMULATIVE PERCENT DISSIMILARITY
Nemertea	**55.00**	4.89	14.09	14.09
Ostracoda	**16.56**	1.11	11.69	25.79
Annelida	**13.00**	**45.11**	11.50	37.29
Kinorhyncha	1.00	4.67	8.59	45.88
Gastrotricha	**11.00**	3.89	8.26	54.14

Group C is a combination of deeper samples from Lovu and Mbokodweni Rivers and Group B consists of Brighton Beach samples. The principal contributor to separation of groups is the Nemertea, which were more than ten times more abundant in Group C than in group B and contributed 14 % to the separation between the two groups. Other groups that were more abundant in Group C than in group A were the Ostracoda and Gastrotricha. Annelida were abundant in both groups and only contributed 11% to the separation between these groups. There were no perfect indicators between Group A and Group C.

5.3 LINKING BIOTIC PATTERNS TO ENVIRONMENTAL FACTORS - MEIOFAUNA

5.3.1 Background

Field *et al.* (1982) presented a strategy for analyzing marine biological survey data and relating the biotic patterns to environmental data. This approach analyses the biological data 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 This section therefore seeks the best possible reconciliation between sediment grain size and COD's and in an attempt to assess the relative importance of each variable in influencing community structure. Table 4.7 shows the measured environmental variables at each sampling station.

5.3.1.1 Grain size

The abundance data for the macrofauna were 4^{th} root transformed and subjected to non-metric MDS, using the Bray-Curtis measure of similarity and the results presented in Figure 5.3a. Warwick (1988b) showed that the two principal natural variables affecting meiofauna distribution offshore (water depth and sediment granulometry) usually affect the meiofauna more by species replacement than by changes in the proportion of major taxa present. In order to assess what part sediment grain size may have played in the observed groupings, the ordination (Figure 5.3b) was replotted with the sediment type ("muddy" and "sandy") shown in places of station names. The "muddy" stations were defined as those, which yielded a percentage mud in excess of 2% in combination with a COD value greater than 0. mg O_2 g-1. The ordination shows a clear predominance of mud in group A, and sand in group B, while group C contains a mixture of both muddy and sandy samples.

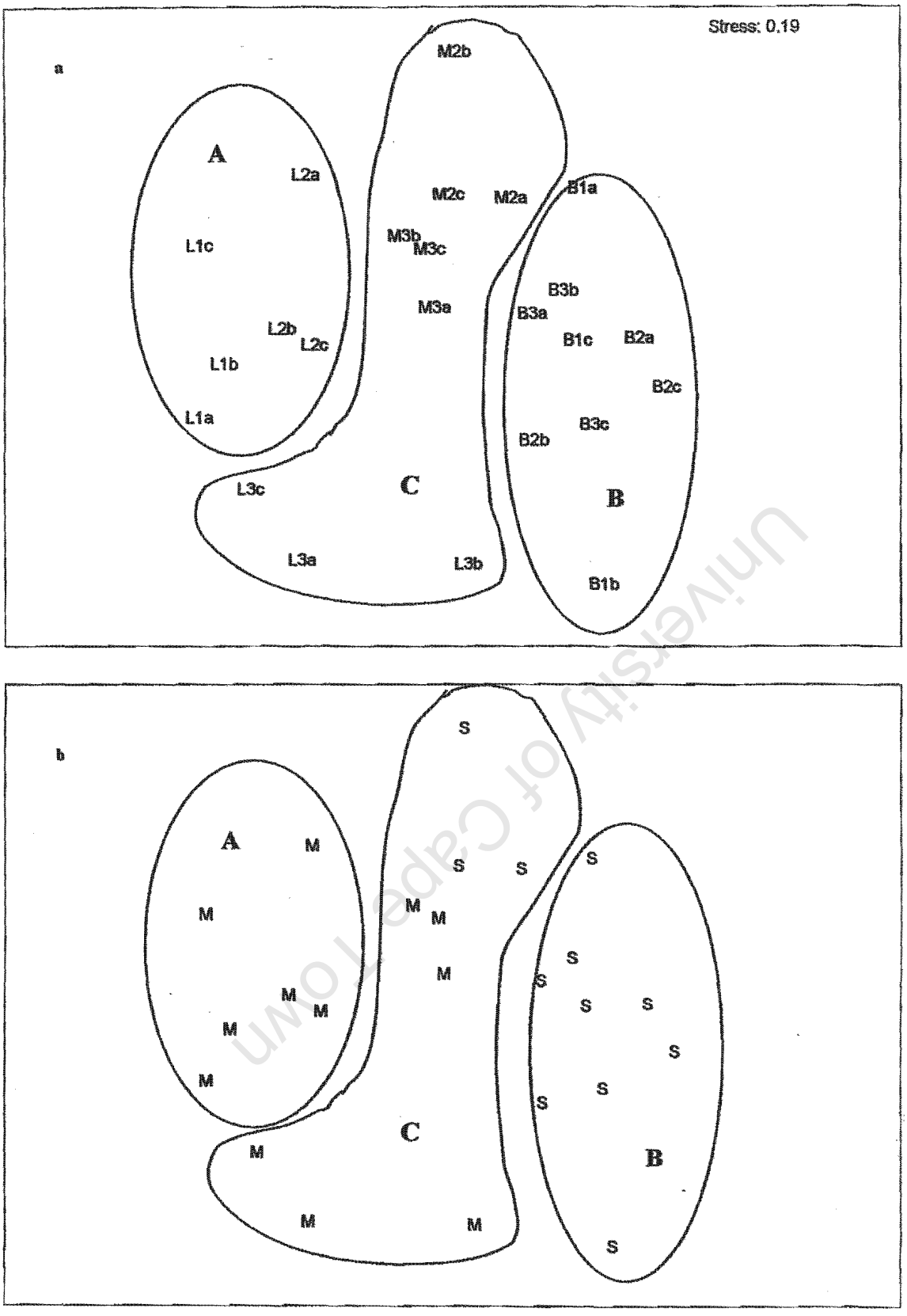
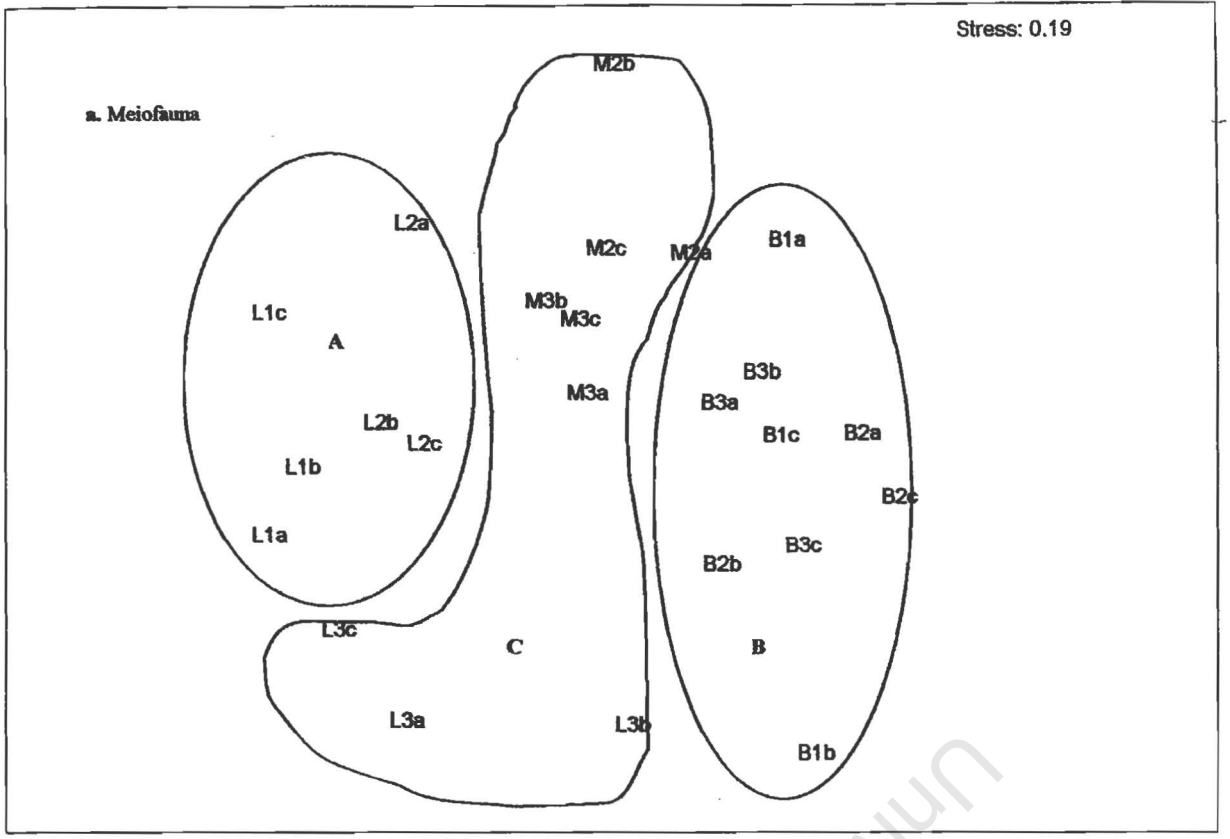


Figure 5.3 (a) MDS plot for the meiobenthic abundance data. (b) Sediment type (M and S for the "muddy" and "sandy" sediments respectively) is indicated in the plot.

5.3.1.2 Chemical Oxygen Demand

The COD values (Table 4.7) varied considerably between stations and showed a clear positive correlation with percentage mud. Sample L2b and L2c had the highest COD values of 1.799 ugO_2g and 3.499 ugO_2g, respectively. These samples also have highest values of percentage mud. Extreme oxygen deficiency (anoxia) is often associated with rotting organic material and may be accompanied by a black layer in the sediment and sulphide smell. Figure 5.4b clearly shows high values (larger circles) to the left of the ordinations. The lower COD values are scattered in the middle and towards the right of the ordination. Group A has largest circles, Group C intermediate circles and Group B the smallest circles of the three groups. As indicated in section 5.3.1.1, Group B is composed of samples from sandy sediments and hence has relatively low values of COD.



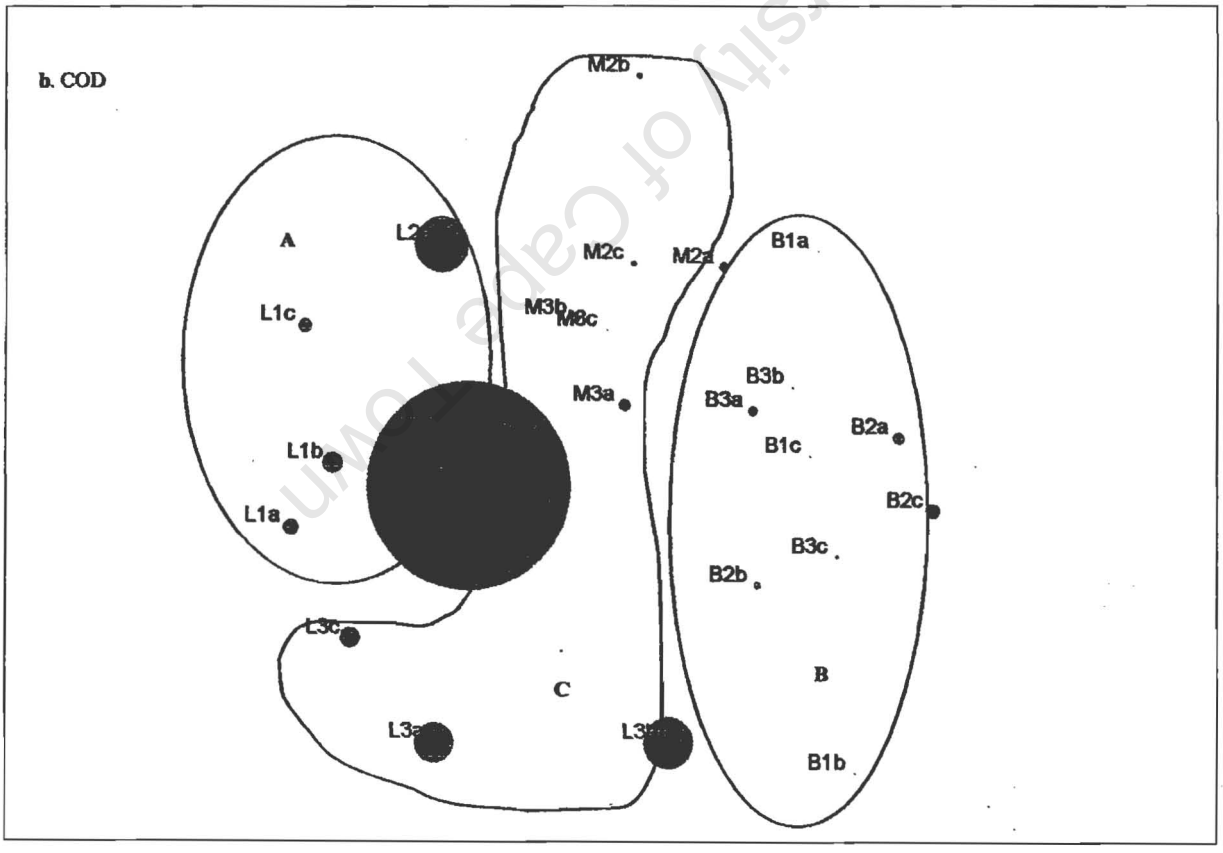
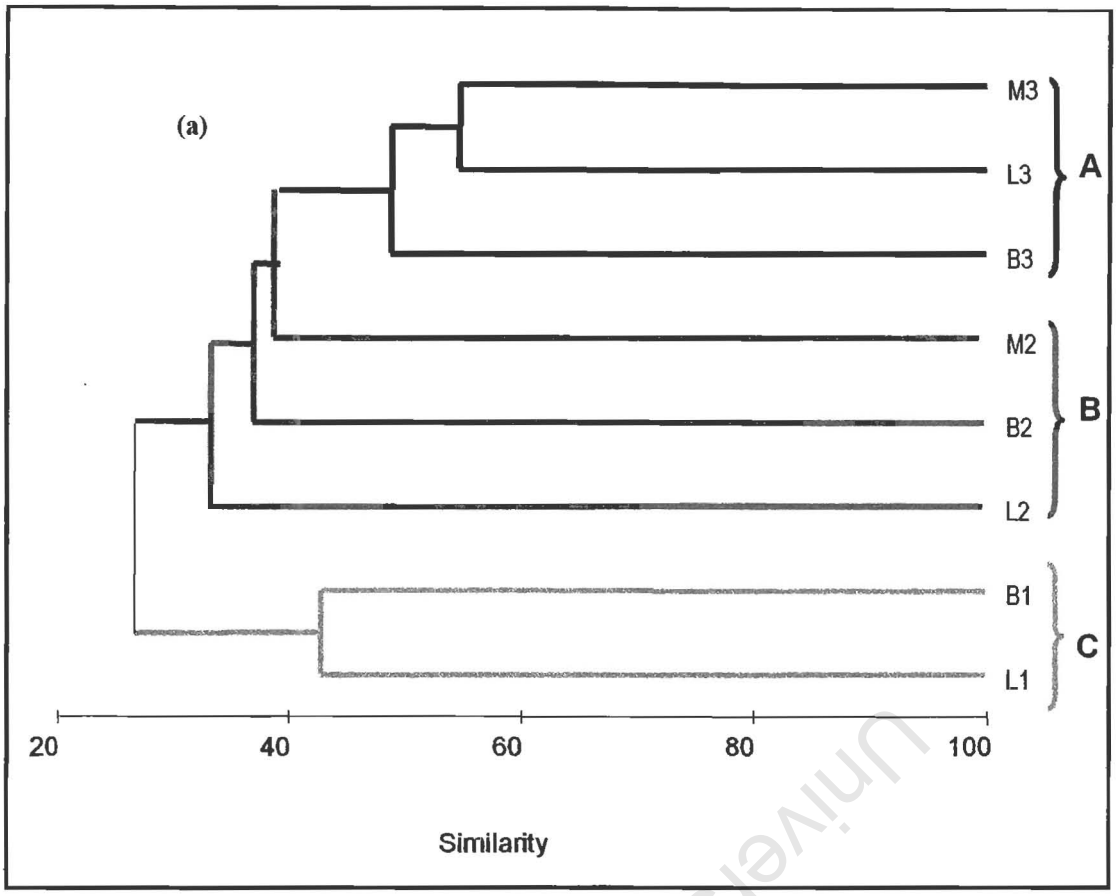


Figure 5.4 (a) MDS plot for the meiofauna abundance data. (b) MDS for COD values (larger circles indicate higher value of COD) superimposed on biotic data.

