Differentiation of copepod assemblages in coastal waters of the Tyrrhenian sea

Multivariate statistics
Copepod assemblages
Coastal waters

Analyse multivariée
Groupements copépodes
Zone côtière

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ABSTRACT

We present an application of a statistical method based on an original homogeneity test, derived by non-parametric maximum entropy techniques, that analyses ecosystems starting from their species composition. The method is applied to zooplankton data collected in different seasons from three adjacent coastal regions in the Tyrrhenian Sea (Mediterranean), with the aim of quantifying statistically significant differences in species composition which could reflect different environmental features.

The analysis revealed significant differences between the study areas. The Gulf of Salerno, a wide mouth embayment open to the flushing of the oligotrophic Tyrrhenian waters, was characterized as a homogeneous area with uniform spatial patterns in copepod assemblages through the seasons. In contrast, the Gulf of Naples appeared to be fragmented into different homogeneous subsystems with boundaries shifting according to the season. The heterogeneous structure of the pelagic system in this environment is probably related to the variable local hydrography and to nutrient enrichment due to land runoff.

Small, but statistically significant, differences in species composition characterizing each homogeneous subsystem were not directly related to precise ecological factors but indicated differences that did not depend on intrinsic fluctuations. Such differences in species composition could indicate stress before modifications in environmental parameters are detectable.

The present method has been compared with other multivariate techniques, including cluster analysis and principal component analysis.

RÉSUMÉ

Différenciation de groupements de copépodes dans une zone côtière de la mer Tyrrhénienne.

Les auteurs présentent une application d'une méthode statistique élaborée par des techniques non paramétriques du maximum d'entropie qui permettent de caractériser les écosystèmes à partir de leur composition en espèces. Dans ce but la distribution spatiale des biocénoses zooplanctoniques a été analysée en différentes saisons et en trois zones côtières de la mer Tyrrhénienne. La méthode a mis en évidence des différences significatives entre les zones étudiées. Le Golfe de Salerne apparaît comme une zone homogène avec une répartition uniforme des copépodes pendant les différentes

périodes d'observation. Le Golfe de Naples, au contraire, est composé de plusieurs sous-ensembles homogènes dont les limites varient avec les saisons. Ces différences sont probablement dues à l'hydrographie variable de cette zone et aux déchets industriels et agricoles qui changent au cours du temps.
L'analyse a été principalement consacrée à la quantification des différences statistiquement significatives dans la composition en espèces qui pourraient refléter différents milieux ambiants et donc être utilisables comme indicateurs précoces de stress.

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INTRODUCTION

Understanding the structure and dynamics of zooplankton in the spatial domain has been a major challenge in oceanographic studies. Above and beyond the shortcomings of traditional sampling tools (Andrew and Mapstone, 1987) and the need for advanced techniques for *in situ* zooplankton studies (Sprules *et al.*, 1992), there remains a need for quantitative criteria for the analysis of zooplankton communities on a wide range of spatial and temporal scales.

The role of physical factors in structuring zooplankton communities has often been recognized, mainly on a large scale. Different zooplankton assemblages have been seen as associated with distinct water masses in frontal areas (*e.g.* Franks, 1992) or in regions with clear physical and/or chemical gradients (Jouffre *et al.*, 1991). Moreover, physical heterogeneity of the environment influences species richness and abundance (LeRoy Poff and Ward, 1990). On the other hand, the predominance of biological rather than physical regulatory forces has often been proposed for stable oceanic environments (McGowan and Walker, 1985).

Both spatial and temporal heterogeneity in plankton communities may also be caused by disturbance: the renewal of resources that ensues permits their utilization by non-dominant competitive species and increases the number of ecological niches (Levin, 1992). However, one of the most widespread signs of ecosystem response to severe stress is a reduction in species diversity (Rapport *et al.*, 1985; Patriti, 1984), in accordance with the «stress hypotheses» summarized by Odum (1985).

Multivariate analysis techniques are standard tools used in the study of community structure to determine patterns and evince the relationships between variables. These methods may be applicable to a wide range of data sets, although each method has some different intrinsic limitations (reviewed by James and McCulloch, 1990).

