

Relationships between taxonomic resolution and data transformations in analyses of a macrobenthic community along an established pollution gradient

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ABSTRACT: Although surveys of soft-bottom macrofauna are an important tool in marine pollution monitoring, the high costs involved have often been criticised. Species identification is time-consuming, and one solution is to identify organisms to a taxonomic level higher than species. This study, using data from a survey in the vicinity of the Valhall oil field in the Norwegian sector of the North Sea, examines the effects of using abundances of different taxonomic levels, and of using different data transformations (used to adjust the relative weightings of rare and abundant taxa) in subsequent multivariate analyses of faunal patterns, and relates the environmental variables to the observed faunal patterns from the different analyses. The study area has a constant water depth, homogeneous bottom sediment and a uniform benthic community. At the time of the survey the platform had been active for 9 yr, and strong gradients in environmental contaminants and related faunal changes were found. Data from 27 stations around the oil platform were analysed at the levels of species, genus, family, order, class and phylum, using a range of data transformations and multivariate techniques. The data matrix contained 156 species grouped into 138 genera, 102 families, 42 orders, 18 classes and 10 phyla. Matrices derived from species, genus and family abundances constructed using the same transformation are very similar, and even at higher taxonomic levels the gradient of change in community structure is still detectable. As the taxonomic level increases the effects of transformations become stronger, so although both taxonomic resolution and transformation affect the results of analyses, the effects of each are different and, to a large extent, unrelated. The highest correlations between matrices derived from measured environmental variables and biotic matrices are between environmental variables related to drilling activity and mildly transformed family abundances, suggesting that analyses of higher taxonomic levels are more likely to reflect a contamination gradient than are analyses based on species abundances. Before any general recommendations regarding taxonomic levels are given for future macrobenthic surveys, there is an obvious need for studies of weak, intermediate and strong gradients in various types of contamination in homogeneous and heterogeneous environments, using the same sampling and analysis methods.

KEY WORDS: Taxonomic resolution · Transformation · Macrobenthos · Environmental variables · Multivariate analysis · Pollution monitoring · Cost-effectiveness

INTRODUCTION

Surveys of soft-bottom macrofauna, integral to a majority of marine pollution monitoring studies, have often been criticised due to the high costs involved (McIntyre 1983, Warwick 1993). One reason is that sampling strategies used are very labour-intensive and have remained unchanged for almost a century (e.g.

Petersen 1915, Blegvad 1932, Jones 1952, Buchanan 1963, Pearson 1975, Heip et al. 1992). Although environmental monitoring and pollution assessment programmes traditionally require identification of the individuals collected to the species level, several studies have found analyses at the level of family to be acceptable, since little information appears to be lost (Warwick 1988a, b, Ferraro & Cole 1995, Vanderklift et al. 1996). This suggests that one way of reducing the cost of benthic surveys could be to shorten the time

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needed to identify the animals, and reduce the expertise required for their identification, by using a lower level of taxonomic resolution, that is, identifying specimens to higher taxonomic levels such as family or phylum.

Several papers have considered the utility of analyses of biological data at higher taxonomic levels using univariate measurements such as diversity indices (Kingston & Riddle 1989, Ferraro & Cole 1992, 1995). However, even in clearly perturbed areas, univariate diversity indices often fail to identify any impact or gradients in pollution, whereas multivariate methods are far more sensitive in discriminating between stations or times (Kingston & Riddle 1989, Gray et al. 1990, Warwick & Clarke 1991, 1992, Olsgard 1993, Olsgard & Gray 1995, *inter alia*). In 1986 the community ecology group at an IOC/GEEP workshop analysed macrofauna data from a putative pollution gradient in Frierfjord and Langesundfjord, Norway (Bayne et al. 1988). One of their findings was that the usual methods of multivariate data analysis appear to be very robust to the aggregation of the species data into higher taxonomic groupings (Warwick 1988a). This observation, made on a single data set, was expanded when Warwick (1988b) analysed a further 3 macrofaunal data sets, describing the species composition of benthic assemblages in relation to gradients of pollution, using both univariate and multivariate analyses on species data aggregated to a range of hierarchical taxonomic levels. The general conclusion from these and other (e.g. Ferraro & Cole 1990, Gray et al. 1990, Warwick et al. 1990, Agard et al. 1993, Smith & Simpson 1993, James et al. 1995, Somerfield & Clarke 1995, Vanderklift et al. 1996) studies of sublittoral benthic macrofaunal communities has been that, where strong gradients exist, little information is lost, even if specimens are identified to the level of phylum.