5.4 MACROFAUNA VERSUS MEIOFAUNA

One of the objectives in this study was to compare patterns of response by macrofauna to environmental conditions to those of meiofauna. This was kept simple by pooling replicates at each station for both the meiofauna and macrofauna abundance data. The sensitivity of measured environmental variables was then considered in the interpretation of these results.

The macrofauna dendrogram based on pooled replicates revealed three groups, A, B and C at the 35% similarity level (Figure 5.5a). Group A consist of three deep stations, Group B links onto this and consists of stations at 35 m depth, while group C consist of shallow stations. The ordination (Figure 5.5b) confirms groups A and C but splits Group B. These results suggest that depth is a more important factor than distance alongshore for the macrofauna at this scale of up to 40 km. This was also evident in the ANOSIM test (chapter 3) of the macrofauna, in that even though both macrofauna and meiofauna show significant differences, depth produced relatively low values of R and significant levels.



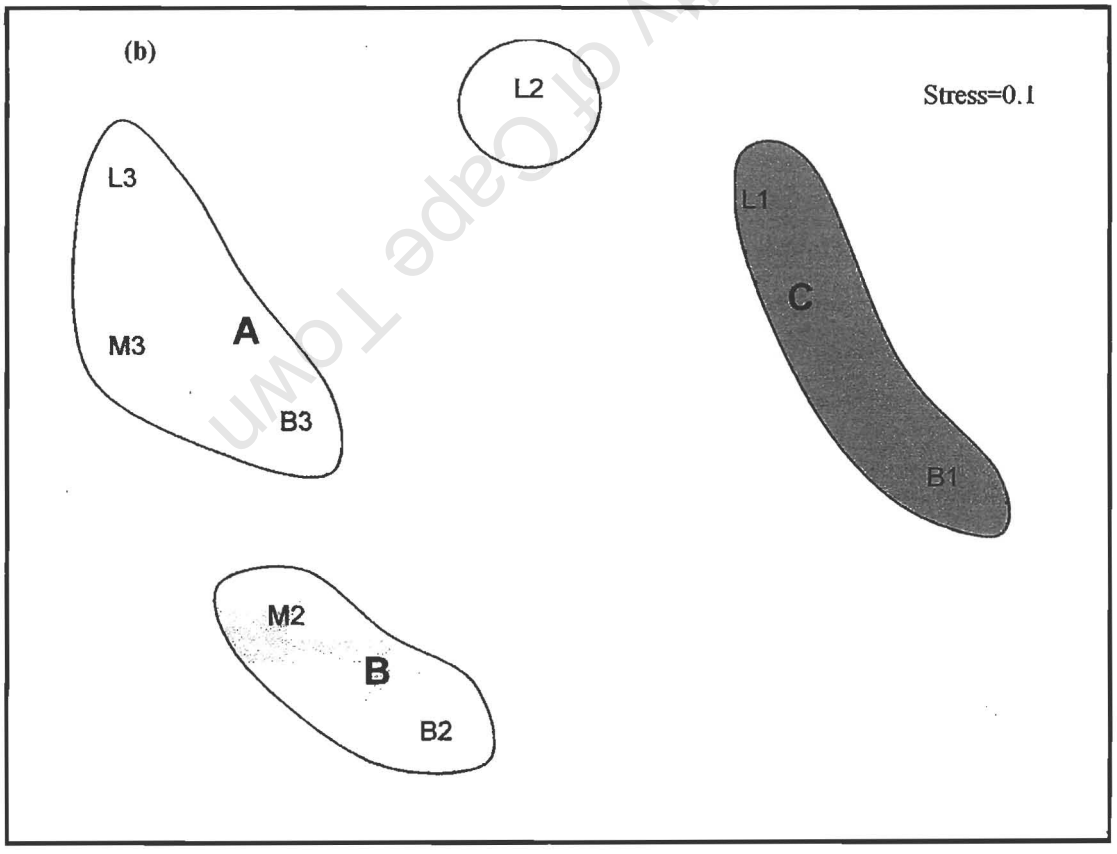
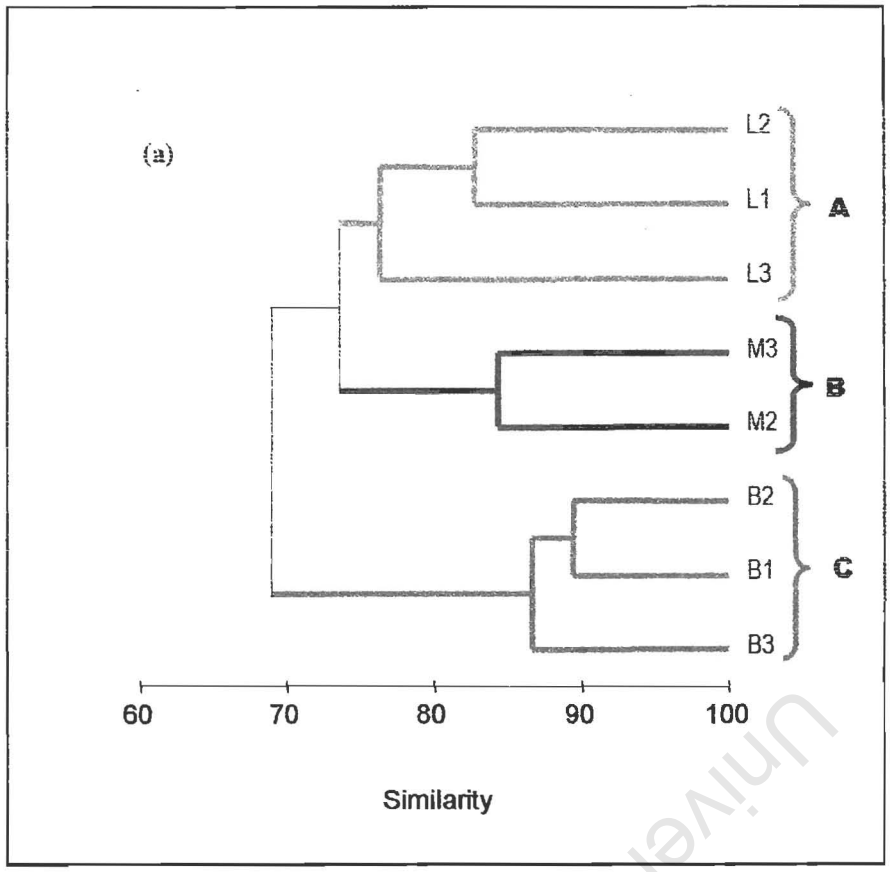


Figure 55 (a) Dendrogram and, (b) ordinations of macrofauna "pooled" replicates for samples taken by a Day grab in May 1999.

The meiofauna replicates were also pooled at each station and the resulting dendrogram is shown in Figure 5.6a. Groups A (L1, L2 and L3); B (B1, B2 and B3) and C (M1, M2 and M3) were identified at the 40% similarity level. The ordination of the same data set (Figure 5.6b) shows a similar pattern with groups A, B and C clustered together. The meiofauna results show each transect to be different. Again even though ANOSIM test (sections 3.2.1 and 3.2.2) of the meiofauna showed that both position alongshore and depth are significant factors, distance alongshore is much more important than depth at this scale.



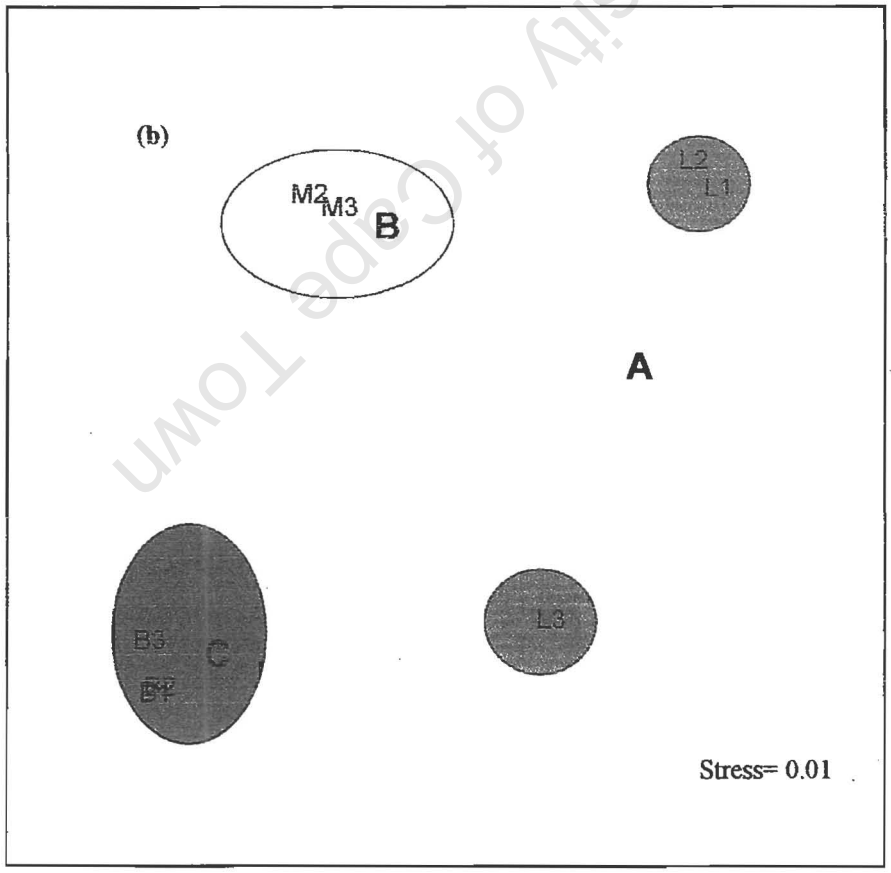


Figure 5.6 (a) Dendrogram and, (b) ordination of "pooled" meiofauna replicates for samples taken by a Day grab in May 1999.

5.5 CONCLUSION

The three groups revealed in cluster analysis of the meiofauna grouped the samples according to the position along the coast. The separation of Lovu station, L3 from other Lovu stations show that there may be other environmental factors, which are responsible for its separation. Apart from sample B2a all other replicates group together. This anomaly was also noticed in the macrofauna case and was related to the possibility that a ship may have drifted from one patch to another during sampling.

The three groups were classified either as "muddy" or "sandy" and the meiofauna groups responsible for the dissimilarity were identified. Harpacticoida and Ostracoda were prominent indicators for sandy sediments. Even though harpacticoids were found in sandy sediments, Annelida were characteristic organisms of the muddy sediments. It may happen that different species of harpacticoids have different sediment type preferences.

Overlaying sediment grain size on the MDS plot showed that Group A, shallower Lovu samples has muddy sediment. The intermediate Group C consists of mud and sand, and Group B consists of sand. The muddy sediments show high Chemical Oxygen Demand (COD) values. These patterns are expected considering the fact that Groups A and C are situated close to riverine sources of mud (Lovu and Mbokodweni) and Group B is situated off Brighton Beach where there is no freshwater influence.

Comparing macrofaunal and meiofaunal sensitivity by pooling replicates showed that the two components react differently to depth. With the macrofauna, even though position along the coast is a major factor, depth was found to be much more important in shaping community structure than position along the coast. This pattern is not evident in the meiofauna, which are

less sensitive to depth than to position along the coast. Again this finding may be related to the fact that the meiofauna was analyzed to taxonomic levels higher than family. Analyzing meiofauna to lower taxonomic levels (as in macrofauna) and comparing sensitivity with that of the macrofauna is a concern for future studies.

CHAPTER SIX

ASSESSING STRESS LEVELS

CHAPTER 6: ASSESSING STRESS LEVELS

6.1 BACKGROUND

Warwick *et al.* (1987) found the distributional (ABC) methods to be sensitive indicators of natural physical and biological disturbance as well as pollution-induced disturbances over both spatial and temporal scales. The curves rank species in order of importance on the x-axis and show the cumulative percentage of each species in numbers or biomass on a cumulative scale (called percentage dominance) on the y-axis. When the community is approaching maturity, the biomass becomes increasingly dominated by one or a few large species, each represented by few individuals (Warwick *et al.* 1993a). The numerical dominants are smaller species. Hence, when plotted as k-dominance curves, 'numerical diversity' is less than 'biomass diversity', so that the line for abundance lies well below the line for biomass, since the dominant species form a much larger proportion of the total biomass than they do of the total numbers (Figure 6.1a).

In theory, under stress (natural physical and biological or pollution-induced disturbance), large competitive dominants are eliminated and the biomass and abundance curves are closely coincident and may cross each other one or more times (Fig 6.1b).

Under severe disturbance, benthic communities become increasingly dominated by one or a few very small opportunistic, r-selected species and few larger individuals are present. Hence, 'numerical diversity' is greater than 'biomass diversity' (Figure 6.1c).

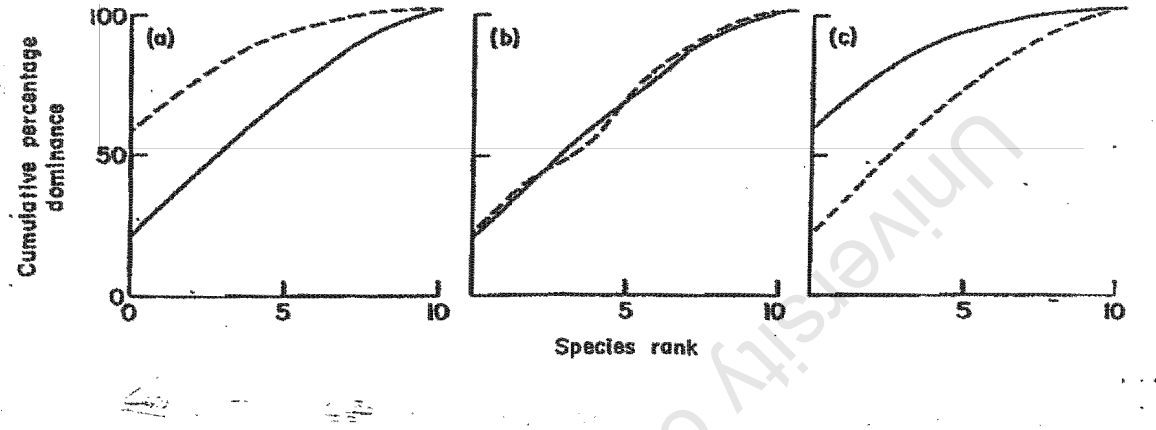


Figure 6.1 Hypothetical k-dominance curves for species abundance showing unstressed (a), moderately (b) and heavily stressed (c) conditions (after Warwick 1986).

Meire and Dereu (1990) defined stress as perturbation applied to a system by a stressor, which is foreign to that system or which may be natural to it, but, in the instance concerned is much greater than usual. Distributional techniques are graphical methods proposed specifically for assessing biological community response to stress (Warwick *et al.* 1993b). This study attempts to investigate the sensitivity of Abundance Biomass Comparison curves (ABC) to natural physical and biological disturbance. Either of these can act in the same manner as pollution-induced disturbance to maintain benthic communities at an immature successional stage, dominated by small opportunistic species. Weston (1990) found a false impression of disturbance when large number of small individuals occur (usually of only one or a very few species) in apparently unperturbed situations. This problem is caused by the over dependence of the elevation of the curves on the dominance of the first ranked species,

and can be mitigated by the use of "partial dominance" curves which ignore the first dominant species in ranking them (Clarke, 1990).

