

# More about Taxonomic Sufficiency: A Case Study using Polychaete Communities in a Subtropical Bay Moderately Affected by Urban Sewage

Pablo Muniz<sup>1,2\*</sup> and Ana M. S. Pires-Vanin<sup>2</sup>

- <sup>1</sup>Sección Oceanología, Facultad de Ciencias, Iguá 4225, 11.400, Montevideo, Uruguay
- <sup>2</sup> Present address of the first author. Instituto Oceanográfico da Univ. de São Paulo (IOUSP), Pça. do Oceanográfico 191, 05508-900. Cidade Universitária, São Paulo, SP, Brazil

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Abstract - The taxonomic sufficiency approach has been proposed as a surrogate for the typical analysis of speciesabundance data, especially in conditions involving prominent pollution gradients. Here, we evaluate the use of taxonomic sufficiency with infralittoral macrobenthic data derived from samples taken in a moderate polluted subtropical environment in southeastern Brazil, analysing five taxonomic levels and including two functional levels throughout polychaete feeding guilds and trophic groups. The data were collected seasonally at nine stations and studied for two abundance data series (0.5 and 1.0 mm sieve mesh-size). The results showed a similar ordination pattern between the two sieve mesh-size, but with the 0.5 mm sieve data a different pattern was observed during austral summer. A slight loss of information was detected using genus, family, polychaete species and their feeding guilds as taxonomic/ functional units. These results together with those of the cost/ benefit ratio, suggested that the family level seemed to be sufficient to detect the impact caused by moderate pollution in this shallow-water, subtropical environment. In additional, through the use of feeding guilds, similar patterns are obtained. Correlation analysis showed that chlorophyll a, total organic matter, zinc, and chromium sediment content were the variables that best explained the biological pattern observed and not always the best correlation coefficient occurring at the species level. The feeding guild approach seems to be useful and generates interpretable results similar to those obtained with the species level of the whole macroinfauna. The results showed an important cost reduction in the sample processing, suggesting that it is possible to adopt a coarser taxonomic level monitoring program even in species-rich communities.

**Key words** – macrobenthos, taxonomic resolution, pollution, monitoring, Brazil

## 1. Introduction

Contamination of the aquatic environment has become a serious problem in many parts of the world, with rivers and bays often seriously affected. Urbanised littoral areas receive effluent discharges resulting, in general, in the contamination of water, sediments and the biota that can affect human health by direct contact or through the food chain. Within aquatic ecosystems, the benthic environment has an important function as an efficient natural trap for several substances and also as a natural regulator of the sedimentary biogeochemical processes. Bottom sediments also constitute a source of nutrients for the water column above them, leading to benthic-pelagic coupling and influencing primary productivity (Jørgensen 1996). Sediments may act as a sink but also as a source of contaminants in these ecosystems.

The macrobenthic fauna are often used in the assessment of anthropogenic impacts because it integrates long-term environmental conditions (Bilyard 1987) but these approaches have been criticised due to the high cost involved (Kingston and Riddle 1989; Warwick 1993). Besides the very labour-intensive sampling methods, the laboratory analyses, *i.e.* sorting and identification of the organisms to the species level, are time-consuming and require the participation of experts in each macrofaunal group, which increases substantially the costs of a monitoring programme. In this sense, Ellis (1985) introduced the concept of "taxonomic sufficiency" which refers to the taxonomic level necessary and sufficient to meet the goals of the

<sup>\*</sup>Corresponding author. E-mail: pmmaciel@fcien.edu.uy or pmmaciel@usp.br

study. The analysis of data at levels higher than those of species have since been proposed as a surrogate for the typical analysis of species-abundance data (Warwick 1988a, b), especially, under conditions involving prominent pollution gradients. Although, in the last years, many studies have tested the taxonomic level sufficient for the assessment of several impacts, most of them have focused on the soft-bottom macrofauna in temperate and cold waters (Bayne et al. 1988; Herman and Heip 1988; Gray et al. 1990; Olsgard et al. 1997, 1998) and especially in relation to oil pollution (Warwick 1988a, b; Fiori and Soares-Gomes 2002). In these studies, a slight loss of information was detected when organisms were identified at higher levels than species, and generally work with the family level produced similar results to those generated with the species abundance data, reflecting the contamination gradient well. It has been argued that taxonomic levels higher than those of species can be used successfully in quantifying the impact on marine hard bottoms (Mistri and Rossi 2000; Pagola-Carte et al. 2002), in sandy beaches (Defeo and Lercari 2004) and also in terrestrial habitats (Pik et al. 1999, 2002). However, as pointed out by Terlizzi et al. (2003), few studies were made either in warm temperate (approximately 6) and/or tropical areas (only one).

The analysis of the trophic structure of benthic communities is a widely used method for determining energy flow in marine sediments. Many authors have demonstrated that the distribution patterns of trophic groups are sensitive to multiple factors, including environmental disturbance, food supply, sediment types, anthropogenic effects, and hydrodynamic conditions (Probert 1984; Gaston and Nasci 1988; Arasaki et al. 2004). In most benthic soft-bottom communities, polychaetes are frequently the main component of the macrofauna (Boesch 1972; Ward and Hutchings 1996), and this is also the case on the Brazilian inner shelf and coastal areas (Paiva 1993; Pires-Vanin et al. 1993; Muniz and Pires 1999, 2000). Classifying benthic animals into feeding categories dates back to the work of Hunt (1925), and this approach has been used extensively in soft-bottom environments (Maurer and Leathern 1981; Dauer 1984; Bianchi and Morri 1985). Along the southern Brazilian coast, Paiva (1993) and Muniz et al. (1998) have attempted to characterize the polychaete fauna of the Ubatuba region according to their assignment to trophic groups. Fauchald and Jumars

(1979) applied the concept of "feeding guilds" as a more comprehensive classification of trophic groups, since it includes both the motility and feeding strategies of the animals. This functional approach permits grouping of species as "ecological units" according to the similarity of their roles in the food web, and may replace the use of species populations in ecological studies (Muniz and Pires 1999). Fauchald and Jumar's classification has been revised for several polychaete families (Dauer *et al.* 1981; Gaston 1987) and, more recently, for several species of the Brazilian coast (Pardo 1995).