Within marine benthic samples there is usually a great range of abundances. Some taxa are dominant, while others are occasional or rare. In multivariate analyses data transformations are often used to adjust the contributions of species to intersample similarities (Clarke 1993). When abundances of higher taxonomic levels are used, it is probable that the dominance patterns are altered. No study has examined the effects of analysing abundances of higher taxonomic levels and employing different transformations concurrently.

Links between faunal patterns and environmental variables have also been neglected in previous investigations of

taxonomic discrimination. Although such links cannot prove cause and effect, relationships may be indicated, especially if the environmental variables are carefully selected. Environmental variables measured generally include those which describe natural changes between stations, e.g. water depth and sediment grain size, and variables which give information on the level of contaminants, e.g. heavy metal content in sediment, oxygen levels in the bottom water and so on. The underlying assumption is that faunal patterns are a function of variations in environmental conditions, and that small changes in the environment will elicit detectable responses in the fauna. This implies that if a number of stations within the same geographical area are exposed to the same environmental variables, we should expect a high degree of faunal similarity between the stations. Although the validity of this assumption can be questioned, major changes in environmental variables should result in detectable changes in faunal composition.

An ideal site for investigating such links would be a homogeneous area of seabed with an introduced gradient of contamination. The area in the vicinity of the Valhall platform in the southern part of the Norwegian sector of the North Sea (Fig. 1) represents an area very close to such an ideal. Water depth is constant, the sediment is homogeneous and the macrobenthic com-

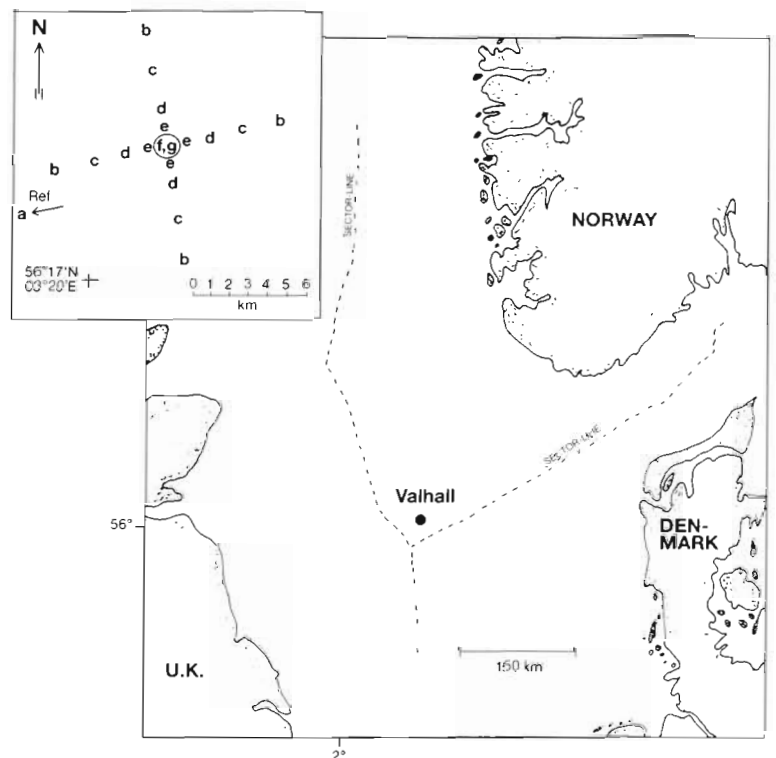


Fig. 1. Location of the Valhall field and (inset) sampling grid. Letters in sampling grid indicate distance to platform: a: reference sites, 10 000 and 15 000 m; b: 6000 m; c: 4000 m; d: 2000 m; e: 1000 m; f, g: 500 m, 250 m

munity is uniform over large areas (Johannessen et al. 1992, Olsgard & Gray 1995). Oil production started at the Valhall field in 1982, discharging drill-cuttings during operations, and by 1991 clear gradients in environmental variables such as total hydrocarbons (THC), barium (Ba) and strontium (Sr) could be detected around the Valhall platform (Fig. 2). Similar gradients in faunal patterns were also detectable (Olsgard & Gray 1995).

Using the high quality data available from the 1991 monitoring survey at the Valhall field (Gjøes et al. 1992, Johannessen et al. 1992), the objectives of this study are: (1) to examine the effects of using abundances of different taxonomic levels, and of using different transformations, in subsequent analyses of faunal patterns and (2) to relate environmental variables to the observed faunal patterns from the different analyses.