6.2 DISTRIBUTIONAL RESULTS

6.2.1 Replicates

Figures 6.2 to 6.4 are graphical representations of the abundance and biomass data of macrofaunal samples from off Lovu River, Mbokodweni River and Brighton Beach plotted as ABC curves. The three sites are interpreted as follows.

Lovu River. Samples L1a, L1b and L1c are "inshore" stations at 25m depths. L1a (W=-0.014) showed a possible slight disturbance with the abundance curve above the biomass curve for most of its length. Sample L1b (W=0.039) showed a marginal disturbance with the abundance curve crossing the biomass curve at one point. Sample L1c (W=0.184) showed an undisturbed condition with the biomass curve above abundance curve throughout its length. For the middle samples (L2a, L2b and L2c) at 35m depths, the sample designated as L2a (W=-0.045) indicated a slightly disturbed state with the abundance curve above the biomass curve for most of its length. Samples L2b and L2c, (W=0.225 and 0.139 respectively) had the biomass curves above the abundance curves, this indicating an undisturbed state. The "offshore" station, i.e. samples L3a, L3b and L3c at 45m depth, with W= -0.008, -0.019 and –0.030 respectively all indicated a possible state of disturbance. The abundance curves appeared above the biomass curves in all three samples (Figure 6.2). The macrobenthic community at these three stations consisted predominantly of small species, with very few large, long-lived organisms present.

Mbokodweni River. Sample M2a, M2b and M2c are 35 m deep and have the W-statistic value of 0.27, 0.254 and 0.165 respectively. They all show the biomass curve to be above the abundance curve. Sample M3a, M3b and M3c at 45 m deep with corresponding W-statistic value of 0.318, 0.107 and 0.32 respectively also show the biomass curve above the abundance curve (Figure 6.3). This suggests an undisturbed state.

Brighton Beach. Samples B1a, B1b and B1c at 25m depth indicate a relatively undisturbed state and have a corresponding values of W=0.139, 0.561 and 0.631 respectively. The middle station, i.e. samples B2a; B2b and B2c at 35m depth generated W-statistic value of 0.139, 0.153 and 0.264 respectively. The deeper stations, i.e. (B3a, B3b and B3c) at 45m depth revealed W-statistic values of 0.206, 0.166 and 0.297 respectively. All graphs for the Brighton Beach samples conformed to the undisturbed ABC curve configuration (biomass curve above the abundance curve).

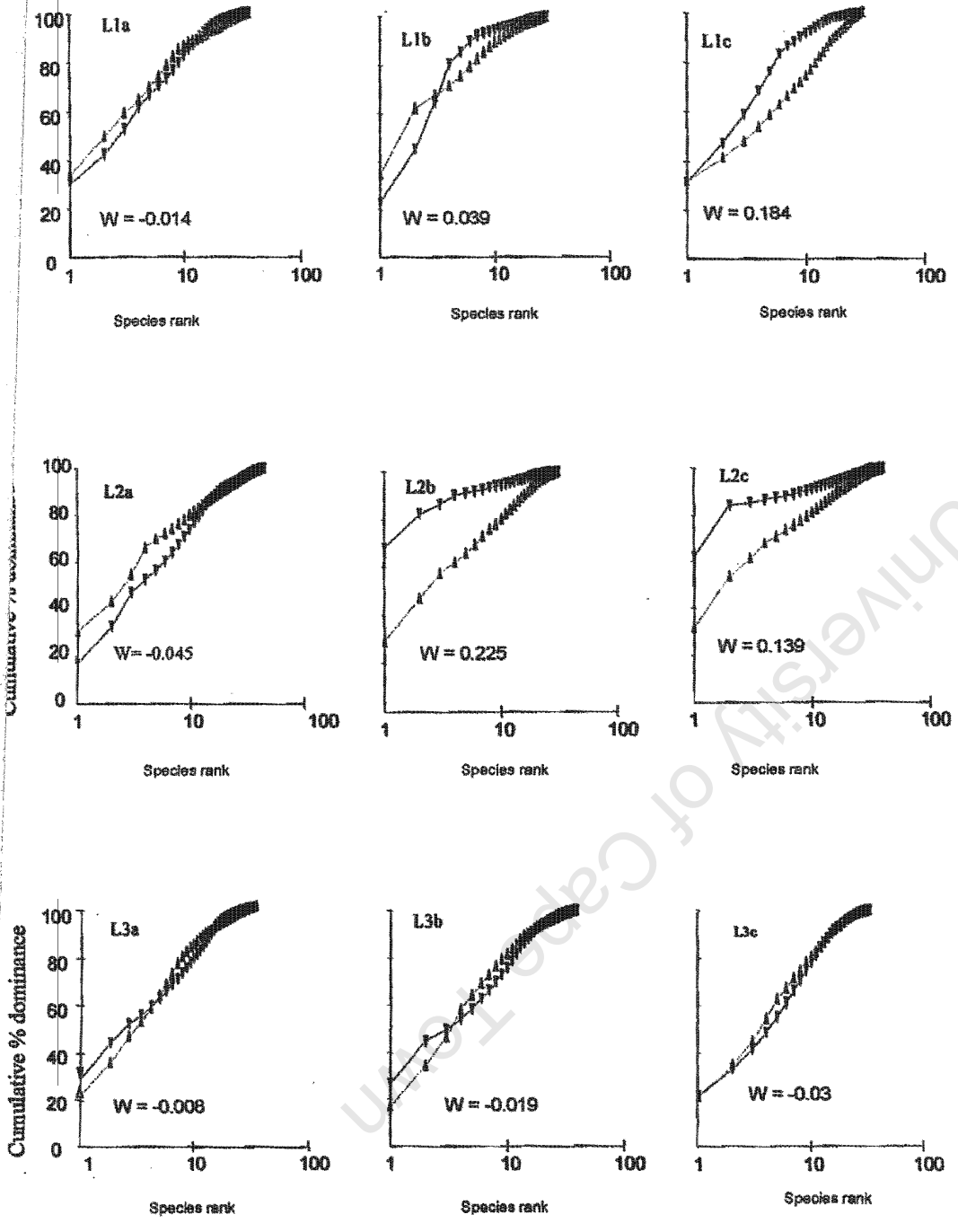


Figure 6. 2 Distributional curves for macrofaunal samples taken of Lovu River mouth, solid triangles indicate biomass and the open triangles indicate abundance.

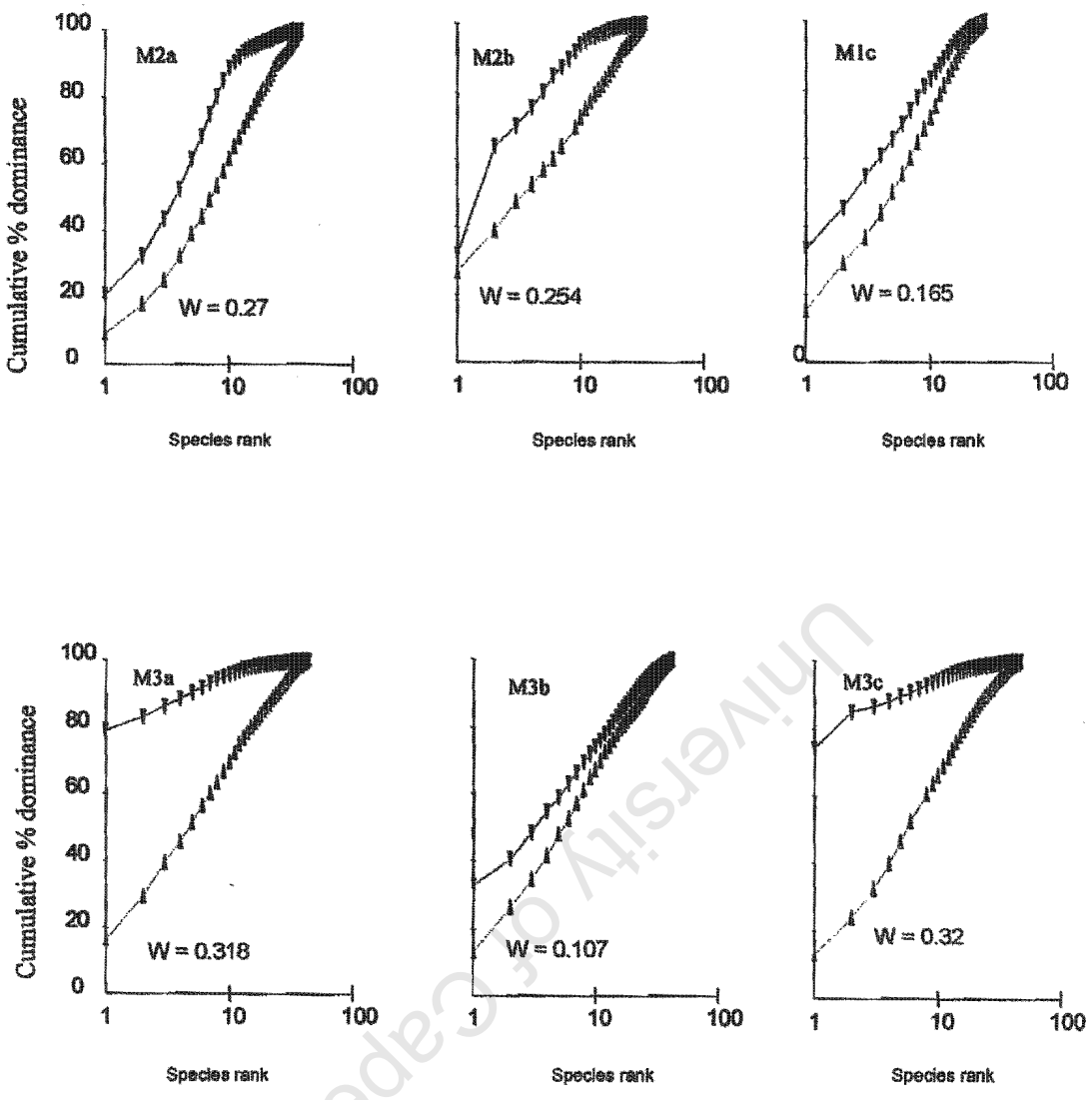


Figure 6. 3 Distributional curves for macrofaunal samples taken off Mbokodweni River mouth. See Figure 6.2 for symbols.

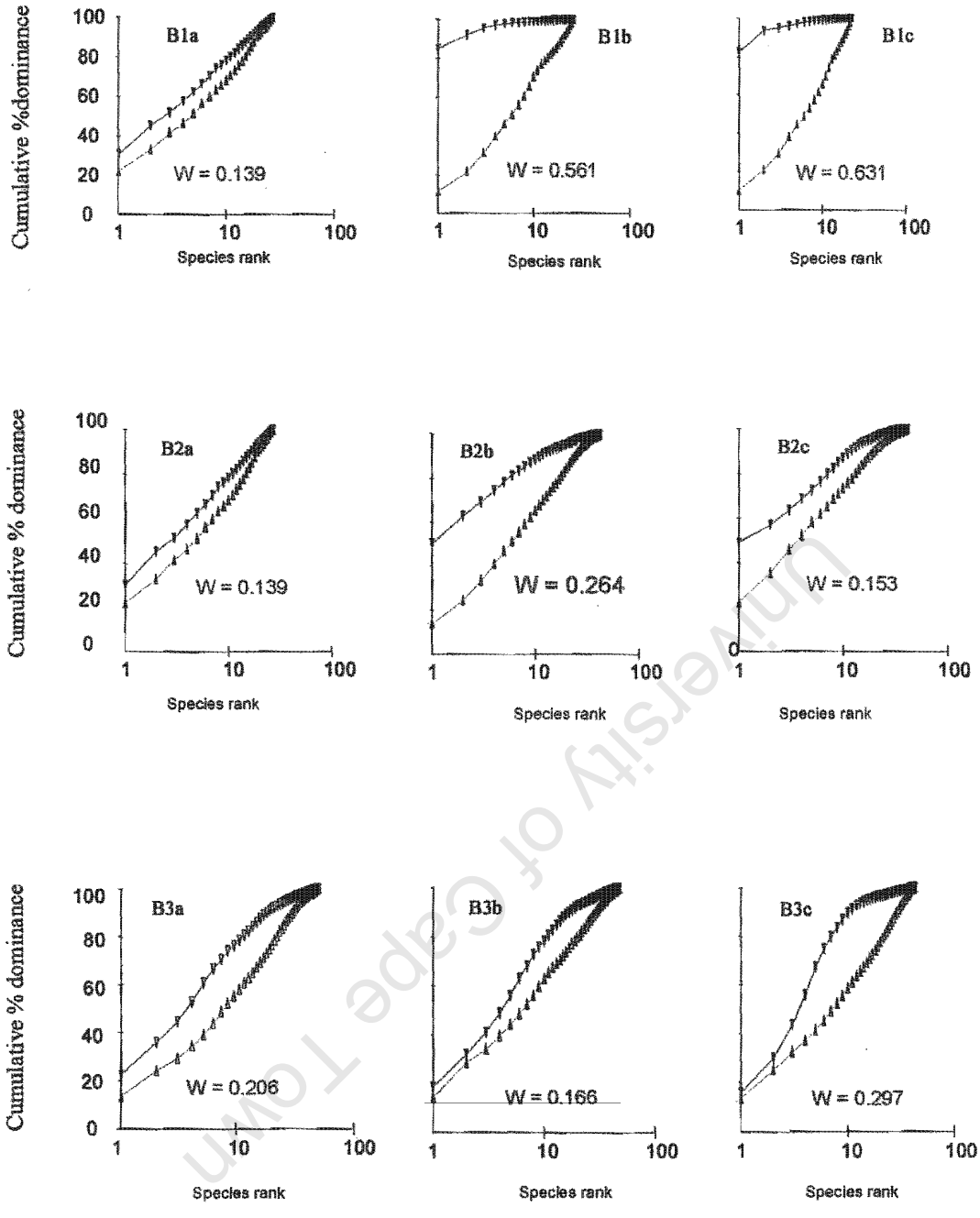


Figure 6.4 Distributional curves for macrofaunal samples taken off Brighton Beach. See Figure 6.2 for symbols.