This study investigates the potential of several approaches to taxonomic sufficiency for detecting moderate impact levels caused by sewage and city runoff in a shallow subtropical macrozoobenthic community. The study was carried out in the Ubatuba region, located on the north coast of the São Paulo State (Brazil), specifically at the inner portions of Ubatuba and Picinguaba bays.

The north coast of the São Paulo State (Brazil) has several enclosed bays strongly affected by increasing tourism and urbanization (Furtado et al. 1987). Due to their physiography, water circulation and dispersion of exotic elements are restricted when compared to open sea areas. Ubatuba Bay is protected from south waves from the open sea (Mahiques 1995). Water circulation is clockwise with the inflow from the south. The input of fluvial sediments is strongly dependent on the rainfall regime leading to a higher contribution during the summer season (Mahiques et al. 1998). Four rivers flow into the bay and greatly influence its water quality (CETESB 1996; Burone et al. 2003; Muniz 2003) especially, during summer and rainy periods, when large amounts of untreated sewage are introduced from Ubatuba City. The innermost region of the bay, near the river mouths, consists of very fine sand with silt and clay, and with moderate organic matter content (Burone et al. 2003). In relation to the contents of heavy metals, hydrocarbons, and faecal sterols, this inner region can be classified from weak to moderately contaminated (Muniz 2003).

The aim of the present study is: (i) to test the possibility of whether the same spatial-temporal patterns can be derived from taxonomic levels higher than species; (ii) as (i) but using functional categories (by means of polychaete's trophic groups and feeding guilds) and only polychaete species; (iii) to determine the most cost-effective method for assessing the ecological effects caused by moderate

pollution in subtropical shallow environments, including the most effective sieve mesh-size (*i.e.* 1.0 or 0.5 mm). As far as we know, this is the first study dealing with taxonomic sufficiency along the southern Brazilian coast, as well as the first one to consider polychaete feeding guilds as functional units for these types of studies.

## 2. Material and Methods

## Sampling and methods

In April, August, and December 2001 and February 2002, sediments of the Ubatuba region from 9 stations were sampled, previously defined in a pilot survey (October 2000). The stations were positioned using the

global positioning system (GPS). Six of them (St. 1 to 6) were located in the inner region of Ubatuba Bay, while one was (St. 7) in the outer region and two (St. 8 and 9) in the neighbouring Picinguaba Bay (Fig. 1). The rationale for selecting the sampling locations was to ensure a similar depth and sediment type and different degrees of anthropogenic impact. St. 1 to 6 were under direct riverine influences, St. 7 without river influence, while St. 8 and 9 in the Picinguaba Bay were used as a reference site. The two bays are approximately 10 km apart on the north coast of the São Paulo state. Although the bays are located between two of the main ports of South America (i.e Santos and Rio de Janeiro), they have a different degree of anthropogenic perturbation. While Picinguaba Bay

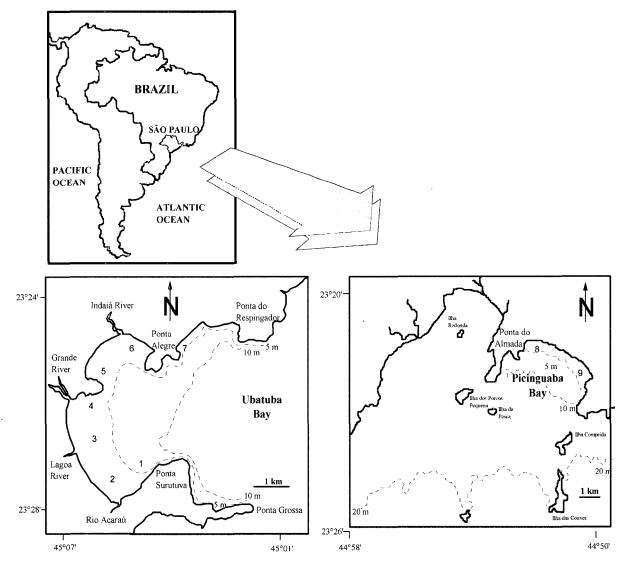


Fig. 1. Map of the study area (North littoral of São Paulo State, Brazil) showing the sampling stations at Ubatuba (St. 1 to 7) and Picinguaba (St. 8 and 9) bays.

constitutes a well preserved site, far from human occupation, owing to its contiguity to a state park (Paiva 2001), Ubatuba Bay presents some ecological and water quality perturbations (CETESB 2000; Burone *et al.* 2003; Muniz *et al.* 2005).

At each station, sediment samples were collected with a manual Kajac corer of 8.0 cm in internal diameter for the analyses of the following factors: granulometric parameters, photosynthetic pigments, total organic matter, total organic carbon, total nitrogen, sulphur, chromium, zinc, copper, hydrocarbons and sterols. The first 3 cm of the sediment column were analysed. Muniz (2003) described in detail the sample conservation and laboratory methods for these sediment variables.

For macrofauna, five replicate samples were taken by using a 0.05 m² van Veen grab at each station (1 to 9). Sediment samples were sieved trough a 0.5 and 1.0 mm square aperture sieve-mesh and preserved in 70% ethanol. In the laboratory animals in the two different fractions were sorted under a stereomicroscope, and subsequently identified to the lowest possible level, generally that of species. Only the time taken to identify the polychaete fauna at the family, genera and species level was recorded since this group was identified by the first author. As the other faunal groups were sent to experts for their identification, quantification of time could not be considered.

#### Data analysis

Species abundance data of the whole macrofaunal community were aggregated to genera, family, and phylum levels. For the polychaete species abundances were also aggregated to feeding guilds and trophic groups. The polychaete trophic groups (TG) and feeding guilds (FG) classification was made according to Fauchald and Jumars (1979) with some modifications introduced by Gaston (1987), Lastra *et al.* (1991), Paiva (1993) and Pardo (1995). The use of polychaetes and their TG and FG as taxonomic/functional units is justified by its dominance in the studied community (Muniz 2003; Muniz *et al.* 2005), as well as by the advanced knowledge of their trophic classification when compared to other groups.