MATERIALS AND METHODS

Macrofauna abundances (pooled data from the 5 replicate van Veen grabs from each station) were aggregated to the levels of genus, family, order, class and phylum following the taxonomic classification of Howson (1987). Ranked matrices of similarities among samples were constructed using the Bray-Curtis similarity measure (Bray & Curtis 1957) and the following transformations: none, square root, fourth root and presence/absence. Ordination was by non-metric multidimensional scaling, MDS, and the goodness-of-fit of the resulting 2-dimensional plots was measured using Kruskal's stress Formula I (Kruskal & Wish 1978, Clarke & Green 1988). Formal significance tests for differences between groups, defined by their distance to the platform, were performed using the ANOSIM permutation test (Clarke & Green 1988, Clarke 1993).

The resulting multivariate patterns were compared using the methods of Somerfield & Clarke (1995), whereby rank correlations between the corresponding elements of pairs of matrices themselves become the elements of a second similarity matrix, which is then used as, for example, an input matrix for a 'second-stage' MDS. The rank correlation used was a modified Spearman rank correlation, the harmonic rank correlation of Clarke & Ainsworth (1993), which down-weights the effects of larger rank dissimilarities.

The relationships between patterns in multivariate community structure and combinations of environmental variables were examined using the BIO-ENV procedure (Clarke & Ainsworth 1993),

which calculates rank correlations between a similarity matrix derived from biotic data and matrices derived from various subsets of environmental variables, thereby defining suites of variables most closely correlated with the observed biotic structure. The following environmental variables were used: depth, median grain size ($Md\phi$), sediment sorting (inclusive standard deviation, SD), sediment skewness and kurtosis, sediment % silt-clay ($<63\ \mu\text{m}$), TOC (total organic carbon), and concentrations of barium (Ba), strontium (Sr), lead (Pb), iron (Fe), copper (Cu), cadmium (Cd), chromium (Cr), zinc (Zn) and THC (total hydrocarbons). The environmental variables were converted to approximate normality using a \log_{10} transformation prior to these analyses.

RESULTS

The species abundance matrix contained 156 species grouped into 138 genera, 102 families, 42 orders, 18 classes and 10 phyla, the largest changes in the number of taxonomic units being between the levels of family and order (41%) and order and class (43%).

MDS ordinations of matrices derived from square root transformed abundances of various taxonomic levels (Fig. 3) appear similar at the levels of species, genus, family and order, indicating that at these levels the overall patterns of community structure are retained. This is also seen in the high correlation values between the species level and the levels of genus, family and order with correlation coefficients of $r_s = 0.99$, 0.99 and 0.97 , respectively (Fig. 3). The ordination plots at the level of class and phylum are less similar, compared to the lower taxonomic levels, and the correlation coefficient

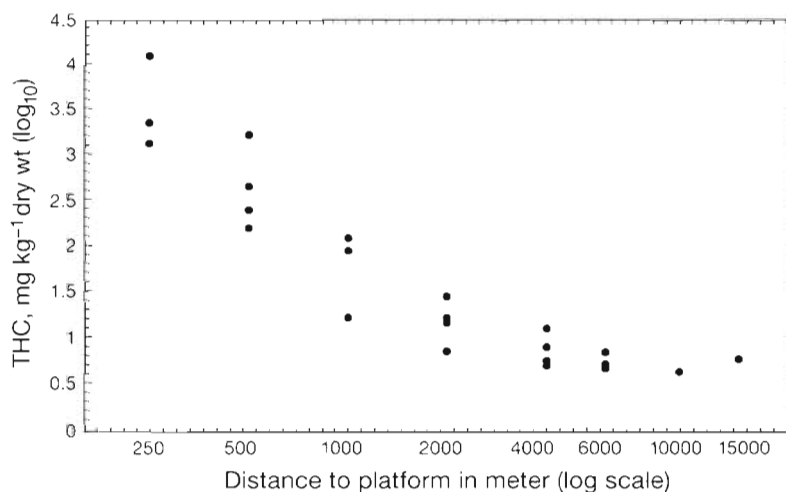


Fig. 2. Relationship between concentration of total hydrocarbons (THC) in the upper 1 cm of the sediment at Valhall in 1991 against the distance from the platform