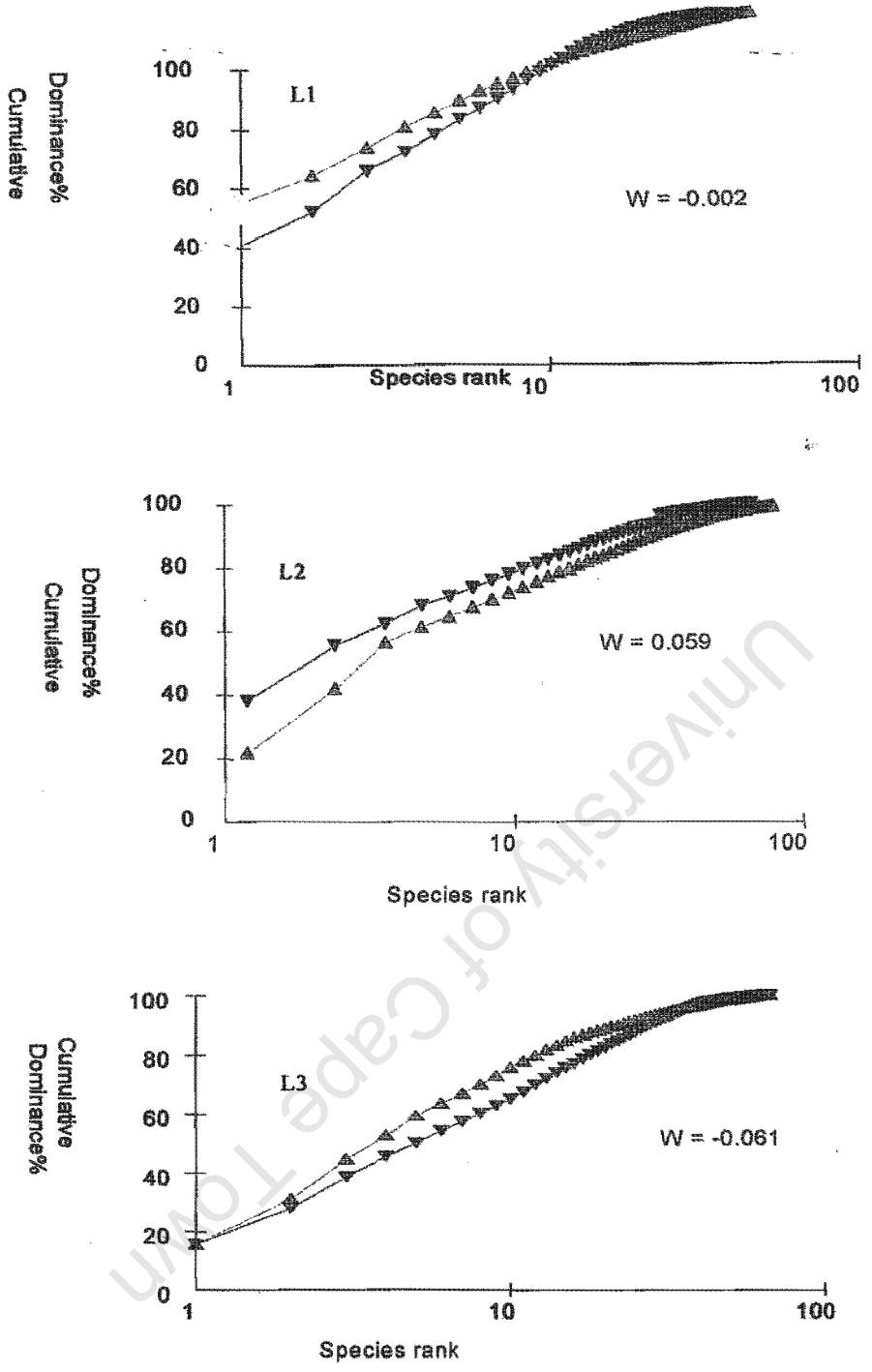


Figure 6.5 Distributional curves for macrofauna samples taken off the Lovu river mouth in May 1999, stations ("pooled" replicates). Darker triangles represent the biomass and lighter triangles represent the abundance.

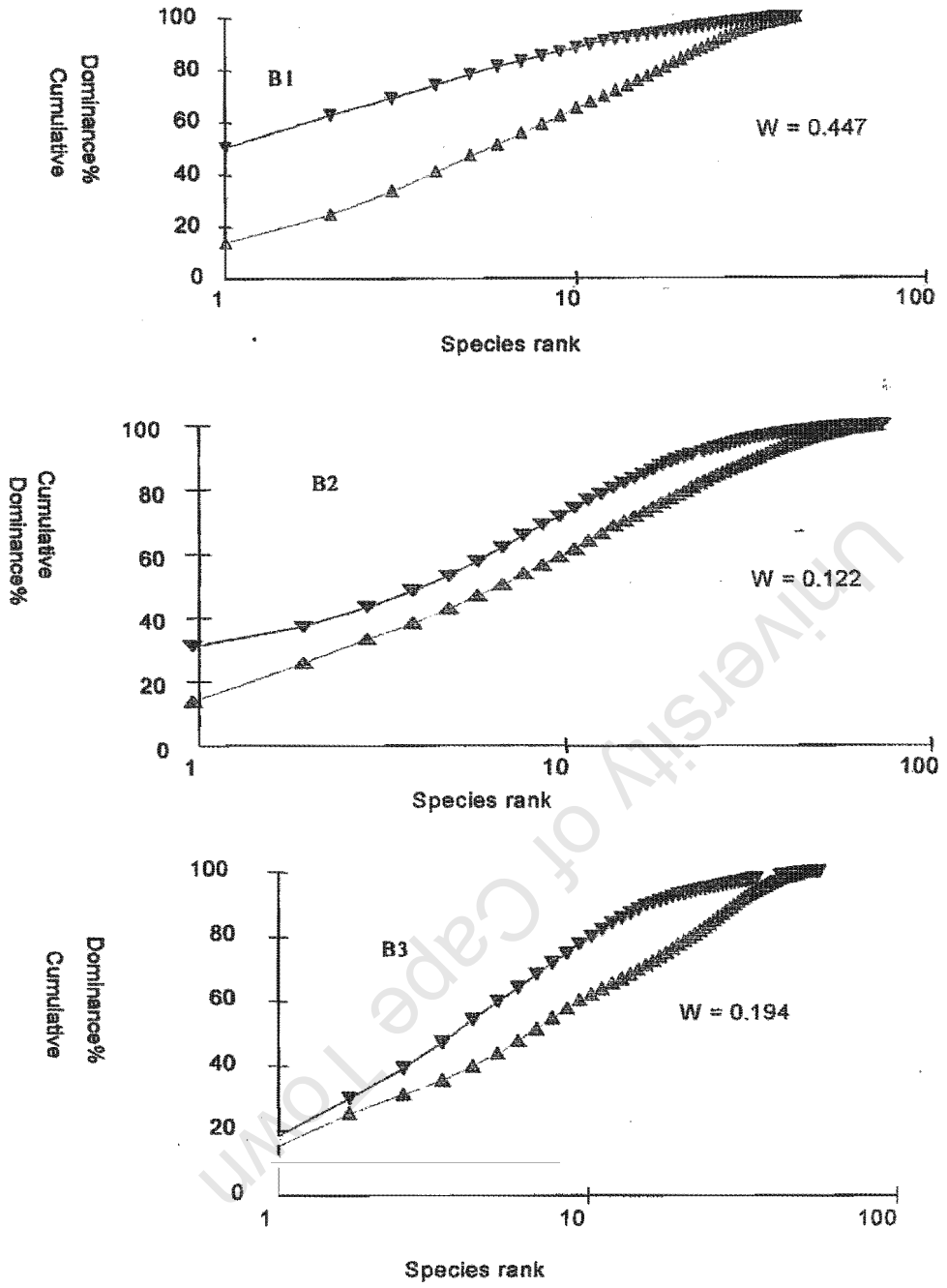


Figure 6.6 Distributional curves for samples taken off the Brighton beach in May 1999, stations ("pooled" replicates). Darker triangles represent the biomass and lighter triangles represent the abundance.

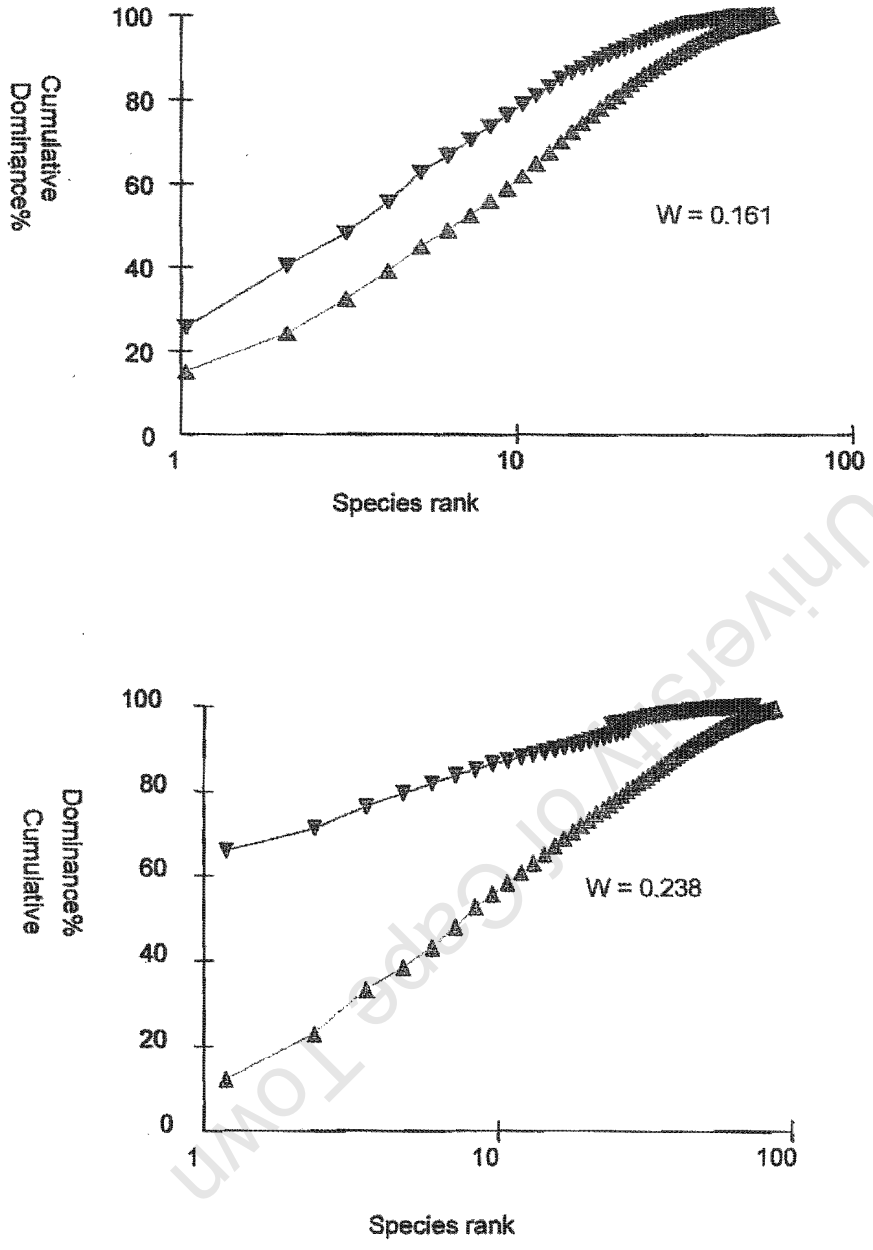


Figure 6.7 Distributional curves for samples taken off the Mbokodweni River mouth in May 1999, stations ("pooled" replicates. Darker triangles represent the biomass and lighter triangles represent the abundance.

6.2.3 Transects

Figure 6.8 is a graphical representation of the Lovu, Mbokodweni Rivers and Brighton Beach transects where data from each station have been combined or pooled, plotted as ABC curves. Of the three sites, Lovu is the only one that showed negative W-statistic value of –0.021. The abundance curve is above the biomass curve, which suggests a disturbed state. Brighton Beach and Mbokodweni transects suggests that they are undisturbed and have W-statistic values of 0.166 and 0.192 respectively. The ANOSIM test (chapter 3) revealed that there are significant differences among these three transect.

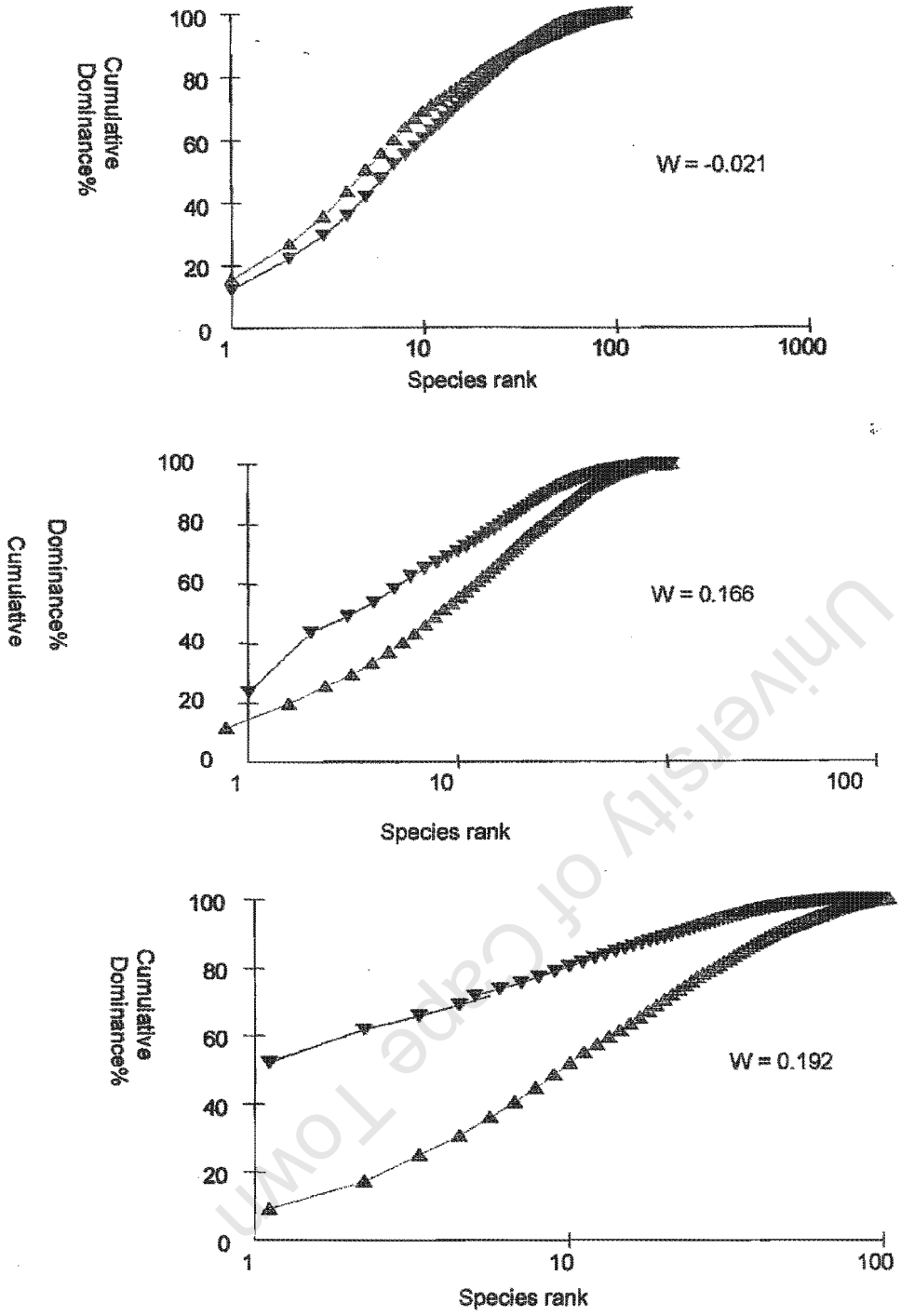


Figure 6. 8 Distributional curves for macrofaunal samples taken off the Brighton beach, Mbokodweni and Lovu river mouth in May 1999 transect (site).