Subsequent calculations were done using the PRIMER package (Clarke and Warwick 1994). Abundance data from the resulting 56 matrices (7 taxonomic/functional levels x 4 surveys x 2 sieve-mesh size) were transformed as following: none, log (x+1), square root, fourth root and

presence/absence, generating a total of 280 matrices. These matrices were analysed using non-metric multidimensional scaling (nMDS) with the Bray-Curtis similarity measure (Bray and Curtis 1957). The goodness-of-fit of the resulting 2-dimensional ordination was measured using Kruskal's stress Formula I (Kruskal and Wish 1978).

The temporal analysis of the variability at different taxonomic levels, with the square root transformed data, was studied through a second-stage MDS ordination (Somerfield and Clarke 1995), on a total of 28 ranked matrices of similarities among samples. By means of this technique, the rank correlations calculated between pairs of similar matrices become the elements of a second matching matrix, which is then used as an input matrix for the second-stage MDS ordination. In this ordination, the relative distances between the symbols (similarity matrices) shows how similar they are, and in this manner patterns in a number of similar matrices (seven types of aggregation and four surveys in this study) can be compared simultaneously (Olsgard *et al.* 1998).

Correlations between similar matrices obtained from species abundances and matrices derived from abundances as aggregated at the higher taxonomic levels were calculated using the non-parametric Spearman rank correlation coefficient (Clarke and Ainsworth 1993). The cost/benefit ratio of Karakassis and Hatziyanni (2000) was also calculated for each data set, using the formula:

$$CB_L = \frac{1 - \rho_L}{(S - t_L)/S}$$

where  $CB_L$  is the ratio at taxonomic level L,  $\rho_L$  is the Speraman correlation coefficient between taxonomic levels,  $t_L$  is the number of taxa present at the taxonomic level and S is the number of species.

According to the aforementioned authors, the ratio permits the selection of the taxonomic level with the minimal loss of information and the least taxonomic effort. It ranges between 0 and 1, and when the value is equal to zero, a high correlation between the specific level and any of the other ones exists, which means that the loss of information is zero.

In order to relate environmental data (contaminants included) to biological data, the BIO-ENV (biotic-environmental matching) procedure was applied (Clarke and Ainsworth 1993). The best matches of abiotic (standardised) and biotic (square root transformed) similarity matrices were

measured using the weighted Spearman rank correlation coefficient ( $\rho_{\text{w}}$ ). The seven taxonomic/functional levels were analysed separately and then compared with the species level results. This approach was done to evaluate if the subset of selected variables that best explain the species pattern is the same and has the same effect at the other levels considered.

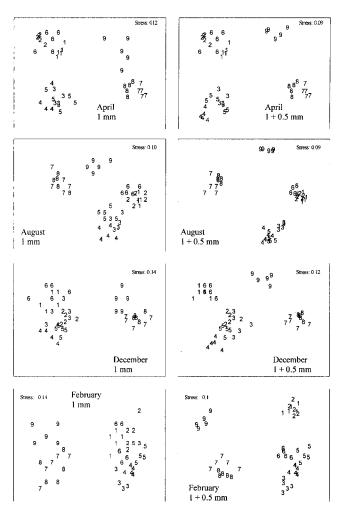
## 3. Results

A total of 47,499 individuals belonging to nine phyla, 88 families, 135 genera, 188 species, 72 polychaete species, 12 feeding guilds and 5 trophic groups were recorded (Appendix 1).

The two series of data generated by the 1.0 and 1.0+0.5 mm sieve-mesh size showed similar results in April and August surveys at the various levels of taxonomic aggregation studied. The differences were more marked during the December and February surveys (Fig. 2), when a large fraction of small individuals was recorded, especially some polychaete opportunistic species, and also when nematode abundance had an important increment (Muniz 2003, Muniz *et al.* 2005). Table 1 shows the differences in abundance and number of species retained both in the 1.0 and in the 1.0+0.5 mm mesh-sieve size for the four surveys. Since, some differences were detected between the two data sets, subsequent results are only referred to in the 1.0+0.5 mm mesh-sieve size data.

The time spent for identification of polychaete fauna was recorded for the second, third, and fourth surveys. Excluding the first survey, we believe that avoiding the possible bias related with the time spent going through the literature to obtain the name on an unfamiliar species for example. It was observed that the cost of identifying species was 6.5 times larger than that of identifying a family and 3 times larger than that of identifying a genus.

The ordination of sites by nMDS, considering all the macrofaunal species, showed first aggregation of the replicates (Fig. 2), and the station groups formed varied according to the two major temporal patterns. These patterns were detected clearly in the 1.0+0.5 mm sievemesh size data set, and basically reflected the difference in the abundance of small-sized individuals retained in the 0.5 mm mesh size (mainly *Mediomastus capensis* together with several spionid species and nematodes, Muniz *et al.* 2005). The pattern observed in April and



**Fig. 2.** nMDS ordinations of replicate grab samples at each station, based on square root transformed abundances species data for each survey. Results for the 1.0 mm and 1.0+0.5 mm data sets. Stress of the two dimensional configuration are indicated.

**Table 1.** Total abundances and number of species, for each one of the four surveys, retained both in 1.0 and 1.0+0.5 mm mesh-sieve size

	mesh-sieve	abundance	species number
April	1.0	4812	121
-	1.0+0.5	11625	139
August	1.0	4644	104
	1.0+0.5	12170	123
December	1.0	3816	104
	1.0+0.5	11478	151
February	1.0	4470	109
·	1.0+0.5	12226	142

August showed that the replicates of station 9 formed a group, station 7 and 8 clustered together forming the second group and stations 1, 2 and 6 formed the third

group; finally stations 3, 4 and 5 formed the last group (Fig. 2). The first two groups remained unchanged in December and February (austral summer, rainy season), but station 2 clustered together with the group formed by stations 3, 4 and 5 in December. In February station 6 clustered together with stations 3, 4 and 5 forming one group (Fig. 2). The observed pattern involved the separation of those stations with riverine influences (more impacted sites) from those displaying marine influences (7, 8 and 9). These grouping sites are in accordance to those obtained from faecal sterols, hydrocarbons, heavy metals, and other sediment variables (Muniz 2003). In this work, it was shown that sewage from these rivers along with city runoff are the main factors responsible for the environmental quality of the Ubatuba Bay system and for some ecological aspects is related to the species distribution (Muniz 2003; Muniz et al. 2005). The above mentioned distribution pattern was more clearly detectable with the 1.0+0.5 mm data set than with the 1.0 mm data set (Fig. 2).