In this study we apply a statistical method based on an original homogeneity test, derived by non-parametric maximum entropy techniques, that analyses ecosystems starting from their species composition (Kullback, 1968; Macchiato *et al.*, 1992). We statistically characterize homogeneous spatial patterns in zooplankton data sets. Although the method can be extended to structure analysis in order to define discriminant descriptors (Legendre and Legendre, 1983), we emphasize here its use as a classification procedure.

Our aim was to quantify any statistically significant differences in the species composition of copepod assemblages from coastal waters in the Tyrrhenian Sea (Mediterranean) which could reflect community responses to environmental differences.

So the method makes it possible to define an operational concept of group; in fact, among n samples characterized by m descriptors, it is possible to find h compatible samples from the same source distribution (homogeneous subsets).

The statistic H, used in this method, maintains all the information contained in each descriptor (species), taking into account sample size and the experimental frequency of each descriptor. It has high sensitivity and can detect small shifts in descriptor frequency distribution, quantifying small differences in abundance patterns. The statistic H is fundamentally different from the indexes derived by the Shannon-Weaver expression. In this analysis we show that it is possible to discriminate among samples that have different species composition, but the same frequency distribution.

The method has the following characteristics:

(i) no transformation or standardization of variables is required;

(ii) in the classification procedure, spatial and/or temporal constraints that are known *a priori* can be taken into account;

(iii) it can support classical multivariate techniques such as ordination or clustering using the statistical significance of its responses and discriminant analysis or correspondence analysis providing the input classification.

The method has been compared with other multivariate classification and ordination methods. In a previous paper, we analysed *Arrenatherum elatius* meadow communities with clustering and Principal Component Analysis (PCA) techniques and the homogeneity test method, showing that our method is able to point out, statistically, the incompatible elements enclosed in a group (Macchiato *et al.*, 1992). Here, we compare our method with clustering and the results of these techniques with PCA. Particularly we would note that the homogeneity test results are unequivocal and the researcher needs no other criteria to accept the null hypothesis.

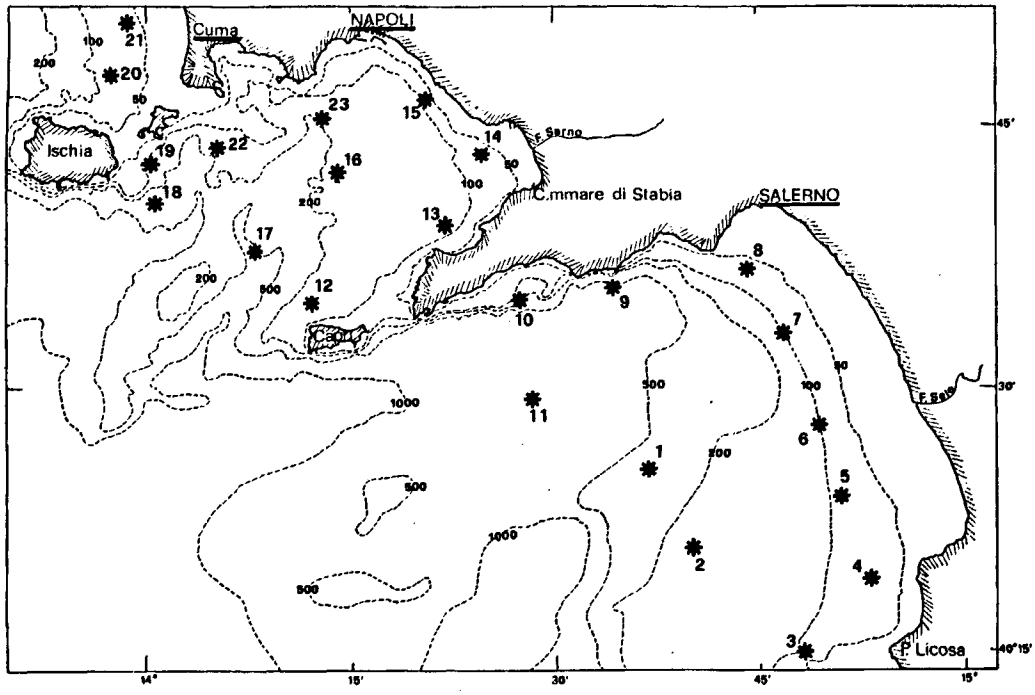


Figure 1

Map of sampled areas.