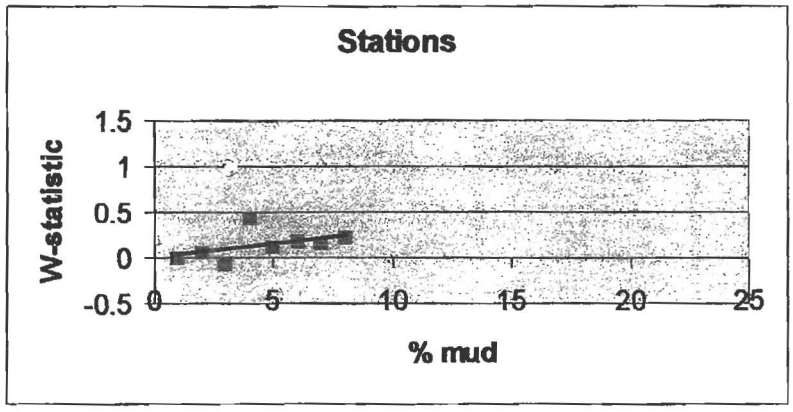
6.3 LINKING THE W-STATISTIC TO ENVIRONMENTAL VARIABLES

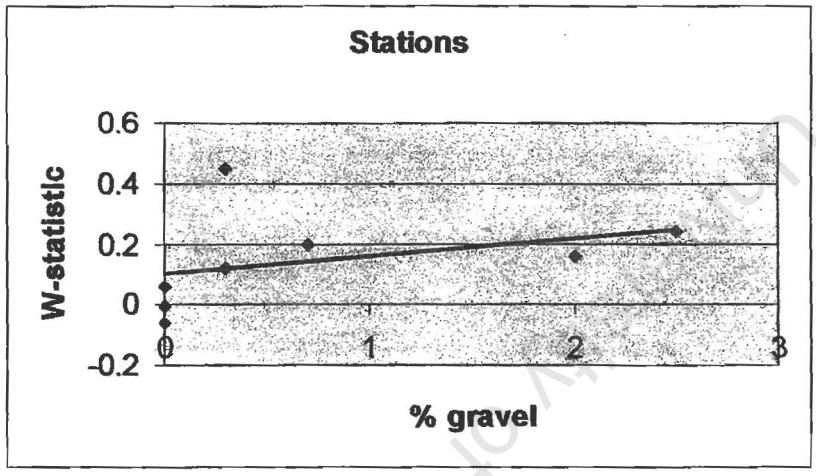
Presenting ABC plots for every sample can be cumbersome when the number of sites, times or replicates is large. It would therefore be convenient to reduce each plot to a single summary statistic. Clearly, some information will be lost in such a condensation: one plots cumulative dominance curves rather than quoting a diversity index precisely because of a reluctance to reduce the diversity information to a single statistic. Nonetheless, Warwick's (1986) contention that the biomass and abundance curves increasingly overlap with moderate disturbance, and transpose altogether for the grossly disturbed condition, is a unidirectional hypothesis and very amenable to quantification by a single summary statistic.

A correlation measure was used to assess whether the W-statistic for each station, % mud, % coarse sand and % gravel vary together, i.e. whether large values of W-statistic are associated with large values of either % gravel, % coarse sand or % mud (positive correlation), whether small values of W-statistic are associated with large values of % mud or % gravel (negative correlation), or whether values in both sets are unrelated (correlation near zero). These correlations were done for every station of Lovu River, Mbokodweni River and Brighton Beach stations. Table 6.1 is a summary of the results of the correlation of W-statistic with % mud and % gravel. Figure 6.9 gives graphical representation of the correlation between the W-statistic and the percentage mud, sand and gravel respectively.

Table 6.1 Results of macrofaunal "pooled" replicates correlation

Station, n=8	Sediment particle size	r^2	p	Significance
L1, L2. L3, B1, B2, B3, M2, M3	% mud	0.078	0.3293	Not significant
L1, L2. L3, B1, B2, B3, M2, M3	% coarse sand	0.014	0.5372	Not significant
L1, L2. L3, B1, B2, B3, M2, M3	% gravel	0.023	0.3886	Not significant





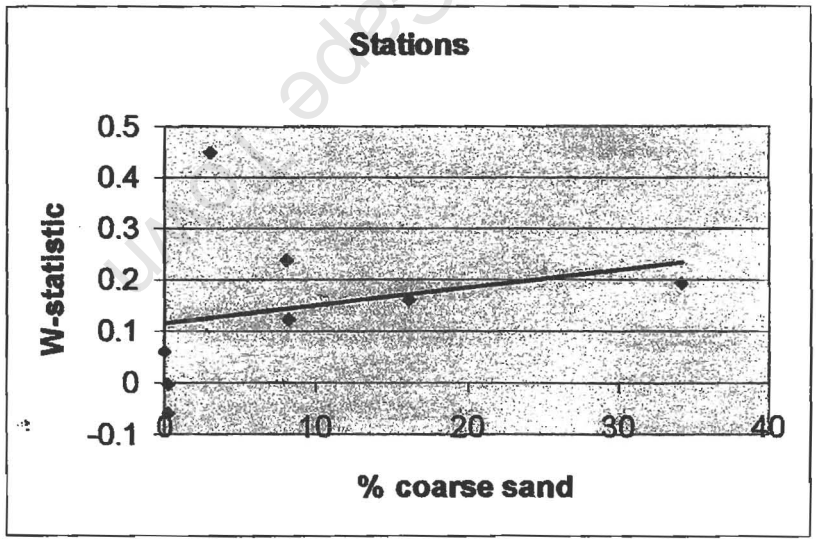


Figure 6. 9 Correlation for the "pooled" data of the W-statistic with % mud, gravel and coarse sand. Dots are co-ordinates.

Percentage mud. The percentage mud was classified as those samples with sediment particle size of less than 0.063mm. From this analysis it was concluded that since p value is greater than 0.10, there is no statistically significant relationship between W-statistic and percentage mud at 90% or higher confidence level. This does not confirm findings of (Winckler, 1999) who found W-statistic to be strongly positively correlated with percentage mud, i.e. as the mud content increases in the sediment, so the W-statistic becomes more positive (undisturbed). This may be related to the fact that conditions are relatively prestine in this study.

Percentage coarse sand. Coarse sand was classified as having a sediment particle size of 0.5 and 1 mm. The values of p and r^2 were found to be 0.5372 and 0.014 respectively. Since the p value is greater than 0.10, there is no statistically significant relationship between the W-statistic and percentage coarse sand at the 90% or higher confidence level.

Percentage gravel. The gravel was classified as having a sediment particle size of more than 2mm. Table 6.1 shows that p = 0.023. Since p value is greater than 0.10 there is no statistically significant relationship between the variables at the 90% or higher confidence level. This again does not confirm findings of Winckler (1999) who found correlations of the W-statistic with percentage gravel.

6.4 CONCLUSION

The graphical representation of the three transects indicated significant differences among them. When treating one replicate at a time it was found that samples, L1a, L1b, L2a, L3a, L3b and L3c are the only ones that indicated moderate disturbance. Despite this there was no sample found which was severely disturbed. Because of the fact that some replicates of the same station showed some disturbance and others not, it was necessary to "pool" the replicates. Station L1 and L3 showed a possible disturbed state and L2 showed an undisturbed state. Mbokodweni and Brighton stations all indicated an undisturbed state as was evident when replicates were treated separately. To find a general picture, the three stations of each site were also combined and treated as different transects. The Lovu transect showed a possible disturbance and possessed a negative W-statistic. Brighton and Mbokodweni transects were found to be undisturbed with positive W-statistic values.

In order to measure stress level, the W-statistic was correlated with three environmental variables, namely; percentage mud, coarse sand and gravel present in a sample for each replicate. For all three transects no significant correlation of W-statistic with any of the environmental variables was found. It is again important to note that the ABC curves are designed to indicate stress due to pollution and all sites used in the current study were relatively unpolluted.

CHAPTER SEVEN

GENERAL CONCLUSION

CHAPTER 7: GENERAL CONCLUSION

In assessing benthic invertebrate community structure, the current study used multivariate and distributional techniques. Multivariate ordination or clustering methods preserve taxon-specific information and are very sensitive in detecting changing community patterns because they are species dependent (Warwick *et al.* 1990). Distributional and univariate summaries may, however, extract universal features which are not a function of the specific taxa present, and may therefore be related to levels of biological "stress" (Clarke 1990). Warwick (1986) suggested that the distribution of numbers and biomass of individuals among species in macrobenthic communities show a differential response to disturbance. This response can be clearly demonstrated by the comparison of *k*-dominance for abundance and biomass, which result in Abundance Biomass Comparison (ABC) curves. These further produce the W-statistic that may be used to measure the impact of stress on biotic communities. The current study uses samples from three short transects, which are believed to be relatively undisturbed to test whether these methods are sensitive to natural changes in community structure. The main findings for the four main aims treated as separate chapters are briefly discussed below.

A *priori* statistical testing was used for both the macrofauna and meiofauna to test the two null hypotheses that: 1. There is no difference between the shallow and the deeper stations, 2. There are no differences among the three transects. The macrofauna test rejected the first null hypothesis and showed a highly significant difference between the shallow and deeper stations in terms of their fauna. The meiofauna test narrowly rejected the null hypothesis. Statistical testing revealed inherent variability among study sites, and it was concluded that natural fluctuations and other unforeseen factors act together to produce the observed community structure. The macrofauna component was more sensitive to the type of sediment

as measured by percentage coarse sand and Chemical Oxygen Demand (COD). On the other hand the meiofauna showed different sensitivity to distance alongshore, depth, type of sediment and COD compared to the macrofauna, but some sensitivity to all four variables. Analysis of similarity for both macrofauna and meiofauna rejected the second null hypotheses and showed that there is inherent variability among transects at different locations alongshore.

Multivariate methods revealed concordance between the analyses of the biomass and abundance data; both grouped the samples in a similar fashion, therefore either component of the biotic data can be used to represent the benthic invertebrate community structure. The use of data aggregated to higher taxonomic levels is not useful when assessing natural variability at a local scale. The dissimilarity among the four groups from the multivariate analysis was related back to the component species in each group of samples and the species responsible for the groupings identified. It emerged that the pelecypod; *Lasaea sp.*, amphipod; *Ampelisca brevicornis, Ampelisca diadema* and *Urothoe sp.* were consistently more abundant in muddy sediments. An unidentified gastropod and *Photis sp.* were characteristic of sandy sediments. One of the secondary aims of the study was to assess the degree of concordance between environmental factors and the biotic patterns. The biological composition of an area is largely affected by the prevalent environmental conditions. Therefore, one of the aims in this study was to assess the degree of concordance between the environmental factors and biotic patterns. Sediment particle size appears to play a key role in influencing benthic community patterns. Another factor contributing to macrobenthic community structure was found to be depth, even though the depth range was narrow (25-45 m). Increasing a scale in both position along the coast and depth, and testing the validity of these small scale findings is a concern for future studies.

Cluster analysis of the meiofauna revealed three major groups based on each transect. Using "pooled" replicates it was found that samples of the same transect are more similar to each other than samples of the same depth. When relating the dissimilarity of the three groups to component species, it was found that the annelids are characteristics of muddy samples. The ostracods and harpacticoids were found to be characteristics of sandy samples. Sediment grain size and COD appear to play a key role in influencing meiobenthic community patterns. When replicates of each station were combined for macrofauna and meiofauna components, the resulting patterns differed. Macrofaunal patterns grouped the samples according to depth and meiofaunal patterns grouped the samples according to position along the coast (transect). The meiofauna appear to be less sensitive to depth than the macrofauna. This anomaly may be related to the fact that the meiofauna was only analyzed to taxonomic level higher than family and the macrofauna analyzed to species level. Analyzing the meiofauna to the same taxonomic level as macrofauna and comparing the two sensitivities is a concern for future studies.

The graphical representations (ABC curves) highlighted some differences among the three transects. The ABC curves indicated the possible influence of sediment disturbance at the Lovu site. This may be due to the fact that Lovu River is large and fine sediments from the river flood may cause periodic disturbance. Correlations were used to elucidate relationships between the W-statistic on the one hand, and the environmental indicators (percentage mud, percentage coarse sand and percentage gravel) of disturbance on the other. There were no significant correlations found between W-statistic and environmental variables. This study has shown that ABC curves appear to be less useful measures of natural disturbance. ABC curves are mainly designed to assess stress due to pollution. It is important to note that not all

categories of sediment particle size were taken into consideration and the observation may have changed if all categories were considered.

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APPENDIX 1

Similarity
Create triangular similarity/distance matrix

Worksheet

File: A:\why1.xls
Sample selection: All
Variable selection: All

Parameters

Analyse between: Samples
Similarity measure: Bray Curtis
Standardise: No
Transform: Square root

Outputs

Worksheet: Sheet1

ANOSIM
Analysis of Similarities

Similarity Matrix

File: Sheet1
Data type: Similarities
Sample selection: All

One-way Analysis

Factor Values

Factor: 3.2.1 Transect
Lovu
Brighton
Mbokodweni

Factor Groups

Sample	3.2.1 Transect
L1a	Lovu
L1b	Lovu
L1c	Lovu
L2a	Lovu
L2b	Lovu
L2c	Lovu
L3a	Lovu
L3b	Lovu
L3c	Lovu
B1a	Brighton
B1b	Brighton
B1c	Brighton
B2a	Brighton
B2b	Brighton
B2c	Brighton
B3a	Brighton
B3b	Brighton
B3c	Brighton
M2a	Mbokodweni
M2b	Mbokodweni
M2c	Mbokodweni
M3a	Mbokodweni
M3b	Mbokodweni
M3c	Mbokodweni

Global Test

Sample statistic (Global R): 0.469
Significance level of sample statistic: 0.1%

Brighton
Mbokodweni

Factor Groups

Sample	3.2.1 Transect
L1a	Lovu
L1b	Lovu
L1c	Lovu
L2a	Lovu
L2b	Lovu
L2c	Lovu
L3a	Lovu
L3b	Lovu
L3c	Lovu
B1a	Brighton
B1b	Brighton
B1c	Brighton
B2a	Brighton
B2b	Brighton
B2c	Brighton
B3a	Brighton
B3b	Brighton
B3c	Brighton
M2a	Mbokodweni
M2b	Mbokodweni
M2c	Mbokodweni
M3a	Mbokodweni
M3b	Mbokodweni
M3c	Mbokodweni

Global Test

Sample statistic (Global R): 0.469
Significance level of sample statistic: 0.1%
Number of permutations: 999 (Random sample from a large number)
Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

Groups	R Statistic	Significance Level %	Possible Permutations	Actual Permutations	Number >= Observed
Lovu, Brighton	0.583	0.1	24310	999	0
Lovu, Mbokodweni	0.642	0.1	5005	999	0
Brighton, Mbokodweni	0.192	7.8	5005	999	77

ANOSIM
Analysis of Similarities

Similarity Matrix

File: Sheet1
Data type: Similarities
Sample selection: All

One-way Analysis

Factor Values

Factor: 3.2.2 Depth
25
35
45

Factor Groups

Sample	3.2.2 Depth
L1a	25
L1b	25
L1c	25
B1a	25
B1b	25

L2b	35
L2c	35
B2a	35
B2b	35
B2c	35
M2a	35
M2b	35
M2c	35
L3a	45
L3b	45
L3c	45
B3a	45
B3b	45
B3c	45
M3a	45
M3b	45
M3c	45

Global Test

Sample statistic (Global R): 0.24
Significance level of sample statistic: 0.3%
Number of permutations: 999 (Random sample from a large number)
Number of permuted statistics greater than or equal to Global R: 2

Pairwise Tests

Groups	R Statistic	Significance Level %	Possible Permutations	Actual Permutations	Number >= Observed
25, 35	0.306	1.9	5005	999	18
25, 45	0.53	0.1	5005	999	0
35, 45	-0.018	51.4	24310	999	513

ANOSIM
Analysis of Similarities

Similarity Matrix

File: Sheet1
Data type: Similarities
Sample selection: All

One-way Analysis

Factor Values

Factor: 3.2.3 Percentage coarse sand
A
B
C

Factor Groups

Sample	3.2.3 Percentage coarse sand
L1a	A
L1b	A
L1c	A
L2a	A
L2b	A
L2c	A
L3a	A
L3b	A
L3c	A
B1a	B
B1b	B
B1c	B
B2a	C
B2b	C
B2c	C
B3a	C
[illegible]	[illegible]

M2c	C
M3a	C
M3b	C
M3c	C

Global Test

Sample statistic (Global R): 0.771
Significance level of sample statistic: 0.1%
Number of permutations: 999 (Random sample from 594914320)
Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

Groups	R Statistic	Significance Level %	Possible Permutations	Actual Permutations	Number >= Observed
A, B	0.983	0.5	220	220	1
A, C	0.69	0.1	293930	999	0
B, C	0.872	0.2	455	455	1

ANOSIM
Analysis of Similarities

Similarity Matrix

File: Sheet1
Data type: Similarities
Sample selection: All

One-way Analysis

Factor Values

Factor: 3.2.4 Chemical Oxygen Demand (COD)
C
A
B

Factor Groups

Sample	3.2.4 Chemical Oxygen Demand (COD)
L1a	C
L1b	C
L1c	C
L2a	C
L2b	C
L2c	C
L3a	C
L3b	C
L3c	C
B1a	A
B1b	A
B1c	A
B2a	A
B2b	A
B2c	A
B3a	A
B3b	B
B3c	B
M2a	B
M2b	B
M2c	B
M3a	B
M3b	B
M3c	B