The loss of information, expressed as a decrease in the Spearman rank correlation coefficient (p) derived from the analysis of a given taxonomic level compared with the species level, showed that higher correlation coefficients occurred when data was untransformed or square-root transformed (Fig. 3). With the five types of transformation, the  $\rho$  remained above 0.90 for genus, family, and polychaete species, and above 0.80 for polychaete feeding guilds (FG). Furthermore, using untransformed or square-root transformed data for the polychaete trophic group (TG) and at the phylum level, the loss of information was also low. By using the other three types of transformation, a marked decrease in p values was observed with a further decrease in taxonomic resolution, being that the lowest value of p occurred when data were transformed by presence/absence and considered at the phylum, polychaete feeding guilds and trophic groups levels (Fig. 3). The low temporal variability in the studied communities could be observed through the analysis of the p values, which in most of the cases were lower in summer than in the other surveys, especially at coarser taxonomic levels. The variability was enhanced by the decrease of taxonomic resolution and the severity of transformation.

As the square-root data transformation showed the highest values of  $\rho$ , the temporal analysis of the variability at different taxonomic levels, studied through a second-

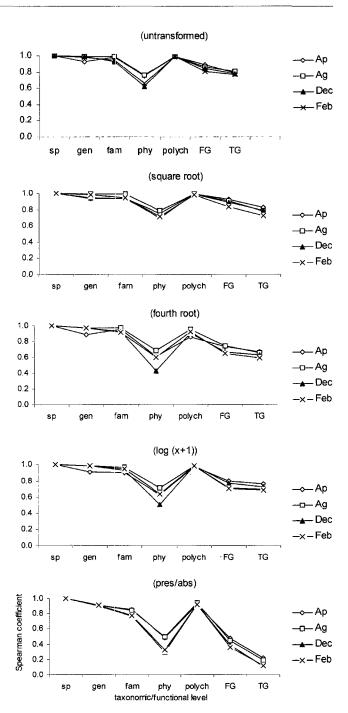
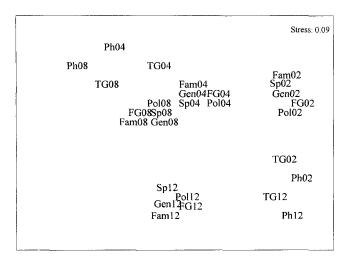


Fig. 3. Spearman correlation coefficients between species abundance matrix and the other matrices derived of the taxonomic and functional levels considered for each one of the four surveys and type of transformations used. sp = species level; gen = genera level; fam = family level; phy = phyla level; polych = polychaete species level; FG = polychaete feeding guild level; TG = polychaete trophic group level; Ap = April survey; Ag = August survey; Dec = December survey; Feb = February survey.

stage MDS ordination, was done only with this type of transformation (Fig. 4). Matrices derived from species,



**Fig. 4.** nMDS "second-stage" ordination of inter-matrix rank correlations for the four surveys. Abundance data based on square root transformed. Taxonomic levels nomenclature are the same of Figure 3. 04 = April survey; 08 = August survey; 12 = December survey and 02 = February survey. Stress of the two dimensional configuration are indicated.

polychaete species, genus, family and to a lesser extent feeding guild (FG) abundances, tend to cluster together, indicating that as the taxonomic level increases, the similarity among the matrices decrease. The more marked differences occurred in the summer surveys (symbols further apart). Although the distribution pattern of the stations was similar throughout the studied period (Fig. 2), some differences were detected when analysed together (Fig. 4), indicating that the communities were more similar at most of the levels of taxonomic/functional aggregation considered than those observed on a temporal scale.

Figure 5 showing the patterns at the different taxonomic/functional levels of aggregation considered for the two data sets (1.0 and 1.0+0.5 mm). We can observe that the patterns were similar with all the levels considered, but were clearer when considering the 1.0+0.5 mm.

The cost/benefit ratio showed lower values for the polychaete species level as well as genus and family levels (Fig. 6). The two data sets (1.0 and 1.0+0.5 mm) presented the same trend comparing the taxonomic levels, but the ratio values were slightly higher in the 1.0 mm than in the 1.0+0.5 mm data set. Taking into account the precision of the results and the decrease in the taxonomic effort, we can suggest that working with the levels mentioned above gives the best results without disturbing the pattern observed for the species level data. Considering

the reduction in the number of taxa/units (considering the 1.0+0.5 mm data set) when compared to the species level (53% for family, 29% for genera and 62% for polychaete species), the constancy of the  $\rho$  values, and the low values of the cost/benefit ratio, it seems to be clear that these levels of taxonomic resolution give the best results in terms of minimising loss of information and precision in interpreting the observed patterns.

The BIO-ENV results showed that the combination of variables with higher correlation coefficients (that best explained the biological pattern observed), almost always included chlorophyll a, total organic matter, zinc, and chromium (Table 2). The maximum values of  $\rho_{xx}$  occurred for the species level (with the exception of April survey), indicating that the biological pattern was best identified with this level of taxonomic resolution. However, the differences in p<sub>w</sub> values for genus, family, polychaete species, and feeding guild levels were minimal when compared to the species level, showing that at these higher levels of taxonomic resolution and at the functional level of feeding guilds, the biological pattern can also be clearly detectable. In general, the polychaete feeding guild level showed  $\rho_{w}$ values that varied between species and genus or family levels, showing that this approach also provided interpretable faunal ordinations. For phyla and polychaete trophic group levels, the lowering of correlation was more severe. Therefore, the identification of macrofauna at genus, family, polychaete species, and feeding guilds showed interpretable ordinations of the stations in this coastal area with a moderate degree of pollution.