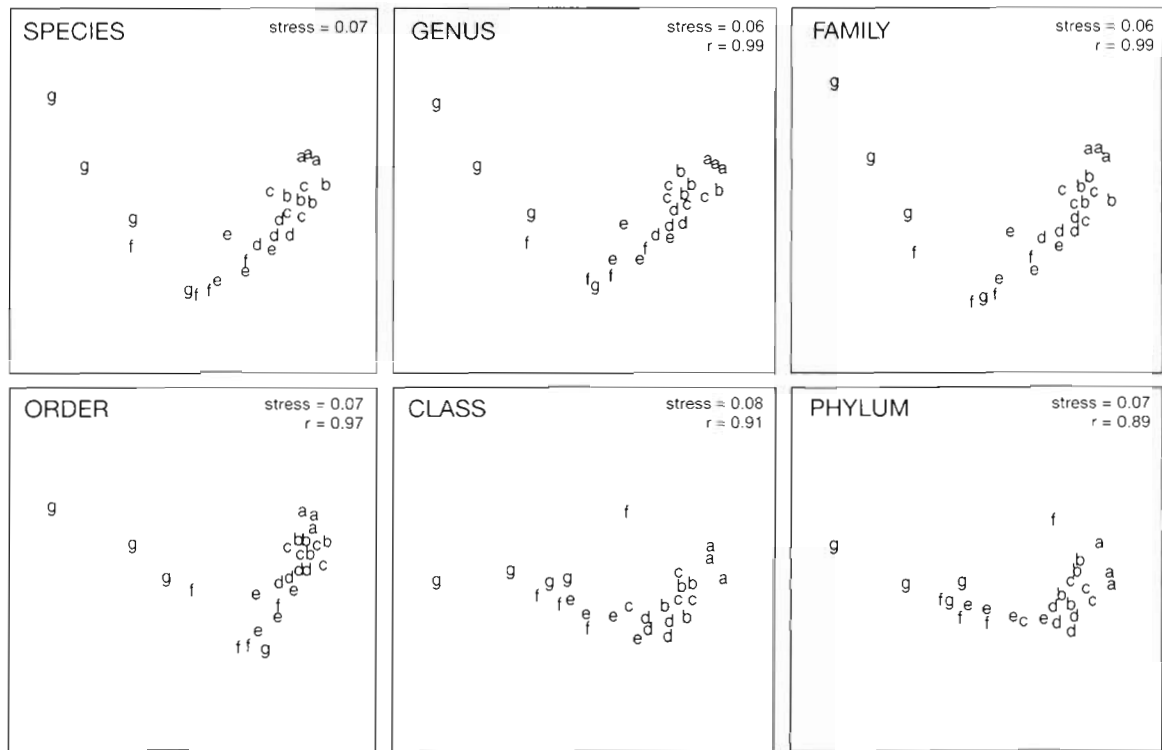
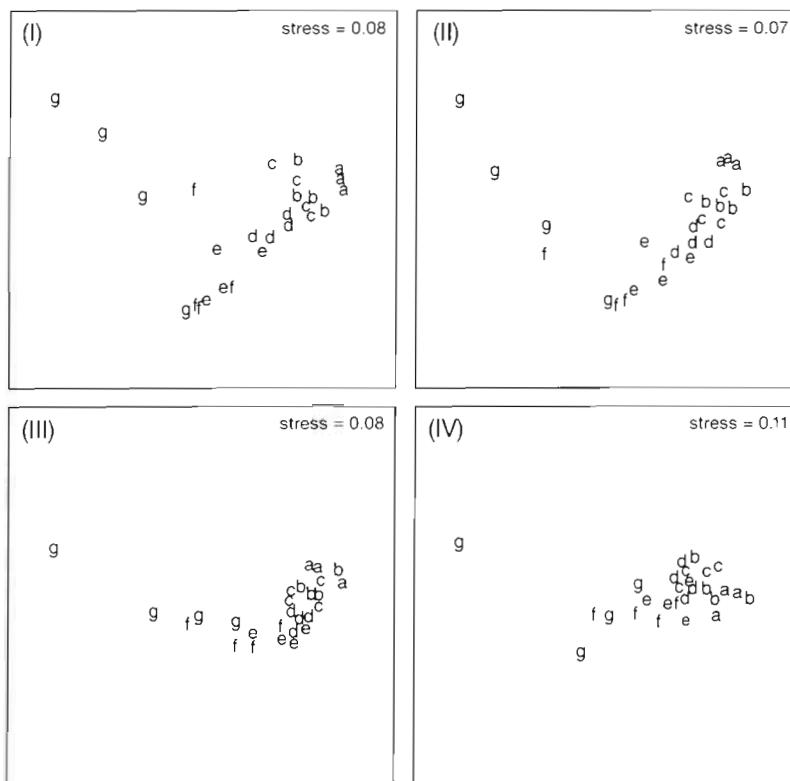