We present the analysis of zooplankton data collected during three cruises; while the samples are not appropriate for proper investigation of the temporal evolution of the zooplankton communities, we shall identify, through the spatial patterns, the manner in which different community structures could express different environmental features.

MATERIALS AND METHODS

Study area

Sampling was conducted in three adjacent areas of the Southern Tyrrhenian Sea (Fig. 1) characterized by different dynamics (Carrada *et al.*, 1980). The Gulf of Salerno (area A) is a wide embayment with a mean depth of 260 m. It has a very narrow shelf in the north; in the south, the shelf is approximately 10 miles wide. The entire Gulf is flushed by oligotrophic Tyrrhenian waters, the area facing the city of Salerno being the only site where occasional features of hydrological confinement are observed. The only relevant freshwater source is the Sele river (71 m^3/s average flow), but the fresh water is rapidly diluted in the Tyrrhenian flow due to the narrowing of the shelf near the river mouth (internal report). The Gulf of Naples (area B) has a mean depth of 170 m, a more complex bottom topography and diversified boundaries that generally force spatial hydrographic gradients. Outfalls of urban wastes along the shore, originating in a highly populated area, result in highly eutrophic conditions in the eastern and northwestern areas. The third sampled area (about 75 m depth), off Cuma (area C), is within the Gulf of Gaeta, north of the Gulf of Naples, and is heavily influenced by the outfall of the Naples treatment plant, which treats > 1/3 of the Naples sewage.

Data

Zooplankton samples were collected in November 1986, March and June 1987 at 23 stations (Fig. 1), by vertical hauls from 50 m to the surface using a Nansen net (1.13 m mouth diameter; 200 μm mesh aperture).

This zooplankton study was part of a national project to evaluate anchovy and sardine stocks in the Southern Tyrrhenian Sea in relation to productive processes within the pelagic ecosystem. The principal aim of research at that time was to obtain an estimate of the stocks of *Engraulis encrasicholus* and *Sardina pilchardus* and to identify correlations between zooplankton biomass and eggs and larvae of fish. A minor effort was devoted to hydrology and to the characterization of phytoplankton communities. Only temperature, salinity and chlorophyll *a* concentrations were recorded in the sampled water masses. The preliminary results of the November cruise were discussed in a previous paper (Mazzocchi *et al.*, 1989).

The present analysis has been performed only on copepods, which accounted on average for more than 80 % of total zooplankton in the present study.

Copepod abundances (ind/m^3) were organized in three matrices, including only adults. Juvenile stages were not taken into account, because of their unbalanced contribution to the numbers of each species as a result of the selective sampling imposed by the net mesh size used. Because of the experimental error, we have considered cumulative frequencies lower than 0.04 % to be indistinguishable from zero. The difference between sampled and examined numbers is

Table 1

Area A *Gulf of Salerno; Area B - Gulf of Naples; Area C - Cuma*
N_1 *Mean abundance with standard deviation of total copepods (adults plus juveniles)*
m_0 *Number of sampled species of adult copepods*
N_0 *Number of elements in the m_0 species*
m_1 *Number of sampled species with relative abundance > 0.04 %*
N_1 *Number of elements in the m_1 species*
Chl *a* *mean values of surface chlorophyll a concentration (range of values in brackets)*