#### 4. Discussion

The results of the present study, compared the patterns produced at the species level with those generated at higher levels, including polychaete feeding guilds and their trophic groups as functional units, showed that the loss of information was relatively low. The same community patterns were observed at the levels of genera, family, polychaete species, and polychaete feeding guilds. Other studies working in subtidal temperate and/or sub-tropical benthic communities have also highlighted the ecological importance of the polychaete species and/or their functional groups (Ward and Hutchings 1996; Muniz and Pires 1999; Paiva 2001). Previous investigations developed in several benthic communities subjected to strong pollution

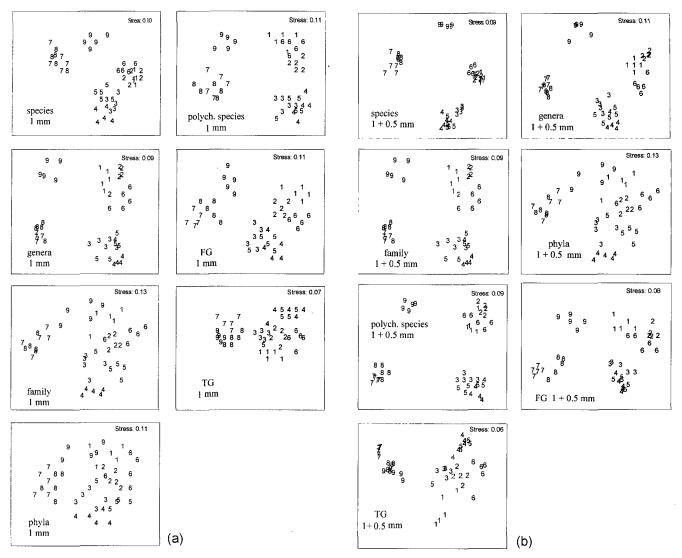
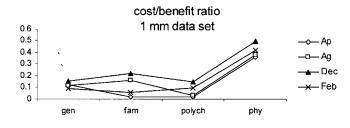


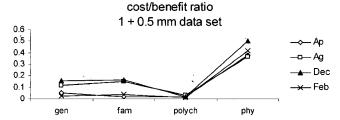
Fig. 5. nMDS ordinations of replicate grab samples at each station based on square root transformed abundances data for August survey. Results for the (a) 1.0 mm data set and (b) 1.0+0.5 mm data set; at species, genera, family, phyla, polychaete species, polychaete feeding guild (FG) and polychaete trophic (TG) group levels. Stress of the two dimensional configuration are indicated.

gradients (Warwick 1988a, b; Ferraro and Cole 1990; Somerfield and Clarke 1995; Olsgard *et al.* 1997, 1998) showed that working at genera, family, order and sometimes class and phylum levels generated a benthic pattern similar to those obtained at the specific level. According to Ferraro and Cole (1990) the biological explanation for taxonomic sufficiency in pollution impact assessments is the hierarchical structure of biological responses to stress. As the disturbance increases, the tolerance of individuals first, then species, genera, families, etc. is decreasing and consequently the impact resulting from increasing stress is manifested at higher levels of biological

organisation, and therefore, the taxonomic level sufficient to assess the impact should increase. This simply means that, as the stress increases, the faunal gradient becomes stronger, and consequently the effects may be detected at lower taxonomic resolution. Furthermore, organisms aggregated to a higher taxonomic level than species may show less natural variability in benthic communities because species are more affected than higher taxa by both seasonal cycles and other drives of natural variability (Warwick 1988a, b).

At phyla and polychaete trophic group levels, the results showed the patterns to be quite different and the





**Fig. 6.** Cost/benefit ratios for the different taxonomic levels for the four surveys considering the two data sets utilised (1.0 mm and 1+0.5 mm). Survey and taxonomic level nomenclature are the same of Figure 3.

community pattern could not be easily recognised. In strongly perturbed sandy beaches, Defeo and Lercari (2004) observed good responses of the macrofauna working at the trophic group level. Perhaps, in the Ubatuba region, the moderate degree of pollution results in low or moderate levels of stress and for this reason the impact was less evident at the phylum and polychaete trophic group levels. Olsgard *et al.* (1988) found similar results in the North Sea benthic communities where the contamination was weak.

Analysing the fauna at a species level, a different abundance pattern of two opportunistic polychaetes retained in the 0.5 mm sieve-mesh size was observed (high proliferation in the austral summer, Muniz 2003; Muniz et al. 2005). The efficiency of a mesh size to sample macrofauna will vary depending on the benthic community. Universally, the recommended sieve-mesh size to study macrofauna is 1.0 or 0.5 mm for shallow water and 0.3 mm for deep sea environments (Gage and Tyler 1991). Hartley (1982) explained that the most important difference between the 1.0 and 0.5 mm mesh is due to the high number of juveniles retained in 0.5 mm. Recently, Thompson et al. (2003) analysing cost-efficiency methods for marine pollution monitoring in Antarctica, recommended the use of 1.0 mm sieves as the most cost-effective compromise between reliability of results and the ease of sample sorting. The authors also found that most of the fauna retained in the 0.5 mm mesh were juveniles of organisms retained in the 1.0 mm mesh. In the Ubatuba region, the differences in abundance and species number between the data set of 1.0 mm and that of 1.0+0.5 mm were important and the abundance patterns were different in the summer surveys. As the use of the 1.0 mm data set did not permit the observation of the proliferation of small opportunistic species during summer, we still recommend the use of a 0.5 mm mesh. However, there is obviously an increase in the sample processing costs.

Another aspect of the present study at issue was the type of transformation used. Data transformation has

**Table 2.** BIO-ENV results for each survey and for each one of the seven taxonomic levels considered. The Subset of environmental variables showing the best pw for each survey and for each taxonomic level are listed. Faunal abundances are square root transformed and environmental variables are standarised.

	April	August	December	February
species	0.781	0.836	0.852	0.832
	chlor a, TOM, N, Cr, Zn	chlor a, pheopig, Cr, Cu	MD, TOM, Cu, Zn	Zn, N, TOM
ganara	0.778	0.782	0.826	0.797
genera	chlor a, TOM, N, Cr, Zn	chlor a, pheopig, Cr	TOM, Cu, Zn, chlor a	Zn, TOM, N
family	0.896	0.775	0.748	0.788
	chlor a, TOM, Cr	chlor a, pheopig, Cr	TOM, Cu, Zn, chlor a	Zn, TOM, N
phyla	0.592	0.581	0.627	0.602
pityta	chlor a, TOM, Cr	Cr, MD	TOM, Cu, C/N	TOM, N, C/S
polychaete	0.825	0.832	0.836	0.824
	chlor a, TOM, N, Cr, Zn	chlor a, pheopig, Cr, Cu, TOC	TOM, Cu, Zn, chlor a	Zn, N, TOM, TOC
FG	0.783	0.741	0.809	0.801
	chlor a, TOM, N, Cr	chlor a, COT, Cr, Cu	TOM, Cu, Zn, chlor a	TOM, N, Zn
TG	0.594	0.622	0.623	0.613
	chlor a, TOM, Cr	chlor a, COT	TOM, Cu, C/N	TOM, N, Cr