Global Test

Sample statistic (Global R): 0.498

Pairwise Tests

Groups	R Statistic	Significance Level %	Possible Permutations	Actual Permutations	Number >= Observed
C, A	0.608	0.1	11440	999	0
C, B	0.694	0.1	24310	999	0
A, B	0.201	3.7	6435	999	36

Similarity
Create triangular similarity/distance matrix

Worksheet

File: A:\MEIPR.PM1
Sample selection: All
Variable selection: All

Parameters

Analyse between: Samples
Similarity measure: Bray Curtis
Standardise: No
Transform: Square root

Outputs

Worksheet: Sheet2

ANOSIM
Analysis of Similarities

Similarity Matrix

File: Sheet2
Data type: Similarities
Sample selection: All

One-way Analysis

Factor Values

Factor: 3.2.1 Transect (Meiofauna)
Lovu
Brighton
Mbokodweni

Factor Groups

Sample	3.2.1 Transect (Meiofauna)
L1a	Lovu
L1b	Lovu
L1c	Lovu
L2a	Lovu
L2b	Lovu
L2c	Lovu
L3a	Lovu
L3b	Lovu
L3c	Lovu
B1a	Brighton
B1b	Brighton
B1c	Brighton
B2a	Brighton
B2b	Brighton
B2c	Brighton
B3a	Brighton
B3b	Brighton
B3c	Brighton

25, 45	0.307	2.7	5005	999	26
35, 45	0.148	4.8	24310	999	47

ANOSIM
Analysis of Similarities

Similarity Matrix

File: Sheet2
Data type: Similarities
Sample selection: All

One-way Analysis

Factor Values

Factor: 3.3.3 Percentage coarse sand (Meiofauna)
A
B
C

Factor Groups

Sample	3.3.3 Percentage coarse sand (Meiofauna)
L1a	A
L1b	A
L1c	A
L2a	A
L2b	A
L2c	A
L3a	A
L3b	A
L3c	A
B1a	B
B1b	B
B1c	B
B2a	C
B2b	C
B2c	C
B3a	C
B3b	C
B3c	C
M2a	C
M2b	C
M2c	C
M3a	C
M3b	C
M3c	C

Global Test

Sample statistic (Global R): 0.496
Significance level of sample statistic: 0.1%
Number of permutations: 999 (Random sample from 594914320)
Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

Groups	R Statistic	Significance Level %	Possible Permutations	Actual Permutations	Number >= Observed
A, B	0.613	0.5	220	220	1
A, C	0.606	0.1	293930	999	0
B, C	0.085	26.2	455	455	119

ANOSIM
Analysis of Similarities

Similarity Matrix

File: Sheet2
Data type: Similarities
Sample selection: All

One-way Analysis

Factor Values

Factor: 3.3.4 Chemical Oxygen Demand (Meiofauna)
C
A
B

Factor Groups

Sample	3.3.4 Chemical Oxygen Demand (Meiofauna)
L1a	C
L1b	C
L1c	C
L2a	C
L2b	C
L2c	C
L3a	C
L3b	C
L3c	C
B1a	A
B1b	A
B1c	A
B2a	A
B2b	A
B2c	A
B3a	A
B3b	B
B3c	B
M2a	B
M2b	B
M2c	B
M3a	B
M3b	B
M3c	B

Global Test

Sample statistic (Global R): 0.552
Significance level of sample statistic: 0.1%
Number of permutations: 999 (Random sample from a large number)
Number of permuted statistics greater than or equal to Global R: 0

Pairwise Tests

Groups	R Statistic	Significance Level %	Possible Permutations	Actual Permutations	Number >= Observed
C, A	0.722	0.2	11440	999	1
C, B	0.506	0.1	24310	999	0
A, B	0.485	0.3	6435	999	2

APPENDIX 2

Biomass of macrobenthos taken by Day grab in May 1999 off the KwaZulu Natal coast

ATION NUMBER	L1a	L1b	L1c	L2a	L2b	L2c	L3a	L3b	L3c	B1a	B1b	B1c	B2a	B2b	B2c	B3a	B3b	B3c	M2a	M2b	M2c	M3a	M3b	M3c
nthura													0			0	0	0						
eromatidae																						0.01		
TOSTRACA											0													
RURA																			0.06					
IDACEA			0						0				0	0	0.3			0						
rosaccus	0	0			0	0	0.03	0		0	0.1	0	0.2	0.2	0	0	0	0	0.06	0.04	0.02	0.09	0	0.09
ERTEA	0	0.8		0	0	0	0.02		0	0			0.1		0		0.2	0.3			0.01	0.02	0.1	0.08
IUROIDEA	0	0	0				0.01	0		0		0	0	0	0	0.3	0.3	0	0.03	0.01	0.04		0.2	0.03
THOBRANCHIA																								2.2
RACODA														0										
coda sp1	0.2	0	0.2	0		0	0.08		0	0		0				0	0	0	0.01	0.01	0.03			
coda sp2	0	0					0.09	0.1								0	0	0						
ECYPODA			1.8										0.8			0.1	0.1	0.2	0.25	0.3	0.32			
linia globulosa								0	0						0				0.13				0	0.01
x	0.1																							0.01
x *bipartitus*	0.4																							
ea							0.05	0	0.2			0		0.3	0									
								0	0.1											1.72				
madeirensis														0.6										
a fasciata																			0.33			0.32		
ta contempta	0.3	0	0.1				0.2																	
a	0		0	0.1	0	0					0.4		0.2	0.4	0.4	0.1	0.4	0.8						0.02
a vidalensis	0.1		0.1	0.1		0		0.1	0				0.4						0.17	0.13				
lea arakana			0.7	0.4			1.3	0	0						0.8	1.1	0.3	1.1	0.41	1.72	0.89	0.41	1.7	
ycardium																								
IATULACEA							0.44	1.2															0	0.01
YHELMINTHES						0																		
CHAETA																								
aretidae													0										0.1	
trosyllis		0					0.01						0											
trosyllis parva				0						0										0				
es																			0.01					
dilidae									0.3		0	0.1		0.2								0.01		0.01
olidae											11					0.4	0.6	0.5						
dia	0.1					0				0.1	0	0.1		0.1	0	0.1	0.1	0	0.06	0.06	0.01	0.04	0	0.01
dia longicaudata		0.2	0.1										0.2			0.2	0.2	0.2						
lidae	0.1	0.7	0	0.1		0		0		0	0		0			0	0	0	0			0.04		
opteridae												0.1											0	0.03
lidae							0.01			0					0									
onensis					0																			
ra				0	0								0										0.2	
sa														0										
patra													0											
siphodonta							0.01	0	0				0.1	0.1	0.1		0	0					0	0.03
													0							0				
ae			0							0			0		0	0	0							
geridae							0.12		0.2														0	0
a	0	0	0.1	0.1	0	0		0		0			0	0.1	0	0.4			0.2	0.02	0.02			0.02
dae				0				0.1										0.3					0.2	
fe				0.1	0.1	0	0.01	0						0		0.4	0.3					0.02		0.02
hoe				0																		0.01	0.1	
idae													0	0										
neris																0	0	0	0	0.01				
na																							0.1	0.01
idae				0						0						0	0					0.01	0.1	0.05
sa depressa																						0.01		
s		0	0		0	0	0.13			0.2				0	0.1	0.7	0.8	0.9	0.33	0.25	0.25		0.1	0.15
s *capensis*																								
s *dibranchus*				0																				
													0.1			0	0	0	0.01			0.09	0.1	
s	0	0	0	0.1	0		0.1	0.1	0.7			0		0	0.1					0.03	0.1		0.1	0.14
conchylega				0	0																	0.01		
eremita				0.1	0	0	0.01						0.1											
ae							0.01									0.1	0	0						
				0	0	0						0										0.01		
cuvieri	0	0																						
	0.1	1	0.9	0.2		0														0.01			0	0.07

Biomass of macrobenthos taken by Day grab in May 1999 off the KwaZulu Natal coast

STATION NUMBER	L1a	L1b	L1c	L2a	L2b	L2c	L3a	L3b	L3c	B1a	B1b	B1c	B2a	B2b	B2c	B3a	B3b	B3c	M2a	M2b	M2c	M3a	M3b	M3c
ACTINARIA												7.2		3.6	3.4							13.6		14.8
AMPHIPODA																								
Amaryllis macrophthalma					0		0.1		0						0				0.01					0.02
Ampelisca						0				0	0		0					0		0.01	0.04	0.02		0.03
Ampelisca brachyceras							0.01						0	0	0									
Ampelisca brevicornis	0.1	0.1	0.1	0.1	0		0.11	0.1	0.1							0	0	0				0.19	0.4	0.19
Ampelisca diadema	0	0	0	0	0	0																0.04		
Ampelisca miops								0	0	0									0					
Ampelisca palmata							0.05										0							
Byblis gaimardi	0						0.16	0.1	0.1					0	0	0	0		0.01	0	0.09	0.04	0.1	0.05
Ceradocus																								
Corophiidae	0			0	0	0	0.02	0	0.1					0	0	0	0	0	0.01	0.01	0.01		0	0.03
Corophium	0	0	0	0	0	0	0.19	0.2	0.2	0				0	0	0	0	0	0.01	0.02	0.05		0	0.2
Cunicus profundus											0	0	0											
Gammaropsis				0			0.06	0					0	0	0		0	0	0.02	0.02	0.05	0.09	0	0.03
Grandidierella		0																				0.1		
Hippomedon						0					0	0												
Maera					0																	0.02		
Mandibulophoxus stimpsoni	0	0	0	0	0	0	0.09	0	0.1	0				0	0	0	0	0	0.01			0.02		0.02
Melita appendiculata																						0.03		
Oedicerotidae											0												0	
Pholis				0			0.09	0	0				0		0							0.01		0.01
Platyschnopus herdmani							0.01						0	0		0								
Urothoe				0			0			0	0	0								0		0		
Urothoe coxalis							0.01												0		0.01	0.01		0
Urothoe elegans							0.01		0	0									0			0.02		0.02
Urothoe pinnata		0					0.02	0	0	0	0	0	0.9		0.1	0	0	0	0.02	0.01	0.05			
ANOMURA			0.4				0.01	0			0	0.1				0.2	0	0.1	0.25	0.12	0.01			
Albunea symnista	0.3			0.1																				
Galathea	0.1			0									0.3	0.3	0	0	0.1	0.1	0.01		0.01	0.7	0.3	0.3
ASCIDEACEA												1												
BRACHYURA									0.1						0									0.31
Calappidae										0														
Dehaanius							0.03	0.1					0.5	0						0.13		0.51	0.1	
Dromidae				0	1.5	1.5	0.2	0.2					0	0	0	0.1	0.1	0				0.25	0	0.23
Philyra			0.4			0																		
Xanthidae	0	0		0	0	0								0.2						0.25				
CARIDEA													1								0.16			
Callianassa					0																			
CHORDATA				0.5									1.1	0		0	0	0			0.06		0.1	
Branchiostoma						0										0	0.1	0.8	0.76	0.03	0.11			
COPEPODA						0					0	0	0	0	0	0	0	0	0			0		
CRINOIDEA			0										0											
CTENOPHORA																						0.01		
CUMACEA																								
Cyclaspis scissa						0	0.02	0	0															
Dic calmani			0							0						0	0		0.01					
Eocuma	0	0	0											0				0	0.02	0.01	0.02			
Iphinoe							0.09			0	0								0.01			0.01	0	0.01
Iphinoe crassipes							0.03				0													
Iphinoe stebbingi	1	0.9	0.5	0.5	0.3	0.5	0.09	0.1	0.1				0	0	0	0	0	0						
ECHINOIDEA						0		0.1				0		0	0									
GASTROPODA		0.2					0.12	0.1	0.1						0								0.2	
Polynices																				0.11	0.12			
ISOPODA																								
Anthuridae	0	0	0	0	0	0	0.02	0	0	0	0			0	0							0	0	0.01
Arcturidae					0	0	0.01	0	0					0	0								0	
Arcturina	0																							
Bopyridae																								0.01
Cirolana							0.02	0	0.1	0	0		0	0.1	0.1	0.1	0	0		0.02			0	0.01
Cyanthura							0.01																	
Idoteidae				0																				

Macrobenthos taken by Day grab in May 1999 off the KwaZulu Natal coast

STATION NUMBER	L1a	L1b	L1c	L2a	L2b	L2c	L3a	L3b	L3c	B1a	B1b	B1c	B2a	B2b	B2c	B3a	B3b	B3c	M2a	M2b	M2c	M3a	M3b	M3c
Oweniidae											1													
Paraonidae																6	4	2						
Pectinaria				3		2			1															
Phyllo						2							4			5	5							
Phyllodoce	1						2				1				15									
Phyllodocidae													5											
Prionospio		3		5							1	1	28	8		2	3					2		
Prionospio malmgreni													2											
Prionospio pinnata			1	3	1	9																		
Sabellaridae								2																
Sabellidae				3	1	7	135	86	50			2	42	49	37	13	17	9	2		7	12	19	25
Scolelepis										1	1													
Scoloplos	3			4	1	2											1		3	1		3	4	3
Serpulidae													16	14	12					1		37	53	36
Sigalion						4		2																
Spionidae								2	3															
Spiophanes			3	3						2				2		3			16	38	21		18	8
Spiophanes bombyx								10																
Spiophanes soederstromi													18	84	49	37	44	33				6		
Stemaspis											1													
Sthenelais boa						1									1	2	4	3	2		2			
Syllidae				2																				
Terebellidae														9	6	7	4	4		2				10
Tharyx	2			187	97	28	33	57	51		2	1				5						1	4	3
Tharyx filibranchia	57	13	13	69			9															3		
PYCNOGONIDA	2						1					1												
SIPUNCULIDA																								
Aplonosoma tricocephala	1					1									5	5	2	4						
Nephasoma rutilofusca	2	1	1	4	13	5	2			1	1	5	4		2	1	1	1	1		3	1	5	3
TANAIDACEA					2		2																35	31
TOTAL COUNT	371	323	197	607	338	441	765	493	520	82	61	47	342	375	350	274	314	287	138	141	150	369	401	421
NUMBER OF TAXA	36	28	30	45	31	40	52	39	33	27	26	23	45	42	43	47	48	43	38	33	28	44	42	47

Meiobenthos taken by a Day grab in May 1999 off the KwaZulu Natal coast. Abundance data.