Cruise	Area	N_1 (Ind/m^3)	m_0	N_0	m_1	N_1	Chl *a* (µg/l)
Nov. '86	A	411 ± 170	67	1 623	37	1 618	0.18 (0.11, 0.28)
	B	700 ± 212	68	2 374	43	2 366	0.96 (0.13, 2.63)
	C	1 240 ± 82	59	758	36	756	(0.32, 0.39)
	Tot	783 ± 164	77	4 755	43	4 740	(0.19, 1.10)
Mar. '87	A	1 086 ± 520	99	5 063	37	5 037	0.52 (0.21, 1.70)
	B	1 574 ± 608	90	6 579	36	6 544	0.93 (0.28, 2.03)
	C	1 693 ± 1 092	70	1 427	26	1 420	(0.56, 1.02)
	Tot	1 451 ± 781	107	13 069	40	13 001	(0.35, 1.58)
Jun. '87	A	1 048 ± 271	67	4 982	25	4 967	0.13 (0.02, 0.21)
	B	975 ± 343	66	4 459	20	4 439	3.98 (0.32, 14.29)
	C	645 ± 272	40	437	17	436	(0.26, 3.77)
	Tot	889 ± 297	78	9 878	26	9 844	(0.20, 6.09)

less than 0.5 %. The resulting matrices have the following dimensions: Nov. [23,43], Mar. [23,40], Jun. [23,26] (Tab. 1). Each element x_i^j of these (samples × species) matrices represents the number of individuals of the i-th species ($i \in \{1,..,m\}$) measured in the j-th sample ($j \in \{1,..,n\}$)

Statistical test

The method, based on maximum entropy techniques, defines among the n samples (each of them characterized by *m* variables) *h* samples ($h \leq n$) which are statistically homogeneous, *i.e.* compatible samples from the same source distribution (homogeneity index test).

Each set of measurements is made up of the frequencies of species in the *n* samples $\mathbf{p}^j = (p_1^j ... p_m^j)$ ($j \in \{1,...,n\}$) where

$$p_i^j = \frac{x_i^j}{N^j}$$

is the frequency of i-th species in the j-th sample ($\sum_{i=1}^m p_i^j = 1$ and N^j the j-th sample size).
It is assumed that the cumulative species composition characterizes the *n* samples, *i.e.*, the frequencies of species can represent the source distribution. It is represented by the vector $\mathbf{g} = (g_1,...,g_m)$ in which

$$g_i = \frac{\sum_{j=1}^n x_i^j}{\sum_{i=1}^m \sum_{j=1}^n x_i^j}$$

with x_i^j the number of elements of the i-th species in the j-th sample ($\sum_{j=1}^m g_i = 1$).

For each sample the statistic H is defined as

$$H^j = \sum_{i=1}^m p_i^j \ln \frac{p_i^j}{g_i}$$

This statistic is fundamentally different from the index

$$I^j = \pm \sum_{i=1}^m p_i^j \ln p_i^j$$

derived by the Shannon-Weaver expression ($\pm \sum_{i=1}^m p_i^j \log_2 p_i^j$)
The term g_i in the denominator preserves the information contained in each frequency p_i^j. In fact, in H^j each p_i^j has been compared with the respective cumulative frequency g_i. In fact, when we fix a source distribution vector $\mathbf{g}$ $\left(\text{different by equiprobalility } \forall i \; g_i = \frac{1}{m}\right)$ and a sample represented by vector $\mathbf{p} = (p_1,...,p_m)$, compatible with $\mathbf{g}$, any vector $\mathbf{p}^*$, obtained from $\mathbf{p}$ by means of a generic permutation, results not homogeneous with $\mathbf{g}$ even if $I(\mathbf{p}) = I(\mathbf{p}^*)$. For example $\mathbf{p}^1 = (0.13, 0.57, 0.30)$ and $\mathbf{p}^2 = (0.57, 030, 0.13)$, have the same information content $I(\mathbf{p}^1) = I(\mathbf{p}^2)$ but have different behaviour if they are compared to a source distribution vector $\mathbf{g} = (0.10, 0.60, 0.30)$.

It is possible to quantify this different behaviour with respect to the source distribution vector by means of a statistical test which verifies if the vectors $\mathbf{p}$ and $\mathbf{g}$ represent the same vector unless the intrinsic fluctuations.