Fig. 3. MDS ordinations of square root transformed abundances of different taxonomic levels. Letters indicate distance to platform: a: reference sites, 10 000 and 15 000 m; b: 6000 m; c: 4000 m; d: 2000 m; e: 1000 m; f, g: 500 m, 250 m. The r-values (see Table 2) are rank correlations between the underlying similarity matrix for the species level and the levels of genus, family, order, class and phylum, respectively



coefficients, compared to species level, are 0.91 and 0.89, respectively (Fig. 3). MDS ordinations of species abundance data subjected to different transformations (Fig. 4) lead to very similar plots for untransformed and square root transformed data, with changes apparent in the plots for fourth root transformed and presence/absence data.

The results of ANOSIM tests (Table 1) show, for the levels of species, genus and family, a general decrease in the value of R (the ANOSIM statistic for a global test of differences between groups) as taxonomic level increases, and as stronger transformations are applied. In a majority of studies, patterns in pairwise differences are used to infer an effect. As stronger transformations, and abun-

Fig. 4. MDS ordinations of species abundances using various transformations: (I) none, (II) square root, (III) fourth root and (IV) presence/absence

Table 1. Summary of results from 1-way ANOSIM. Values of ANOSIM statistic (*R*) for global tests for differences between groups in each matrix ($p < 0.001$ in all cases except presence/absence of phyla), and a summary of the pairwise tests which were not significant ($p > 0.05$)

	None			Square root			Double square root			Presence/absence		
	Stns	<i>R</i>	<i>p</i>	Stns	<i>R</i>	<i>p</i>	Stns	<i>R</i>	<i>p</i>	Stns	<i>R</i>	<i>p</i>
Species	Global <i>R</i> = 0.576			Global <i>R</i> = 0.574			Global <i>R</i> = 0.491			Global <i>R</i> = 0.417		
	b, c	-0.208	0.914	b, c	-0.313	0.943	b, c	-0.167	0.829	a, b	0.167	0.171
	e, f	-0.052	0.571	e, f	0.052	0.343	d, e	0.073	0.343	b, c	-0.031	0.571
Genus	Global <i>R</i> = 0.573			Global <i>R</i> = 0.569			Global <i>R</i> = 0.490			Global <i>R</i> = 0.412		
	b, c	-0.208	0.914	b, c	-0.240	0.886	b, c	-0.073	0.686	b, c	0.094	0.343
	e, f	-0.063	0.600	e, f	0.000	0.400	d, e	0.135	0.171	c, d	0.187	0.114
Family	Global <i>R</i> = 0.572			Global <i>R</i> = 0.567			Global <i>R</i> = 0.483			Global <i>R</i> = 0.401		
	b, c	-0.250	1.000	b, c	-0.281	0.914	b, c	-0.167	0.771	b, c	0.000	0.514
	e, f	-0.042	0.571	e, f	0.042	0.314	d, e	0.167	0.143	d, e	0.000	0.600
Order	Global <i>R</i> = 0.535			Global <i>R</i> = 0.556			Global <i>R</i> = 0.526			Global <i>R</i> = 0.474		
	b, c	-0.156	0.914	b, c	-0.177	0.857	b, c	0.052	0.371	a, b	0.157	0.171
	e, f	-0.094	0.800	e, f	0.021	0.429	e, f	0.187	0.143	a, e	0.333	0.114
Class	Global <i>R</i> = 0.500			Global <i>R</i> = 0.595			Global <i>R</i> = 0.560			Global <i>R</i> = 0.434		
	b, c	-0.115	0.800	b, c	-0.187	0.943	a, b	0.370	0.114	a, b	-0.204	1.000
	c, d	0.146	0.114	e, f	0.010	0.429	b, c	-0.125	0.714	a, c	0.167	0.229
Phylum	Global <i>R</i> = 0.482			Global <i>R</i> = 0.545			Global <i>R</i> = 0.447			Global <i>R</i> = 0.078		
	a, c	0.167	0.200	a, c	0.259	0.143	a, c	0.352	0.114	No overall differences		
	b, c	-0.125	0.857	b, c	-0.146	0.943	b, c	-0.052	0.600			

dances of higher taxonomic levels, are used, more pairwise differences are not significant ($p > 0.05$: Table 1), indicating that the ability of ANOSIM to discriminate between stations decreases. The above patterns are less obvious for the levels of order, class and phylum, but in all cases the ability of ANOSIM to discriminate between stations is lowest at the level of phylum.