variable effects on the final results of multivariate patterns and its use depends upon the type of data considered (Olsgard et al. 1997, 1998; Karakassis and Hatziyanni 2000). These authors suggested together with Clarke and Warwick (1994) that the choice of transformation is more a biological than a statistical task, and that universal strategies cannot be recommended. The type of transformation determines the relative contribution of the differences, both qualitative and quantitative, among the samples. The present results suggested that the more appropriate transformation was square-root transformed or untransformed for the community studied. Strong transformations, like fourth root,  $\log (x+1)$  or presence/absence minimised too much the quantitative differences among the species (or other taxonomic units) in cases such as the Ubatuba region, where the differences were more of the quantitative than the qualitative order. These effects were more evident as the level of taxonomic resolution decreased.

These results are important given the potential for time and cost reduction in environmental monitoring programmes. Savings of time and the cost associated with taxonomic aggregation are difficult to estimate, since the time taken to identify fauna is directly related to the number of taxonomic units and the expertise of the available personnel. Ferraro and Cole (1995) and Thompson et al. (2003) reported time savings of about 50% for family level identification and up to 90% for the phylum level. These authors estimated the savings by considering the ratio of the number of higher taxa to the number of species and assuming that the time spent to identify the fauna is directly related to the number of categories in which they must be placed. This approach could be underestimating the time saved because species identification is more difficult and time consuming than genera and family. In the present study, only the time taken in identifying each category for the polychaete fauna was computed and the results showed that the time spent to identify species was 6.5 times larger than that of the family and 3 times larger than that of genus.

According to Karakassis and Hatziyanni (2000), the cost/benefit ratio implies that there is a difference in the rate of loss of information and in the decrease in the number of taxa present at each level. In this sense, a marked change in information loss or in the number of taxa may identify the optimal level for the analysis. In the Ubatuba region, the most marked change in the index

value occurred between family and phyla levels. Among genus, family and polychaete species levels, the index values were similar. Moreover, in some cases, family and polychaete species levels were better than those of the genus level. Nevertheless, we should not forget that the index is based on the assumption that species level identification provides the most information (Karakassis and Hatziyanni 2000). Therefore, the index really selected the second best level. However, is the species level always the best?

The BIO-ENV results showed that aggregation of data at the level of the phyla and polychaete trophic group produce the lowest correlation coefficients in the four surveys analysed. At other taxonomic levels, the results obtained were very close to those based on species level data. Moreover, in the April survey, family seemed to be the best level (highest correlation), but also polychaete species and feeding guild levels had higher correlation coefficients than species and genus levels. Thus, the results suggest that data aggregated at these taxonomic and/or functional levels are no less informative than those of the species level in this type of study, adding weight to the results of previous studies (Warwick 1988a, b; Ferraro and Cole 1990, 1995; Vanderklift et al. 1996; Olsgard et al. 1997, 1998; Gomez Gesteira et al. 2003; Thompson et al. 2003; Defeo and Lercari 2004). The redundancy of information in species level macrobenthic fauna data sets was reflected in the small effect that the change of taxonomic resolution has on multivariate patterns. Furthermore, the results showed that working with a functional approach (polychaete feeding guilds in this case) leads to a realistic response of the macrobenthic communities, similar to those obtained with the traditional approach of species level data. However, the use of this functional approach does not permit saving costs in this type of study, since species identification is needed to classify the organisms in feeding types and guilds.

The second-stage MDS analyses for the Ubatuba region assigned the objective differences among all the matrices (square root transformed data only) derived from the different taxonomic/functional levels and surveys considered in this study. It was shown that for each separate survey the ordinations derived from species, genus, family, polychaete species, and feeding guilds were, in most cases, similar. At the level of phyla and trophic groups, the similarities became less obvious. The present results confirmed the

postulation of Olsgard *et al.* (1997, 1998), who suggested that in areas with weak pollution, the correlation between species and phyla levels were low, implying that finer taxonomic levels should be used.

Considering that the knowledge of species diversity in many habitats is inadequate or that some groups widely used in environmental studies are far from being taxonomically well known (Terlizzi et al. 2003), the use of taxonomic levels higher than species seems to be an appropriate approach. It is also true when different people participate in sorting and identification of the fauna, since species identification is more error prone than identification to higher taxa (Ellis and Cross 1981). Then, sorting efficiency among different people can be improved with coarser taxonomic resolution (Thompson et al. 2003). This is important in times of widespread demise of taxonomy (Boero 2001) and when there are not enough taxonomists for the different groups that are part of macrofaunal communities. It is more useful to obtain correct information on taxa higher than species that incorrect information at the species level.

Although, these results can be used to make general recommendations of the usefulness of working with taxonomic levels higher than species, some considerations should be taken into account. As was highlighted by Terlizzi et al. (2003) the knowledge of species, their biology and ecology, is indispensable also to defining the possible sufficient taxonomic level in monitoring studies. In the Ubatuba region in the course of species identification, two new polychaete species were disclosed and are now in the description stage (Muniz 2003). The use of the taxonomic sufficiency concept must not be interpreted as a substitution for species based studies and yes as a helpful method in monitoring programmes. Moreover, it would be desirable that it be applied when a species baseline data has already been obtained. In poorly known ecosystems, the "rule" should be to acquire detailed information and then study if the taxonomic sufficiency is or is not applicable. Also, there are some pollution investigations for which species level data may be required, as for example if one is interested in determining the effects of a pollutant or a pollution event at the species level.

In conclusion, taxonomy sufficiency appears to be a useful concept in subtropical shallow communities submitted to a moderate impact from domestic sewage and urban activities. In rich polychaete communities like the Ubatuba

region, the feeding guild approach seems to be useful and generates interpretable results similar to those obtained with species, genus, and family levels of the whole macroinfauna community. As a tool for increasing the statistical power of this type of studies and efficiently interpreting the natural and the man-induced variability in benthic communities, it would be desirable that the cost saved with the taxonomic sufficiency approach be reallocated to additional replication both in space and time. The final decision about the taxonomic resolution to which level the fauna must be identified depends on the research objectives. Considering that, as the present study is one of the first developed in South America, more examples from different situations and localities will be necessary before this approach is applied as a regular rule in monitoring programmes. Finally, we would like to highlight that this study does not intend to discourage the interest in taxonomy as was pointed out by Maurer (2000) in his recent "Viewpoint" article entitled, "The dark side of taxonomic sufficiency (TS)". Nevertheless, this type of approach will be perfectly applicable without remorse in those situations where species information are redundant to the study objectives as in the field of environmental management and/or monitoring programmes.