The hypothesis of homogeneity among the *n* samples is equivalent to the null hypothesis

$$H_{exp}^{tot} \in \left[P^{tot}(H_{sim}^{k\ tot}) \;\; k \in \{1,...,Q\}\right]$$

with a confidence level of 1%.

H^{tot}_{exp} is the experimental cumulative value of the statistic H, calculated from the data matrix as

$$H^{tot}_{exp}(N^1,\ldots,N^n,m) = \sum_{j=1}^{n}\sum_{i=1}^{m} p_i^j \ln \frac{p_i^j}{g_i}$$

and $P^{tot}(H^{k\ tot}_{sim})$ is the probability distribution function, obtained by simulation. Starting from the source distribution vector **g**, we simulate Q matrices with dimension [n,m] and calculate for each simulated matrix $H^{k\ tot}_{sim}(k \in \{1,\ldots,Q\})$ determining the distribution function $P^{tot}(H^{k\ tot}_{sim})$. P^{tot} represents the probability that all the analysed samples make up a homogeneous set.

When the *n* samples are not homogeneous, we find the homogeneous subset that contains the highest number of samples, excluding one sample at time. An iterative procedure, for each new input data set constituted by *h* samples ($h < n$), determines the new source distribution vector and the new distribution function. The characteristics of the distribution function have been previously analysed and the relationships between the matrix dimension [*h*, *m*] and the number of simulations, Q, have been determined (Macchiato *et al.*, 1992).

The procedure has been automated. The software ECOSYS, written in Fortran for system VAX/VMS, is available, free of charge, upon request.

Data analysis

We analysed three sample sets and since the matrices are of different sizes (due to seasonal effects) but have a similar species frequency distribution (only few species abundant and many species rare), we fixed a normalized size common to the three collections. Taking into account the number of descriptors (dimension *m*) the normalized size was fixed at 5000 elements for each collection.

To characterize the spatial patterns, we determined a sample classification by means of the homogeneity test (the maps of homogeneous patterns are shown in Figures 2-4 and the frequency percentages of major species, for each homogeneous subsets, are summarized in the Appendix A), calculating also, for each cruise, the diversity index value for the 23 stations (Tab. 2).

To compare this method with other classic multivariate techniques, we determined the spatial patterns by means of clustering (dendrograms are shown in Figure 5).

In addition, we positioned, for each cruise and for each gulf, the samples in the reduced space of the principal axes (PCA), in order to point out the different pattern obtained by homogeneous subsets and by clusters. (Examples for both gulfs in the November and June cruises are shown in Figures 6a, 6b). In this way we are able to compare the different techniques of grouping, pointing out the presence of gradients or privileged directions.

In the homogeneity test procedure, it is theoretically possible to consider all possible subsets. However the number is huge and, when constraints are known *a priori*, it is helpful to take this latter information into account, so as to reduce the number of examined groups and identify subgroups related to the characteristics of the problem. In this analysis, in order to evidence spatial homogeneity in a region of the Tyrrhenian Sea that includes zones with different characteristics, we divided the samples into two groups, one for the stations in the Gulf of Naples, including stations 20 and 21 (area C) and one for the stations in the Gulf of Salerno. Furthermore, if we found two homogeneous subsets that contained the same number of samples, we selected the subset with contiguous samples.

Table 2

Diversity index values.

Sample	I(NOV)	I(MAR)	I(JUN)
1	2.24	2.53	1.28
2	2.39	2.19	2.17
3	2.13	1.75	2.30
4	2.52	2.22	1.57
5	2.51	2.74	1.85
6	2.58	2.56	1.90
7	2.36	2.54	1.93
8	2.31	2.65	1.95
9	2.23	2.53	1.71
10	2.48	2.61	1.76
11	2.41	2.49	1.96
12	2.53	2.05	1.55
13	2.36	1.69	1.35
14	2.65	2.18	1.40
15	2.49	1.81	1.26
16	2.52	2.42	1.37
17	2.48	2.27	1.49
18	2.35	2.53	1.40
19	2.89	2.44	1.21
20	2.70	2.41	1.70
21	2.73	2.45	1.75
22	2.13	2.44	1.54
23	2.65	2.56	1.40