Rank correlations (Table 2) between similarity matrices based on different taxonomic levels and different transformations tend to be lower between matrices derived from abundances of higher taxonomic levels using strong transformations. A 'second-stage' MDS ordination of the matrix in Table 2 produces a 'fan-pattern' (Fig. 5), showing separation of groups horizontally for taxonomic levels and separation of groups vertically for transformations. This shows that, while both affect the results of subsequent analyses, the effects of each are different and, to a large extent, unrelated. Matrices derived from species, genus and family abundances constructed using the same transformation

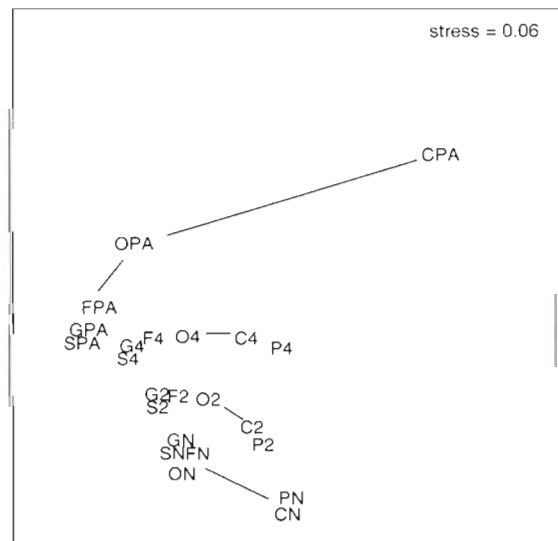


Fig. 5. 'Second-stage' MDS of inter-matrix rank correlations (Table 2), presence/absence of phyla omitted

Table 2. Pairwise harmonic rank correlations between similarity matrices derived from abundances of species (S), genera (G), families (F), orders (O), classes (C) and phyla (P) using no (N), square root (2), fourth root (4) and presence/absence (PA) transformations

S2	0.95																									
S4	0.88	0.97																								
SPA	0.82	0.93	0.98																							
GN	0.99	0.95	0.88	0.82																						
G2	0.95	0.99	0.97	0.92	0.95																					
G4	0.89	0.97	0.98	0.97	0.89	0.97																				
GPA	0.83	0.92	0.97	0.98	0.83	0.92	0.98																			
FN	0.99	0.95	0.88	0.82	0.99	0.95	0.89	0.82																		
F2	0.96	0.99	0.96	0.90	0.96	0.99	0.96	0.91	0.96																	
F4	0.89	0.97	0.98	0.95	0.89	0.97	0.99	0.95	0.89	0.97																
FPA	0.83	0.92	0.95	0.95	0.83	0.92	0.95	0.96	0.83	0.92	0.97															
ON	0.99	0.93	0.86	0.80	0.99	0.93	0.86	0.80	0.99	0.94	0.87	0.81														
O2	0.97	0.98	0.93	0.88	0.97	0.98	0.94	0.88	0.97	0.99	0.95	0.89	0.96													
O4	0.89	0.95	0.95	0.91	0.89	0.96	0.96	0.92	0.89	0.96	0.97	0.93	0.88	0.96												
OPA	0.77	0.83	0.86	0.86	0.77	0.84	0.87	0.87	0.77	0.84	0.88	0.88	0.75	0.84	0.93											
CN	0.87	0.81	0.76	0.72	0.87	0.82	0.77	0.72	0.87	0.82	0.78	0.73	0.87	0.82	0.77	0.68										
C2	0.91	0.91	0.87	0.82	0.92	0.91	0.87	0.82	0.92	0.92	0.88	0.83	0.90	0.91	0.88	0.78	0.94									
C4	0.90	0.93	0.91	0.86	0.90	0.93	0.92	0.87	0.90	0.94	0.92	0.88	0.88	0.93	0.93	0.83	0.82	0.94								
CPA	0.61	0.63	0.63	0.60	0.61	0.64	0.64	0.61	0.61	0.64	0.64	0.61	0.59	0.64	0.66	0.61	0.50	0.61	0.73							
PN	0.87	0.81	0.76	0.72	0.87	0.82	0.77	0.72	0.87	0.82	0.78	0.73	0.87	0.82	0.77	0.69	0.99	0.93	0.82	0.50						
P2	0.91	0.89	0.85	0.81	0.91	0.89	0.86	0.81	0.91	0.90	0.86	0.81	0.90	0.90	0.86	0.77	0.95	0.98	0.91	0.59	0.96					
P4	0.85	0.88	0.87	0.84	0.85	0.89	0.88	0.84	0.85	0.89	0.89	0.86	0.84	0.89	0.89	0.82	0.81	0.91	0.67	0.82	0.93	0.95				
PPA	0.38	0.46	0.50	0.50	0.38	0.42	0.51	0.52	0.37	0.47	0.52	0.54	0.35	0.45	0.52	0.54	0.24	0.41	0.59	0.70	0.25	0.42	0.71			
	SN	S2	S4	SPA	GN	G2	G4	GPA	FN	F2	F4	FPA	ON	O2	O4	OPA	CN	C2	C4	CPA	PN	P2	P4			