ION NUMBER	L1a	L1b	L1c	L2a	L2b	L2c	L3a	L3b	L3c	B1a	B1b	B1c	B2a	B2b	B2c	B3a	B3b	B3c	M2a	M2b	M2c	M3a	M3b	M3c
INA		4	2	10	1	4	4		1	6		3	3	6	5	8	9		19	11	8	4	7	2
IIPODA	1	2		21	6	7	5		2				2	3			1	1			6		1	3
LIDA	6	3	9	18	15	14		3		22	25	35	60	30	33	62	60	79	29	39	34	18	22	11
ARIA					8	8	3			2		9		6	2									
oda other				3				3		15		3	4		4	6	4	4	2	3	3			1
ACEA			1																					
ROSTRICA				8						12		4	1	4	4	5	3	2	34	38	17	1	2	7
cticoida	11	8	13	7	4	8	146	114	88	120	112	90	85	130	136	131	81	105	81	66	77	112	115	141
DA			1	2																5	2		1	
HYNCHA				14	2	5		1			5	14	8		4	2	6	3	4			4		
USCA											5													
TODA	178	135	426	129	167	172	184	206	202	307	427	288	401	361	375	307	302	298	264	225	277	163	123	204
RTEA/PLT	55	32	20	11	11	16	49	81	84	8	2	2		1		11	13	7	32	40	45	69	49	46
CODA	4	2	5	10	2	1			1	3		5				2			28	29	26	9	30	26
OMASTIGOPHORA										18							1							
GRADA					2	2				9			1				2		7	6	4	4	7	2
COUNT	6	7	8	11	10	10	6	6	6	11	6	10	9	8	8	9	11	8	10	10	11	9	10	10
ER OF TAXA	255	186	477	233	220	237	391	408	378	522	576	453	565	541	563	534	492	499	500	462	497	384	357	443

APPENDIX 3

PRIMER 2002/03/22

Similarity
Create triangular similarity/distance matrix

Worksheet

File: A:\WHY1.PM1
Sample selection: All
Variable selection: All

Parameters

Analyse between: Samples
Similarity measure: Bray Curtis
Standardise: No
Transform: Square root

Outputs

Worksheet: Sheet1

Similarity
Create triangular similarity/distance matrix

Worksheet

File: A:\WHY1.PM1
Sample selection: All
Variable selection: All

Parameters

Analyse between: Samples
Similarity measure: Bray Curtis
Standardise: No
Transform: Fourth root

Outputs

Worksheet: Sheet2

CLUSTER
Hierarchical Cluster analysis

Similarity Matrix

File: Sheet2
Data type: Similarities
Sample selection: All

Parameters

Cluster mode: Group average
Use data ranks: No

Samples

1 L1a
2 L1b
3 L1c
4 L2a
5 L2b
6 L2c
7 L3a
8 L3b
9 L3c
10 B1a
11 B1b
12 B1c

16 B3a
17 B3b
18 B3c
19 M2a
20 M2b
21 M2c
22 M3a
23 M3b
24 M3c

Combining

17+18 -> 25 at 84.37
16+25 -> 26 at 79.81
23+24 -> 27 at 70.94
8+9 -> 28 at 67.84
14+15 -> 29 at 66.88
20+21 -> 30 at 65.01
1+2 -> 31 at 62.19
5+6 -> 32 at 60.32
7+28 -> 33 at 59.38
19+30 -> 34 at 57.97
3+31 -> 35 at 57.37
4+32 -> 36 at 56.51
26+29 -> 37 at 52.25
22+27 -> 38 at 50.2
13+37 -> 39 at 48.47
11+12 -> 40 at 45.33
34+39 -> 41 at 41.83
33+38 -> 42 at 41.66
35+36 -> 43 at 41.49
41+42 -> 44 at 36.74
10+40 -> 45 at 33.96
43+44 -> 46 at 32.98
45+46 -> 47 at 25.61

Outputs

Plot: Plot1

Similarity
Create triangular similarity/distance matrix

Worksheet

File: A:\WHY1.PM1
Sample selection: All
Variable selection: All

Parameters

Analyse between: Samples
Similarity measure: Bray Curtis
Standardise: No
Transform: Fourth root

Outputs

Worksheet: Sheet3

Similarity
Create triangular similarity/distance matrix

Worksheet

File: A:\WHY1.PM1
Sample selection: All
Variable selection: All

Parameters

Analyse between: Samples
Similarity measure: Bray Curtis

Outputs

Worksheet: Sheet4

CLUSTER
Hierarchical Cluster analysis

Similarity Matrix

File: Sheet2
Data type: Similarities
Sample selection: All

Parameters

Cluster mode: Group average
Use data ranks: No

Samples

1 L1a
2 L1b
3 L1c
4 L2a
5 L2b
6 L2c
7 L3a
8 L3b
9 L3c
10 B1a
11 B1b
12 B1c
13 B2a
14 B2b
15 B2c
16 B3a
17 B3b
18 B3c
19 M2a
20 M2b
21 M2c
22 M3a
23 M3b
24 M3c

Combining

17+18 -> 25 at 84.37
16+25 -> 26 at 79.81
23+24 -> 27 at 70.94
8+9 -> 28 at 67.84
14+15 -> 29 at 66.88
20+21 -> 30 at 65.01
1+2 -> 31 at 62.19
5+6 -> 32 at 60.32
7+28 -> 33 at 59.38
19+30 -> 34 at 57.97
3+31 -> 35 at 57.37
4+32 -> 36 at 56.51
26+29 -> 37 at 52.25
22+27 -> 38 at 50.2
13+37 -> 39 at 48.47
11+12 -> 40 at 45.33
34+39 -> 41 at 41.83
33+38 -> 42 at 41.66
35+36 -> 43 at 41.49
41+42 -> 44 at 36.74
10+40 -> 45 at 33.96
43+44 -> 46 at 32.98
45+46 -> 47 at 25.61

Outputs

SIMPER
Similarity Percentages - species contributions

Worksheet

File: A:\WHY1.PM1
Sample selection: All
Variable selection: All

Parameters

Standardise data: No
Transform: None
Cut off for low contributions: 90.00%
Factor name: 4.1.1 Cluster groupings

Factor groups
B
D
A
C

Group B

Average similarity: 41.34

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
75	96.83	20.59	3.20	49.80	49.80
145	52.33	2.33	0.42	5.63	55.43
146	25.33	2.07	0.63	5.02	60.45
96	33.33	1.96	0.46	4.73	65.18
83	10.17	1.86	2.80	4.49	69.67
40	12.17	1.60	1.65	3.87	73.54
6	12.50	1.48	0.86	3.57	77.11
7	5.50	1.24	2.33	3.01	80.11
30	19.50	1.06	1.03	2.57	82.68
65	6.67	0.87	1.10	2.11	84.79
94	5.50	0.74	1.16	1.79	86.58
102	7.17	0.70	0.41	1.68	88.26
14	3.83	0.56	1.81	1.36	89.62
88	4.33	0.48	1.62	1.15	90.78

Group D

Average similarity: 44.01

64	6.00	5.53	1.49	17.59	37.94
149	3.00	3.20	6.94	10.18	48.12
21	4.00	3.15	1.19	10.02	58.14
4	8.00	2.80	0.58	8.89	67.03
88	2.33	1.60	6.94	5.09	72.12
43	1.67	1.23	0.58	3.93	76.04
73	1.33	0.93	0.58	2.96	79.01
145	1.00	0.62	0.58	1.96	80.97
121	0.67	0.62	0.58	1.96	82.93
71	1.67	0.62	0.58	1.96	84.90
38	1.33	0.62	0.58	1.96	86.86
13	1.33	0.62	0.58	1.96	88.82
16	0.67	0.62	0.58	1.96	90.78

Group C

Average similarity: 37.15

Species	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
136	29.44	4.05	0.77	10.91	10.91
89	17.44	3.27	0.95	8.81	19.72
126	19.56	2.88	0.97	7.76	27.49
40	8.00	2.48	1.62	6.67	34.16
152	11.44	2.24	0.98	6.03	40.19
57	10.44	1.64	0.72	4.42	44.61
62	5.56	1.52	1.06	4.09	48.70
64	7.11	1.50	1.64	4.03	52.72
5	6.67	1.07	0.79	2.88	55.60
38	6.89	0.86	0.67	2.31	57.92
134	7.78	0.84	0.33	2.27	60.18
61	10.11	0.82	0.48	2.20	62.38
39	4.67	0.81	1.26	2.18	64.56
92	5.56	0.80	0.58	2.16	66.73
22	7.11	0.75	0.44	2.02	68.75
27	4.11	0.73	0.67	1.96	70.71
109	2.89	0.71	0.73	1.91	72.62
98	2.44	0.70	1.95	1.89	74.52
147	2.89	0.70	0.79	1.89	76.41
65	3.33	0.66	0.86	1.77	78.18
36	3.22	0.60	1.11	1.62	79.80
21	2.67	0.56	0.92	1.51	81.30
83	3.33	0.54	0.81	1.44	82.75
144	3.56	0.53	0.77	1.43	84.17
75	2.89	0.41	0.76	1.11	85.28
26	2.44	0.39	0.63	1.04	86.32
4	2.56	0.36	0.43	0.97	87.29
129	4.78	0.33	0.33	0.89	88.18
138	1.56	0.31	0.73	0.83	89.01
13	1.78	0.31	0.70	0.82	89.83
97	3.78	0.30	0.30	0.79	90.63

Groups B & D

Average dissimilarity = 81.19

Species	Group B Av.Abund	Group D Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
75	96.83	9.17	10.35	2.38	12.75	12.75
6	12.50	73.17	6.85	2.33	8.43	21.18
145	52.33	24.83	5.92	1.05	7.29	28.47
126	1.83	54.50	5.66	1.38	6.97	35.43
40	12.17	50.50	4.85	1.56	5.97	41.41
96	33.33	0.33	3.52	0.87	4.34	45.75
129	0.00	21.00	2.78	0.93	3.43	49.18
61	1.00	20.50	2.74	0.87	3.37	52.55
146	25.33	2.00	2.70	0.98	3.33	55.88
27	0.50	21.83	2.41	2.08	2.97	58.85
30	19.50	1.00	2.32	0.59	2.85	61.70
83	10.17	22.67	1.93	1.30	2.37	64.08
62	1.83	11.33	1.26	1.32	1.55	65.62
141	0.33	9.67	1.24	0.72	1.53	67.16
94	5.50	11.67	1.01	1.44	1.25	68.40
152	0.33	10.00	0.99	0.80	1.21	69.62
151	0.00	7.67	0.96	0.98	1.18	70.80
111	1.00	9.33	0.92	0.85	1.14	71.93

39	4.33	8.33	0.87	1.22	1.07	74.13
73	0.00	5.67	0.74	1.04	0.91	75.04
7	5.50	2.33	0.73	2.31	0.90	75.94
67	6.67	1.00	0.71	0.87	0.88	76.82
65	6.67	1.33	0.67	1.42	0.82	77.64
45	0.83	5.67	0.65	0.84	0.80	78.44
134	1.00	4.33	0.60	0.72	0.74	79.18
100	5.17	0.33	0.57	1.00	0.70	79.88
9	0.00	6.33	0.56	0.44	0.69	80.57
68	0.17	3.83	0.54	0.45	0.67	81.24
14	3.83	6.83	0.50	1.61	0.61	81.85
3	0.67	4.67	0.48	0.90	0.59	82.44
21	0.83	3.67	0.47	0.70	0.58	83.02
22	3.33	0.00	0.45	0.68	0.55	83.58
88	4.33	1.83	0.43	0.89	0.52	84.10
89	2.33	3.33	0.42	1.18	0.51	84.62
4	0.50	3.00	0.40	0.81	0.49	85.10
143	3.17	0.67	0.34	0.80	0.42	85.53
101	2.83	0.00	0.34	0.47	0.41	85.94
92	0.00	2.33	0.32	0.56	0.39	86.33
53	2.67	2.17	0.32	1.62	0.39	86.72
25	0.00	2.50	0.32	0.50	0.39	87.11
57	0.00	2.67	0.31	1.65	0.39	87.50
16	0.00	2.50	0.30	0.72	0.37	87.87
64	2.00	3.50	0.30	1.28	0.37	88.24
36	0.00	2.67	0.29	1.75	0.36	88.60
8	0.00	2.33	0.27	0.67	0.33	88.93
18	0.67	2.33	0.27	0.96	0.33	89.26
147	0.33	2.33	0.26	1.03	0.32	89.58
51	2.17	0.00	0.26	0.44	0.32	89.90
123	2.33	0.00	0.25	0.74	0.31	90.21

Groups B & A

Average dissimilarity = 92.71

Species	Group B Av.Abund	Group A Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
75	96.83	0.00	23.00	3.10	24.81	24.81
145	52.33	1.00	9.77	0.81	10.54	35.34
96	33.33	0.00	6.38	0.86	6.89	42.23
146	25.33	0.00	5.32	1.04	5.74	47.97
30	19.50	1.00	4.80	0.58	5.18	53.14
6	12.50	0.00	3.13	1.09	3.38	56.52
40	12.17	0.67	2.64	1.19	2.85	59.37
83	10.17	1.33	2.06	1.59	2.22	61.59
102	7.17	1.00	2.02	0.74	2.18	63.77
4	0.50	8.00	1.87	0.98	2.02	65.79
7	5.50	0.00	1.39	2.29	1.50	67.30
65	6.67	0.67	1.35	1.52	1.46	68.75
67	6.67	0.00	1.29	0.77	1.39	70.14
64	2.00	6.00	1.09	1.33	1.18	71.32
100	5.17	0.67	1.08	1.03	1.17	72.49
94	5.50	0.67	1.06	1.59	1.14	73.63
22	3.33	0.00	1.03	0.69	1.12	74.75
152	0.33	4.33	0.99	2.45	1.06	75.81
39	4.33	0.00	0.96	0.84	1.04	76.85
21	0.83	4.00	0.87	1.29	0.93	77.78
88	4.33	2.33	0.81	0.82	0.88	78.66
14	3.83	1.33	0.76	0.87	0.82	79.48
149	0.33	3.00	0.69	1.42	0.75	80.22
143	3.17	0.00	0.68	0.81	0.73	80.95
101	2.83	0.00	0.66	0.47	0.71	81.67
109	1.67	0.00	0.64	0.43	0.69	82.36
89	2.33	0.33	0.59	1.03	0.64	83.00
53	2.67	0.00	0.54	0.88	0.59	83.58
142	2.17	1.00	0.53	0.99	0.57	84.16
51	2.17	0.00	0.50	0.43	0.54	84.70
93	0.00	2.00	0.50	0.65	0.54	85.23
13	0.83	1.33	0.48	0.90	0.52	85.75
123	2.33	0.00	0.48	0.76	0.52	86.27
87	2.00	1.33	0.46	1.14	0.50	86.77
95	1.83	0.00	0.43	0.50	0.47	87.24
71	0.33	1.67	0.42	0.90	0.46	87.69
103	1.67	0.00	0.42	0.54	0.46	88.15

152	0.33	11.44	1.86	1.08	2.14	54.72
57	0.00	10.44	1.60	1.14	1.84	56.56
134	1.00	7.78	1.53	0.60	1.76	58.31
61	1.00	10.11	1.41	0.67	1.62	59.93
40	12.17	8.00	1.31	1.03	1.50	61.43
102	7.17	1.22	1.28	0.78	1.47	62.90
22	3.33	7.11	1.22	1.09	1.40	64.30
83	10.17	3.33	1.19	1.27	1.37	65.66
38	0.50	6.89	1.02	0.99	1.17	66.83
5	0.00	6.67	0.99	1.19	1.14	67.97
62	1.83	5.56	0.99	1.23	1.13	69.10
67	6.67	1.44	0.98	0.89	1.13	70.23
7	5.50	0.00	0.94	2.33	1.08	71.31
92	0.00	5.56	0.89	0.97	1.02	72.33
64	2.00	7.11	0.84	0.95	0.96	73.29
39	4.33	4.67	0.80	1.19	0.92	74.21
65	6.67	3.33	0.80	1.58	0.92	75.13
100	5.17	0.00	0.75	0.91	0.87	76.00
94	5.50	2.33	0.74	1.42	0.85	76.85
121	1.33	4.56	0.72	0.60	0.82	77.67
27	0.50	4.11	0.69	0.93	0.79	78.46
129	0.00	4.78	0.68	0.71	0.78	79.24
109	1.67	2.89	0.66	1.16	0.76	80.00
14	3.83	0.33	0.62	0.98	0.71	80.71
97	0.00	3.78	0.58	0.68	0.67	81.38
88	4.33	1.44	0.56	0.80	0.65	82.03
144	0.00	3.56	0.54	1.14	0.62	82.65
86	0.33	3.22	0.50	0.44	0.57	83.22
111	1.00	3.00	0.50	0.61	0.57	83.79
36	0.00	3.22	0.48	1.45	0.56	84.35
147	0.33	2.89	0.48	1.17	0.55	84.90
101	2.83	0.00	0.46	0.47	0.53	85.43
143	3.17	0.44	0.45	0.79	0.52	85.95
4	0.50	2.56	0.45	0.86	0.52	86.47
20	0.00	2.89	0.45	0.66	0.52	86.98
26	0.17	2.44	0.44	0.75	0.51	87.49
53	2.67	1.56	0.42	1.17	0.49	87.97
21	0.83	2.67	0.39	1.20	0.45	88.42
13	0.83	1.78	0.36	1.04	0.42	88.84
51	2.17	0.00	0.35	0.44	0.40	89.24
123	2.33	0.00	0.34	0.75	0.39	89.63
142	2.17	1.44	0.34	0.90	0.39	90.03