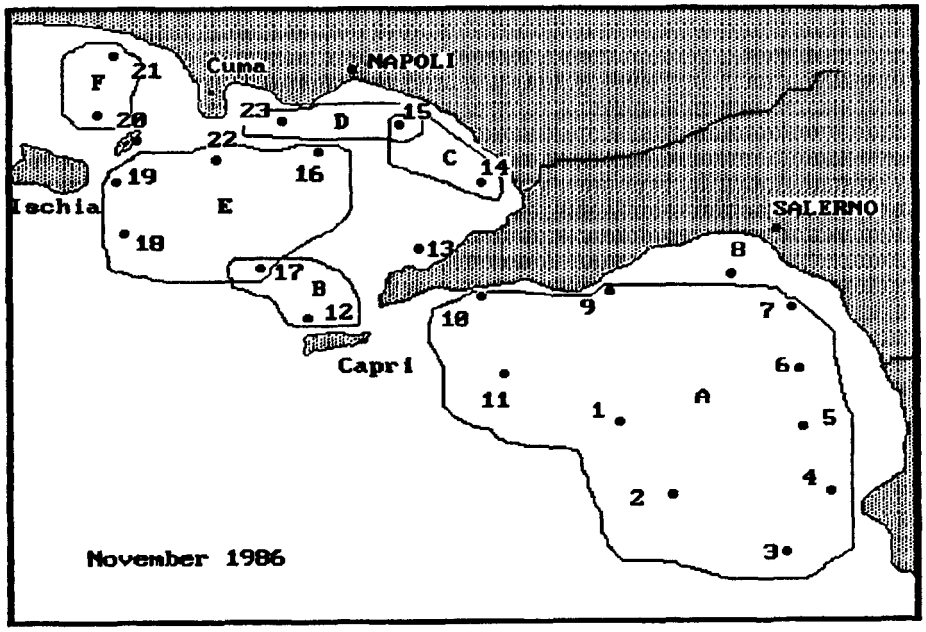
In the clustering procedure, for each cruise, we partitioned the samples into two groups: stations 1-11 for area A and stations 12-23 for areas B and C, obtaining six data sets. For each of them, we calculated the resemblance matrix for the samples, using the euclidean distance, and applied to this matrix the complete linkage clustering in order to determine the dendrogram. We verified that the results were non dependent by choice of resemblance function and clustering method.

To determine the ordination of the samples in the reduced space, we calculate the resemblance matrix for the descriptors, using the covariance coefficient, its set of eigenvalues and eigenvectors and the sample coordinates along the principal axes (PCA).

For the classical multivariate analysis, we used the software MULVA-4 (Wildi and Orloci, 1980).

Figure 2

Homogeneous subsets (HS) pattern for November cruise (Labels A-F).



RESULTS

We analysed each collection with two multivariate classification techniques, taking into account only the spatial contiguity constraint among samples, to show the spatial patterns of zooplankton communities.

Starting from the values of the diversity index, it was not possible to individuate subgroups, since these values indicated only the different number of species sampled on three occasions (seasonal effect).

The homogeneous subsets and clusters, obtained with the two classification techniques, are discussed below.

November 1986 – Total copepod abundances were generally low in the sampled areas, with the exception of the values recorded at the two stations off Cuma (Tab. 1). The most abundant species, *Clausocalanus furcatus*, accounted for 23 % of adult copepods for all samples combined; its dominance characterized most of the homogeneous groups of stations displayed by the mathematical analysis (homogeneous subsets **A, B, E, F** in Figure 2). These groups were differentiated according to rank order of minor species. Only the more coastal stations in the Gulf of Naples (stations 14, 15, 23) were distinguished by a peculiar species association: *Paracalanus parvus, Clausocalanus paululus* and *Paracalanus nanus*. At the stations off Cuma (20, 21), *C. furcatus* and *Temora stylifera* were important, both comprising more than 18 % of the total copepod assemblages in that area. In the Gulf of Salerno, the analysis showed up a remarkable uniformity in community structure characterized by the relative importance of *C. furcatus* (29 %) and *C. paululus* (14 %). The only stations not included in any groups were station 13 in the Gulf of Naples, characterized by high percentage of *Farranula rostrata,* and station 8 in the Gulf of Salerno, characterized by *P. nanus* dominance.