tend to cluster together, indicating that transformation has more of an effect than the level to which abundances are identified, although as the taxonomic level increases the effects of subsequent transformations become stronger (symbols are further apart).

BIO-ENV shows (Table 3) that matrices derived from all taxonomic levels and transformations, with only a few exceptions, are most highly correlated with the environmental variables THC, TOC, Ba, Sr and Zn. The highest correlations with a single variable are generally with total hydrocarbons (THC). These results strongly indicate that impact related to oil-drilling activities is affecting community structure in the vicinity of the platform. It is particularly interesting that the highest correlation ($r_s = 0.850$) is that between THC, TOC and Ba (all associated with drilling muds) and the matrix derived from family abundances constructed using a square root transformation (Table 3). Increasing or decreasing either the taxonomic level or the transformation degrades the match, suggesting that, for this particular study, analyses utilising square root transformed family abundances best reflect the relationship to the measured environmental variables.

DISCUSSION

Patterns in soft-bottom benthic communities at varying levels of taxonomic discrimination are of impor-

tance in view of the high potential for time and cost savings in environmental monitoring programmes. Only a few studies have examined in detail time consumption in relation to levels of taxonomic discrimination. In a study of macrobenthic communities, from the Southern California Bight, Ferraro & Cole (1995) found that costs of genus, family, order and phylum level identification were, respectively, 23, 55, 80 and 95% less than species level identification. However, the relationship between time savings and taxonomic level is not a straightforward one. The time spent dividing the organisms into families, as compared to identification to species, will depend on the number of species within the various families, whether the numerically dominant species belong to several taxonomically complicated families or to a few taxonomically facile families, and on the taxonomic expertise available (Ferraro & Cole 1990). The potential for saving time, and thereby money, will therefore vary from case to case.

Naturally, such gains may only be realised if responses to gradients in pollution are detectable at higher taxonomic levels. The general conclusion from previous studies (Ferraro & Cole 1990, Gray et al. 1990, Warwick et al. 1990, *inter alia*) has been that for sublittoral soft sediment benthic macrofaunal communities, surprisingly little information is lost, even in cases where specimens are identified to the level of phylum. Using more objective techniques, Somerfield & Clarke

Table 3. Summary of results from BIO-ENV. The subset of environmental variables showing the highest overall correlation with various biotic matrices constructed using a range of taxonomic levels and transformations. Maximum values for each separate transformation in **bold**

Transformation	Species	Genus	Family	Order	Class	Phylum
None	THC, Ba, TOC $r_s = 0.797$	THC, TOC, Ba $r_s = 0.800$	THC, TOC, Ba $r_s = \mathbf{0.801}$	THC, TOC, Ba $r_s = 0.774$	THC, Ba $r_s = 0.605$	THC $r_s = 0.605$
Square root	THC, Ba, TOC $r_s = 0.833$	THC, Ba, TOC $r_s = 0.849$	THC, Ba, TOC $r_s = \mathbf{0.850}$	THC, TOC, Ba $r_s = 0.847$	THC, Ba $r_s = 0.752$	THC, Ba, TOC $r_s = 0.736$
Double square root	THC, Zn, Ba $r_s = 0.798$	THC, Zn, Ba $r_s = 0.814$	THC, Ba, TOC $r_s = 0.810$	THC, Zn, Ba $r_s = \mathbf{0.827}$	THC, TOC, Ba, Pb $r_s = 0.799$	THC, Zn, Ba, Pb $r_s = 0.745$
Presence/absence	THC, Sr, Zn, Ba $r_s = 0.713$	THC, Zn, Ba $r_s = 0.725$	Zn, Ba $r_s = \mathbf{0.728}$	THC, Zn $r_s = 0.658$	THC, Pb $r_s = 0.699$	Pb, Zn, Sorting, Sr $r_s = 0.412$