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Appendix 1. List of the species collected in the Ubatuba region with the taxonomic levels considered in the study. Feeding guild nomenclature according to Fauchald and Jumars (1979). CMJ = carnivore motile jawed; SDT=surface deposit-feeder discretely motile tentaculate; SMX=surface deposit-feeder motile with eversible pharynge; HDJ=omnivore discretely motile jawed; SDJ=surface deposit-feeder discretely motile jawed; BMX=subsurface deposit-feeder motile with eversible pharynge; CDJ=carnivore discretely motile jawed; BDJ=subsurface deposit-feeder discretely motile jawed; FDT=suspension-feeder discretely motile tentaculate; FST=suspension-feeder sessile tentaculate; HMJ=omnivore motile jawed; CMX=carnivore motile with eversible pharynge; SST=surface deposit-feeder sessile tentaculate; SMJ=surface deposit-feeder motile jawed.

Phylum	Family	Genera	Species	Feeding guild
Coelenterata	Edwarsiidae	Renilla	Renilla reniformis	
		Edwarsia	Edwarsia sp.1	
Nematoda			nematodos n.i	
Annelida	Polynoidae	Harmothoe	Harmothoe lunulata	CMJ
		Eunoe	Eunoe papillosa	CMJ
			Eunoe serrata	CMJ
	Pholoidae	Pholoe	Pholoe minuta	СМЈ
	Sigalionidae	Sigalion	Sigalion taquari	CMJ
			Sigalion sp.1	СМЈ
		Sthenelais	Sthenelais sp.1	CMJ
	Amphinomidae	Pseudeurythoe	Pseudeurythoe ambigua	CMX
	Pilargidae	Parandalia	Parandalia tricuspis	CMJ
		Sigambra	Sigambra grubii	CMJ
		Cabira	Cabira incerta	CMJ
		Ancistrosyllis	Ancistrosyllis jonesi	CMJ
	Syllidae	Exogone	Exogone arenosa	HMJ
		Typosyllis	Tiposyllis hyalina	СМЈ
	Nereiridae	Nereis	Nereis broa	HDJ ,
		Neanthes	Neanthes cf. succinea	HDJ
			N. bruaca	HDJ
	Nephtyidae	Nephtys	Nephtys squamosa	СМЈ
		Aglaophamus	Aglaophamus juvenalis	CMJ
	Glyceridae	Glycera	Glycera americana	CDJ
			G. oxycephala	CDJ
		Hemipodus	Hemipodus rotundus	CDJ
	Goniadidae	Goniada	Goniada littorea	CDJ
			Goniada brunnea	CDJ
		Glycinde	Glycinde multidens	CDJ
	Onuphidae	Diopatra	Diopatra cuprea	CDJ
	F		D. cf. tridentata	CDJ
		٠.	D. spiribranchis	CDJ
		Onuphis	Onuphis eremita oculata	CDJ
	Eunicidae ,	Eunice	Eunice rubra	BDJ
	Eumerdae	Lunice		
			E. prayensis	BDJ
		Marphysa	Marphysa sanguinea	BDJ
	Lumbrineridae	Ninoe	Ninoe brasiliensis	SMJ
		Lumbrineris	Lumbrineris tetraura	СМЈ
			Lumbrineris sp.	CMJ
		Aglaurides	Aglaurides sp.	CMJ
	Arabellidae	Notocirrus	Notocirrus cf. lorum	СМЈ

(Appendix 1. Continued)

Phylum	Family	Genera	Species	Feeding guild
	Orbiniidae	Nainereis	Nainereis setosa	BMX
		Leitoscoloplos	Leitoscoloplos robustus	BMX
		Haploscoloplos	Haploscoloplos sp.	BMX
		Protoaricia	Protoaricia sp.	BMX
		Phylo	Phylo felix	BMX
	Paraonidae	Cirrophorus	Cirrophorus branchiatus	SMX
		-···- <b>F</b> ·····	C. americanus	SMX
		Aricidae	Aricidae (Acmira) taylori	SMX
	Spionidae	Spiophanes	Spiophanes missionensis	SDT
	Spiomaac	Scolelepis	Scolelepis squamata	SDT
		<del>-</del>		
		Paraprionospio	Paraprionospio pinnata	SDT
	Magelonidae	Magelona	Magelona posterelongata	SDT
			M. papillicornis	SDT
	5	** 41 1	M. variolamellata	SDT
	Poecilochaetidae	Poecilochaetus	Poecilochaetus australis	SDT
	Chaetopteridae	Spiochaetopterus	Spiochaetopterus nonatoi	SDT
	Cirratulidae	Tharyx Cimifornia	Tharyx sp.	SDT
	Elaballigaridas	Cirriformia Piromis	Cirriformia sp.	SDT SDT
	Flabelligeridae	Pherusa	Piromis cf. arenosus Pherusa sp.	SDT
	Opheliidae	r nerusa Armandia	Armandia cf. agilis	BMX
	Ophemuae	Armanata	A. maculata	BMX
			Armandia sp.1 (n. sp.)	BMX
	Capitellidae	Mediomastus	Mediomastus capensis	BMX
	Capitomaao	Notomastus	Notomastus lobatus	BMX
	Maldanidae	Axiothella	Axiothella brasiliensis	BMX
		Clymenella	Clymenella dalesi	BMX
		Aschys	Aschys sp.1	BMX
	Oweniidae	Owenia	Owenia cf. fusiformis	SDT, FDT
			Owenia sp.1 (n. sp.)	SDT,FDT
		Myriochele	Myriochele heeri	SDT
	Pectinariidae	Pectinaria	Pectinaria (Pectinaria) sp.	BMX
			Pectinaria (P.) laelia	BMX
	Ampharetidae	Ampharete	Ampharete sp.	SST
		Isolda	Isolda pulchella	SST
Sipuncula	Aspidosiphonidae	Aspidosiphon	Aspidosiphon albus	***
	Sipunculidae	Sipunculus	Sipunculus nudus	
	Golfingiidae	Thysanocardia	Thysanocardia catharinae	
			Thysanocardia sp.	
Cheliceriformes	Ammotheidae	Achelia	Achelia besnardi	
	Phoxichiliidae	Anoplodactylus	Anoplodactylus cf. pygmaeus	
			Anoplodactylus cf. strictus	
			Anoplodactylus sp.	
		Pycnossoma	Pycnossoma sp.	
Crustacea	Pinnotheridae	Pinnixa	Pinnixa sayana	