The clustering for the Gulf of Naples showed only two groups, with two stations excluded: stations 20 and 13 (Fig. 5a). In contrast with the homogeneous pattern of the Gulf of Naples, stations (20, 21) (the area off Cuma) were not grouped together. Stations (14, 15, 23) constituted a single group, masking the different species composition in the couples (14, 15) and (15, 23) as shown in Appendix A.

As shown in Figure 6a, clusters and homogeneous subsets have different positions with respect to the principal axes. Particularly we note the position of stations (20, 21) (homogeneous subset), which constituted an isolated group in the IV quadrant, and the position of stations (16, 17, 18, 19, 22) (homogeneous subset) in the II quadrant. Furthermore, the ordination in the reduced space shows clearly the transitional role of station 15 with respect to stations 13, 14 and 23: along the II principal axis station 15 moves farther from stations 14 and 23 and closer to station 13; in fact, stations 13 and 15 are a homogeneous subset with a confidence level smaller than 1 %. In the Gulf of Salerno, the cluster procedure showed a uniformity, but it hides the singularity of station 8, linking it to sample 7 (Fig. 5b).

During the sampling, the water column was mixed down to the 50-55 m depth. Surface chlorophyll *a* values were low, ranging between 0.11 µg/l and 2.63 µg/l (Tab. 1).

March 1987 – An increase in total copepod abundances in all the sampled areas was observed. The mean values were the same as in November, the Cuma stations being the richest (Tab. 1). The major species was *Oithona similis*; its association with three *Clausocalanus* species (*C. paululus, C. pergens* and *C. arcuicornis*) characterized the overall area. The mathematical analysis detected homogeneous groups due to minor differences in the rank order of less abundant species (Fig. 3). Only stations 13 and 15 (homogeneous subset **K**) were characterized by the highest dominance of *O. similis* (48 %) and by the significant presence of neritic species as *Euterpina acutifrons*, *Calocalanus styliremis* and *Acartia clausi*.

For this cruise, the dendrograms (Fig. 5c) for the Gulf of Naples showed three groups in which we could distinguish homogeneous subsets, for example the subset **I** enclosed in

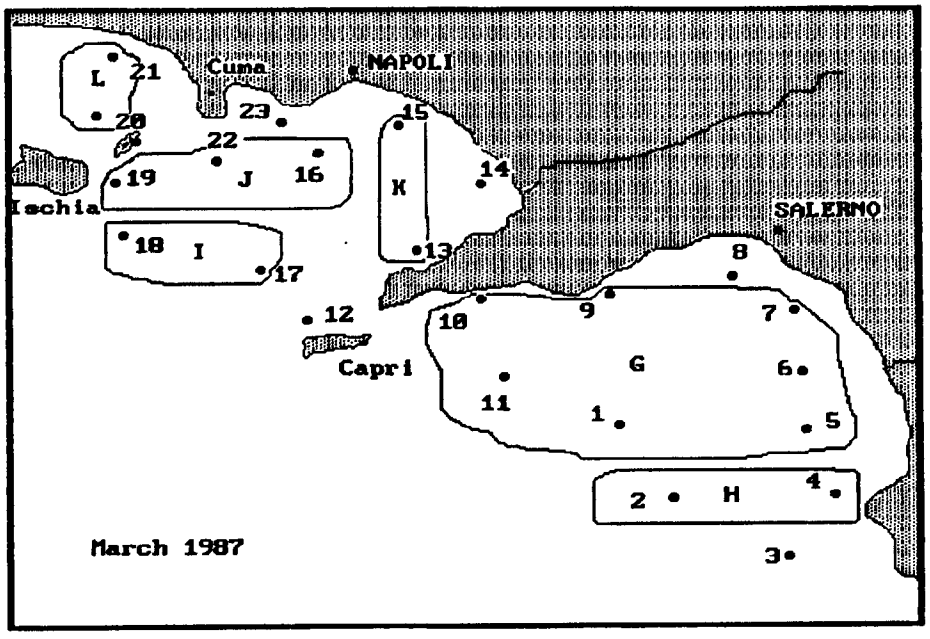


Figure 3

Homogeneous subsets (HS) pattern for March cruise (Labels G-L).