Groups D & C

Average dissimilarity = 79.02

Species	Group D Av.Abund	Group C Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
6	73.17	0.00	9.57	3.44	12.11	12.11
40	50.50	8.00	5.70	1.59	7.21	19.32
126	54.50	19.56	5.31	1.23	6.72	26.04
136	1.00	29.44	3.61	1.14	4.57	30.62
61	20.50	10.11	3.21	0.96	4.06	34.67
129	21.00	4.78	3.18	1.03	4.03	38.71
145	24.83	0.00	3.12	1.01	3.95	42.65
83	22.67	3.33	2.50	1.25	3.17	45.82
27	21.83	4.11	2.27	1.69	2.87	48.69
89	3.33	17.44	2.10	1.07	2.66	51.35
152	10.00	11.44	1.71	1.28	2.16	53.51
141	9.67	0.00	1.44	0.71	1.83	55.34
134	4.33	7.78	1.42	0.79	1.80	57.14
94	11.67	2.33	1.33	1.50	1.68	58.82
75	9.17	2.89	1.31	0.89	1.66	60.48
57	2.67	10.44	1.25	1.35	1.58	62.06
111	9.33	3.00	1.15	1.00	1.45	63.51
151	7.67	0.22	1.10	0.99	1.39	64.90
62	11.33	5.56	1.08	1.33	1.36	66.27
39	8.33	4.67	0.98	1.33	1.24	67.50
22	0.00	7.11	0.91	0.84	1.16	68.66
38	0.17	6.89	0.86	0.98	1.09	69.75
14	6.83	0.33	0.86	2.68	1.09	70.83
73	5.67	0.11	0.85	1.06	1.08	71.91
5	0.50	6.67	0.83	1.23	1.05	72.96
92	2.33	5.56	0.77	1.12	0.98	73.93

9	6.33	0.56	0.67	0.49	0.85	75.70
64	3.50	7.11	0.63	0.96	0.80	76.50
68	3.83	0.00	0.62	0.44	0.78	77.28
121	0.33	4.56	0.57	0.54	0.72	78.00
21	3.67	2.67	0.57	0.86	0.72	78.72
3	4.67	0.56	0.54	0.91	0.68	79.40
144	1.67	3.56	0.54	1.14	0.68	80.08
4	3.00	2.56	0.52	1.10	0.65	80.74
97	0.50	3.78	0.51	0.74	0.64	81.38
109	0.00	2.89	0.43	1.15	0.54	81.92
65	1.33	3.33	0.41	1.29	0.52	82.45
86	0.17	3.22	0.39	0.40	0.50	82.95
25	2.50	0.33	0.38	0.54	0.48	83.43
7	2.33	0.00	0.38	0.44	0.48	83.91
20	0.00	2.89	0.38	0.67	0.48	84.39
26	0.00	2.44	0.37	0.79	0.46	84.85
16	2.50	0.11	0.35	0.74	0.44	85.29
147	2.33	2.89	0.34	1.27	0.43	85.71
18	2.33	1.00	0.33	0.99	0.42	86.14
8	2.33	0.11	0.32	0.72	0.40	86.54
36	2.67	3.22	0.31	1.33	0.39	86.93
150	1.83	0.89	0.30	0.89	0.37	87.31
82	1.50	1.11	0.28	1.07	0.36	87.66
13	1.17	1.78	0.27	1.12	0.35	88.01
146	2.00	0.56	0.27	0.76	0.34	88.34
87	2.33	1.33	0.27	1.24	0.34	88.68
76	1.50	1.33	0.26	0.94	0.33	89.02
60	2.00	0.00	0.26	1.06	0.33	89.34
53	2.17	1.56	0.25	1.18	0.31	89.66
128	1.67	0.56	0.25	1.08	0.31	89.97
11	1.67	0.89	0.25	0.56	0.31	90.28

Groups A & C

Average dissimilarity = 85.15

Species	Group A Av.Abund	Group C Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
136	0.00	29.44	7.52	1.15	8.83	8.83
89	0.33	17.44	5.59	1.26	6.56	15.39
126	0.67	19.56	4.93	1.26	5.79	21.19
134	0.67	7.78	3.62	0.58	4.25	25.43
57	0.00	10.44	2.99	1.15	3.51	28.94
152	4.33	11.44	2.70	0.87	3.17	32.11
61	0.00	10.11	2.53	0.71	2.98	35.09
40	0.67	8.00	2.53	1.91	2.97	38.05
4	8.00	2.56	2.35	1.08	2.76	40.81
62	0.00	5.56	2.15	1.09	2.53	43.34
22	0.00	7.11	1.95	0.84	2.29	45.63
38	1.33	6.89	1.80	1.14	2.11	47.74
5	0.00	6.67	1.77	1.20	2.07	49.82
92	0.00	5.56	1.69	1.01	1.99	51.81
64	6.00	7.11	1.56	1.49	1.83	53.64
27	0.00	4.11	1.50	0.90	1.76	55.40
39	0.00	4.67	1.36	1.30	1.60	57.00
121	0.67	4.56	1.20	0.59	1.41	58.41
129	0.00	4.78	1.17	0.73	1.38	59.79
109	0.00	2.89	1.15	1.07	1.35	61.14
147	0.00	2.89	1.11	1.15	1.30	62.45
97	0.00	3.78	1.06	0.69	1.25	63.69
26	0.00	2.44	0.99	0.72	1.16	64.86
65	0.67	3.33	0.98	1.24	1.15	66.01
144	0.00	3.56	0.98	1.22	1.15	67.16
149	3.00	0.11	0.96	1.62	1.12	68.28
21	4.00	2.67	0.93	1.21	1.09	69.37
83	1.33	3.33	0.90	1.27	1.06	70.43
20	0.33	2.89	0.87	0.77	1.02	71.45
94	0.67	2.33	0.86	0.71	1.01	72.46
36	0.67	3.22	0.80	1.82	0.94	73.40
86	0.00	3.22	0.79	0.39	0.92	74.32
75	0.00	2.89	0.76	1.13	0.89	75.21
111	0.00	3.00	0.74	0.51	0.86	76.07
93	2.00	0.00	0.68	0.64	0.80	76.87
88	2.33	1.44	0.62	0.91	0.73	77.60
42	1.67	0.44	0.59	1.21	0.70	78.29

Macrobenthos taken by Day grab in May 1999 off the KwaZulu Natal coast

STATION NUMBER	L1a	L1b	L1c	L2a	L2b	L2c	L3a	L3b	L3c	B1a	B1b	B1c	B2a	B2b	B2c	B3a	B3b	B3c	M2a	M2b	M2c	M3a	M3b	M3c
Paranthura													1			1	1	2						
Sphaeromatidae																						1		
LEPTOSTRACA											1													
MACRURA																			5					
MYSIDACEA			2						1				1	1	26			1						
Gastrosaccus	2	4			3	3	3	5		9	7	2	15	21	1	3	4	5	7	4	4	5	2	6
NEMERTEA	1	1		4	4	2	3		1	4			3		4		1	3			1	2	4	4
OPHIUROIDEA	1	1	2				1	2		3		1	5	1	1	3	2	4	2	2	2		1	2
OPISTHOBRANCHIA																								1
OSTRACODA														1										
Ostracoda sp1	19	3	19	1		1	2		2	2		1				1	3	4	1	1	1			
Ostracoda sp2	2	8					2	2								1	2	3						
PELECYPODA			10										2			1	2	6	4	6	5			
Cavolinia globulosa								1	1						1				1				2	1
Donax	1																							1
Donax bipartitus	13																							
Lasaea							4	1	4			1		6	6									
Pitar								1	1											3				
Pitar madeirensis														1										
Siliqua fasciata																			1			1		
Sunetta contempta	2	1	2				2																	
Tellina	1		1	3	7	1					3		1	2	2	1	2	5						1
Tellina vidalensis	2		2	3		12		3	1				2						1	1				
Timoclea arakana			1	1			2	1	2						1	3	2	7	3	5	5	3	6	
Trachycardium																								
PENNATULACEA							1	5															2	2
PLATYHELMINTHES						1																		
POLYCHAETA																								
Ampharetidae													2										5	
Ancystrosyllis		4					10						8											
Ancystrosyllis parva				7						2										1				
Nonides																			1					
Aphroditidae									10		1	1		1								3		2
Arenicolidae											1					8	7	11						
Armandia	3					2				7	1	4		4	4	1	5	3	3	5	2	3	15	4
Armandia longicaudata		12	8										13			13	17	21						
Capitellidae	11	88	6	9		3		2		2	1		2			6	2	1	1			4		
Chaetopteridae												1											3	2
Cirratulidae							7			2					3									
Dendronereis					1																			
Glopatra				2	1								4										3	
Oorvillea														13										
Epidiopatra													1											
Eteone sphodonta							3	2	3				23	24	5		15	14					4	4
Eunice													1							2				
Eusiridae			5							2			2		2	1	4							
Flabelligeridae							3		5														3	1
Glycera	1	1	5	13	7	13		5		2			1	8	8	3			4	4	2			3
Glyceridae				9														2					4	
Glycinde				22	15	3	1	1						7		4	2					2		2
Harmothoe				5																		2	3	
Hesionidae													6	4										
Lumbrineris																2	3	2	1	1				
Mageiona																							7	2
Maldanidae				2						1						5	5					4	3	2
Marphysa depressa																						3		
Nephtys		1	4		3	6	5			1				3	5	29	46	39	10	17	8		5	10
Nephtys capensis																								
Nephtys dibranchus				5																				
Nereis													6			14	12	12	6			11	3	
Onuphis	5	6	2	14	6		13	18	22			2		4	6					2	9		7	10
Onuphis conchylega				2	9																	3		
Onuphis eremita				69	34	97	2						7											
Opheliidae							3									10	13	11						
Orbinia				11	12	8						2										2		
Orbinia cuvieri	16	1																						
Owenia	1	1	1	2		3														1			2	1

Macrobenthos taken by Day grab in May 1999 off the KwaZulu Natal coast

STATION NUMBER	L1a	L1b	L1c	L2a	L2b	L2c	L3a	L3b	L3c	B1a	B1b	B1c	B2a	B2b	B2c	B3a	B3b	B3c	M2a	M2b	M2c	M3a	M3b	M3c
ACTINARIA												2		1	1							1		1
AMPHIPODA									5															
Amarylis macrophthalma					4		17								4				1					6
Ampelisca						3				18	6		7					5		4	7	2		6
Ampelisca brachyceras							3						13	7	7									
Ampelisca brevicornis	35	17	11	10	2		114	59	111							14	10	9				47	52	56
Ampelisca diadema	4	8	5	3	7	6			6													14		
Ampelisca miops								8		2									1					
Ampelisca palmata							38										5							
Byblis gaimardi	3						45	19	11					2	2	5	11		5	1	11	9	28	19
Ceradocus																								
Corophiidae	2			3	12	9	7	1	17					9	15	5	2	4	1	2	4		10	15
Corophium	18	4	7	4	6	34	86	85	71	2				13	11	8	8	7	7	7	11		16	45
Cunicus profundus											3	2	4											
Gammaropsis				11			22	10					6	3	4		5	4	10	12	6	21	8	7
Grandidierella		1																				23		
Hippomedon						2					1	4												
Maera					3																	5		
Mandibulophoxus stimpsoni	19	13	5	12	6	6	51	24	43	4				8	7	3	4	5	3			11		7
Melita appendiculata																						7		
Oedicerotidae											6												2	
Photis				6			36	2	11				16		11							4		3
Platyschnopus herdmani							4						2	2		2								
Urothoe				2			1			2	5	2								1		1		
Urothoe coxalis							3												3		5	6		2
Urothoe elegans							4		12	3									2			19		11
Urothoe pinnata		2					39	11	10	4	4	5	18		32	5	4	5	12	4	23			
ANOMURA			5				3	4			3	1				6	1	4	2	2	1			
Albunea symnista	3			1																				
Galathea	3			3									37	39	3	1	3	5	2		1	61	34	28
ASCIDEACEA												2												
BRACHYURA									2						3									13
Calappidae										1														
Dehaanius							2	1					1	1						3		3	4	
Dromiidae				4	5	7	2	2					3	1	2	5	1	2				4	2	3
Philyra			4			1																		
Xanthidae	2	2		1	2	1								1						2				
CARIDEA													1								1			
Callianassa					2																			
CHORDATA				1									1	1		1	1	1			1		2	
Branchiostoma						1										1	3	5	9	1	3			
COPEPODA						3					1	3	1	5	21	13	12	9	1			1		
CRINOIDEA			1										1											
CTENOPHORA																						1		
CUMACEA																								
Cyclaspis scissa						5	4	13	17															
Dic calmani			2							1						1	1		1					
Eocuma	1	1	4											2				2	2	1	3			
Iphinoe							2			2	2								1			11	10	11
Iphinoe crassipes							11				3													
Iphinoe stebbingi	126	113	63	77	59	141	1	30	24				3	2	8	4	5	4						
ECHINOIDEA						1		1				1		1	1									
GASTROPODA		2					1	2	2						1								1	
Polynices																				2	1			
ISOPODA																								
Anthuridae	3	11	2	1	4	2	9	9	10	1	3			1	2							4	4	5
Arcturidae					1	3	2	1	7					3	6								4	
Arcturina	1																							
Bopyridae																								1
Cirolana							6	3	3	1	1		3	6	7	4	3	4		2			2	2
Cyanthura							1																	
Idoteidae				1																				

13	1.33	1.78	0.57	1.26	0.67	79.66
87	1.33	1.33	0.55	1.00	0.65	80.31
98	1.33	2.44	0.55	1.55	0.65	80.95
138	0.00	1.56	0.52	1.17	0.61	81.57
142	1.00	1.44	0.51	1.01	0.60	82.16
113	0.33	1.67	0.50	0.45	0.59	82.75
17	0.00	1.78	0.48	0.76	0.57	83.32
55	0.00	1.11	0.44	0.90	0.51	83.83
14	1.33	0.33	0.44	0.94	0.51	84.34
30	1.00	1.33	0.44	0.92	0.51	84.86
150	0.00	0.89	0.43	0.51	0.50	85.36
112	0.00	1.56	0.42	0.68	0.50	85.85
73	1.33	0.11	0.42	1.33	0.49	86.35
53	0.00	1.56	0.42	0.91	0.49	86.84
76	0.33	1.33	0.40	0.73	0.47	87.31
107	0.00	1.33	0.38	0.61	0.45	87.75
82	0.33	1.11	0.38	0.70	0.44	88.20
67	0.00	1.44	0.37	0.62	0.43	88.63
102	1.00	1.22	0.36	1.22	0.42	89.05
151	1.00	0.22	0.36	0.76	0.42	89.47
145	1.00	0.00	0.35	1.08	0.41	89.88
59	0.67	1.00	0.34	0.92	0.40	90.28

PRIMER 2002/03/22

SIMPER
Similarity Percentages - species contributions

Worksheet

File: A:\MEIPR.PM1
Sample selection: All
Variable selection: All

Parameters

Standardise data: No
Transform: None
Cut off for low contributions: 90.00%
Factor name: 5.1.1 Cluster groupings (Meiofauna)

Average dissimilarity = 31.50

Species	Group C Av.Abund	Group B Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
12	205.33	340.67	14.38	2.03	45.66	45.66
13	55.00	4.89	5.36	2.59	17.00	62.66
3	13.00	45.11	3.55	1.49	11.26	73.92
8	104.44	111.11	2.88	1.52	9.14	83.06
14	16.56	1.11	1.68	1.32	5.32	88.39
7	11.00	3.89	1.13	0.91	3.58	91.97