## (Appendix 1. Continued)

Phylum	Family	Genera	Species	Feeding guild
			Pinnixa rapax	
			Pinnixa sp.1 (n. sp.)	
		Pinnotheres	Pinnotheres emiliai	
	Paguridae	Pagurus	Pagurus sp.	
	Upogebiidae	Upogebia	Upogebia sp.	
	Corophiidae	Photis	Photis longicaudata	
		Cheiriphotis	Cheiriphotis megacheles	
		Ampelisciphotis	Ampelisciphotis podophthalma	
		Cerapus	Cerapus sp.	
		Gammaropsis	Gammaropsis sp.	
	Platyischopiidae	Tiburonella	Tiburonella viscana	
	Ampeliscidae	Ampelisca	Ampelisca cristata	
	•	•	Ampelisca paria	
			Ampelisca brevisimulata	
			Ampelisca pugetica	
			Ampelisca romigi	
			Ampelisca sp.	
	Ischyroceridae	Erithonius	Ericthonius brasiliensis	
	Phoxocephalidae	Microphoxus	Microphoxus cornutus	
	Phoxocephalopsidae	Puelche	Puelche orensanzi	
	Caprellidae	Caprella	Caprella sp.	
	Megaluropidae	Gibberosus	Gibberosus myersi	
	Dexaminidae	Atylus	Atylus minikoi	
	Liljeborgiidae	Listriella	Listriella titinga	
	Oedicerotidae	Monoculodes	Monoculodes nyei	
	Synopiidae	Tyron	Tyron sp.	
	Kalliapseudidae	Hemikalliapseudes	Hemikalliapseudes cavooreni	
		Psammokalliapseudes	Psammokalliapseudes mirabilis	
	Bodotriidae	Cyclaspis	Cyclaspis reticulata	
	•		Cyclaspis oxyura	
			Cyclaspis dentifrons	
			Cyclaspis sp.1	
	Diastylidae	Anchistylis	Cyclaspis sp.2 Anchistylis sp.1	
	Diastylidae	Anchistylis Diastylis	Diastylis planifrons	
		Diasiyiis	Diastylis sp.1	
	Nannastacidae	Campylaspis	Campylaspis sp.1	
		Cumella	Cumella sp.1	
	Cirolanidae	Eurydice	Eurydice littoralis	
	Munnidae	Uromunna	Uromunna cananeia	
	Idoteidae	Synidotea	Synidotea marplatensis	
		Edotea	Edotea sp.	
	Sphaeromatidae	Ancinus	Ancinus brasiliensis	
		Paracerceis	Paracerceis sculpta	

(Appendix 1. Continued)

Phylum	Family	Genera	Species	Feeding guild
Mollusca	Naticidae	Natica	Natica pusilla	
	Olilvidae	Olivella	Olivella puelcha	
			Olivella sp.	
		Eulima	Eulima mulata	
	Eulimidae	Melanella	Melanella arcuata	
	Retusidae	Volvulella	Volvulella paupercula	
	Cylichnidae	Acteocina	Acteocina inconspicua	
	Acteonidae	Acteon	Acteon pelecais	
	Vitrinellidae	Solariorbis	Solariorbis bartschi	
			Solariorbis shimeri	
	Columbellidae	Anachis	Anachis obesa	
	Tornidae	Macromphalina	Macromphalina argentina	
	Calyptraeidae	Calyptraea	Calyptraea centralis	
	Periplomatidae	Periploma	Periploma compressa	
		1	Periploma sp.	
	Ungulinidae	Diplodonta	Diplodonta punctata	
	g	- <sub>1</sub> ,	Diplodonta sp.	
	Corbulidae	Corbula	Corbula caribaea	
	Mytilidae	Amigdalum	Amigdalum cf. papyrium	
	Solenidae	Solen	Solen tehuelchus	
	Lucinidae	Codakia	Codakia costata	
	Baomaco	Ctena	Ctena pectinella	
		Divaricella	Divaricella quadrisulcata	
	Cuspidariidae	Cardiomya	Cardiomya perrostrata	
	Veneridae	Chione	Chione subrostrata	
	Veneriaae	Tivela	Tivela mactroides	
		111010	Tivela sp.	
	Mactridae	Mactra	Mactra isabelleana	
	Machidae	macii a	Mactra janeiroensis	
			Mactra sp.	
	Tellinidae	Tellina	Tellina exerythra	
	Temmaae	Tettina	Tellina versicolor	
			Tellina punicea	
			Tellina martinicensis	
			Tellina sp.	
		Strigilla	Strigilla pisiformis	
	Nucinellidae	Nucula	Nucula semiornata	
	Thraciidae	Thracia	Thracia similis	
	Lyonsiidae	Entodesma	Entodesma alvarezi	
	Cooperellidae	Cooperella	Cooperella atlantica	
	Dentaliidae	Dentalium	Dentalium americanum	
	Demandae	Demanum	Dentalium gouldii	
Echinodermata	Amphiuridae	Amphipholis	Amphipholis subtilis	
Echinodelmata	Ampinuridae	Amphiodia Amphiodia	Amphiodia atra	
		<del>-</del>		
	Onhinatidaa	Amphiura Haminhalia	Amphiura fibulata	
	Ophiactidae Ophiactidae	Hemipholis Ophiozoma	Hemipholis elongata	
	Ophiuridae	Ophiozoma Astropactor	Ophiozoma sp.	
	Astropectiniidae	Astropecten Luidia	Astropecten marginatus	
Chandata	Luidiidae		Luidia senegalensis	
Chordata	Branchiostomidae	Branchiostoma	Branchiostoma platae	