(1995) demonstrated that analyses at the levels of genus and family produce similar results to analyses at the species level, while there were marked differences, but still interpretable patterns, at the level of phylum. The results of the present study are consistent with these previous studies, indicating that in the vicinity of the Valhall field in 1991 a gradient of community structure, related to a gradient of increasing distance from the centre of drilling activity, was detectable at all taxonomic levels, and that the details of the gradient were less clear in analyses based on abundances of higher taxonomic levels such as classes and phyla. Analyses at the level of class or phylum, therefore, may be sufficient for detecting gross disturbances but may not reveal subtle differences in the benthic communities associated with low levels of contamination.

It may be that there are sound biological reasons for examining changes in community structure at higher taxonomic levels. Warwick (1988b) suggested that there are possible theoretical advantages to conducting multivariate analyses at higher levels (e.g. phyla) in studies of anthropogenic effects, in that gradients in natural environmental variables, such as water depth and sediment granulometry, are more likely to influence the fauna by species replacement than by changes in proportions of major taxa. Analyses of higher taxonomic levels are, therefore, more likely to reflect a contamination gradient than are analyses based on species abundances, as the latter are likely to be complicated by natural environmental heterogeneity. Ferraro & Cole (1990) also suggested that grouping animals to higher taxa may dampen natural variability in faunal patterns, improving the ability of subsequent analyses to assess small pollution impacts. If there is a relationship between environmental heterogeneity and changes in community structure at higher taxonomic levels, it could be that the level of phylum may be useful for studies of pollution impacts in environmentally complicated areas, but so far no investigations have examined this. It may also be that there is a

hierarchical structure in biological responses to stress, in which, as stress increases, the adaptability of individuals, then species, genera, families and so on, is exceeded in turn, and so increasing stress is manifested at increasingly higher levels of biological organisation depending on the strength of the pollution gradient and the length of the pollution history (Ferraro & Cole 1990). A complicating factor is that, in areas with a long pollution history, some species can adapt to high levels of contamination, and therefore be encountered in environments in which they might not be expected to survive (Luoma et al. 1983, Grant et al. 1989, Bryan & Langston 1992, Somerfield et al. 1994). The results of the present study indicate that, in the environmentally homogeneous area sampled, it was environmental factors related to the extraction of oil and gas, such as heavy metals and hydrocarbons, that were affecting benthic community structure at all taxonomic levels, but it is interesting that the highest correlations were centred on mildly transformed family abundances.

The 'second-stage' MDS analyses for the Valhall 1991 study give an objective and informative presentation of the differences between all the similarity matrices derived from different taxonomic levels using various transformations. The finding that the degree of transformation is as important to the outcome of consequent analyses as is the taxonomic level to which the fauna is identified is of interest in the light of the debate relating to the use of higher taxonomic levels in pollution studies, and suggests that the choice of transformation in studies related to taxonomic discrimination should be carefully evaluated. The results of this study are in keeping with the predictions made by Clarke & Warwick (1994) that intermediate transformations are likely to give the best balance between a 'narrow view' of community structure based only on abundances of a few dominant taxa, and thus unduly influenced by large fluctuations in population numbers, and a 'wide view' based on all species, thus giving too much weight to random occurrences of the rarest taxa.

In conclusion, this study demonstrates that the faunal patterns obtained with multivariate analyses of the data from Valhall in 1991 show a high degree of consistency up to the level of orders, although gross effects are detectable at the level of phyla, adding weight to the argument that analyses at higher taxonomic levels are potentially useful in many routine pollution monitoring programmes. In more heterogeneous areas, or areas with weaker pollution gradients, it is possible that community patterns will be less obvious at higher levels of taxonomic resolution, compared to the present study. Therefore, before any general recommendations are given for future macrobenthic monitoring surveys there is an obvious demand for studies using the same quantitative assessments which involve strong, intermediate and weak gradients, in homogeneous and heterogeneous environments subjected to various types of contamination, using rigorously standardised analytical protocols.

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