the group (18, 17, 20) or the subset **K** in the group (15, 18, 19, 16). Furthermore, also in this case, stations (20, 21) (area C) did not belong to the same group. For the Gulf of Salerno (Fig. 5d), we obtained a grouping different from the homogeneous pattern. The homogeneous subset **H** was different from **G** for *Oithona similis* frequency percentages, 37 % and 16 % respectively; station 3 was the only sample characterized by 57 % of *Oithona similis* and by 5 % of *Calocalanus contractus*. By comparison, the clusters showed the similarity among all samples (characterized by *Oithona similis* dominance) pointing out the link between stations (9, 10) which have a number of individuals higher than others (about 700 elements compared to a mean value of 400).

The mean surface chlorophyll *a* values were the same as in the previous cruise in the Gulf of Naples, whereas a slightly increase was recorded in the Gulf of Salerno and at stations off Cuma (Tab. 1).

June 1987 – With regard to copepod abundances, mean values were higher in the Gulf of Salerno and much lower at the Cuma stations (Tab. 1). *Paracalanus parvus* and *Acartia clausi* were the most abundant species in this period, comprising 42 % and 20 % of total adult copepod numbers, respectively. The analysis selected a higher number of homogeneous groups, all clearly dominated by *P. parvus*. Only at stations 12 and 19 (homogeneous subset **R**), close to Ischia and Capri Islands, respectively, was *A. clausi* first in rank order (Fig. 4). The groups were separated by the relative importance of less abundant (*Oithona similis, Centropages typicus, Calocalanus styliremis, Clausocalanus pergens*) or secondary species.

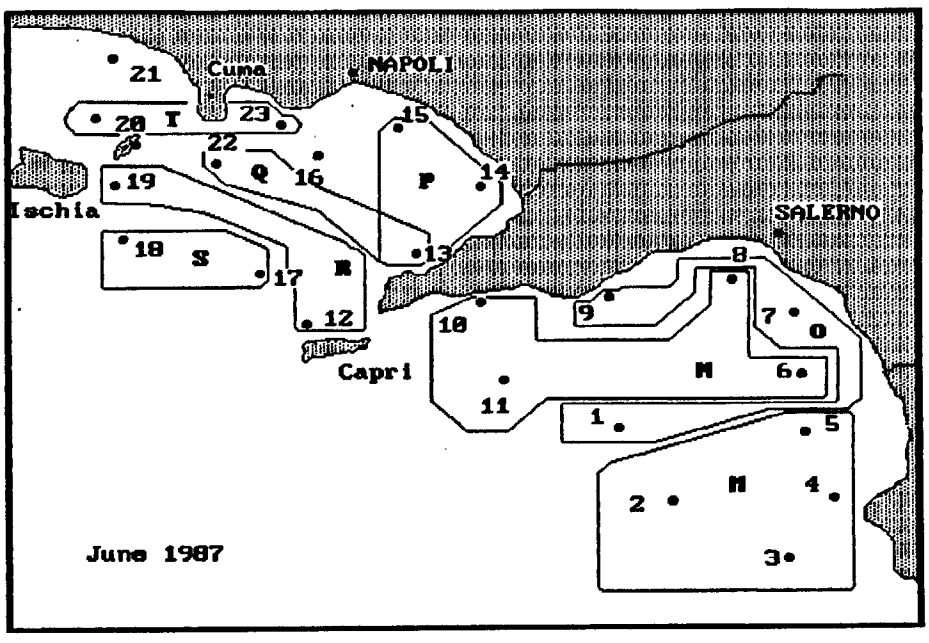


Figure 4

Homogeneous subsets (HS) pattern for June cruise (Labels M-T).

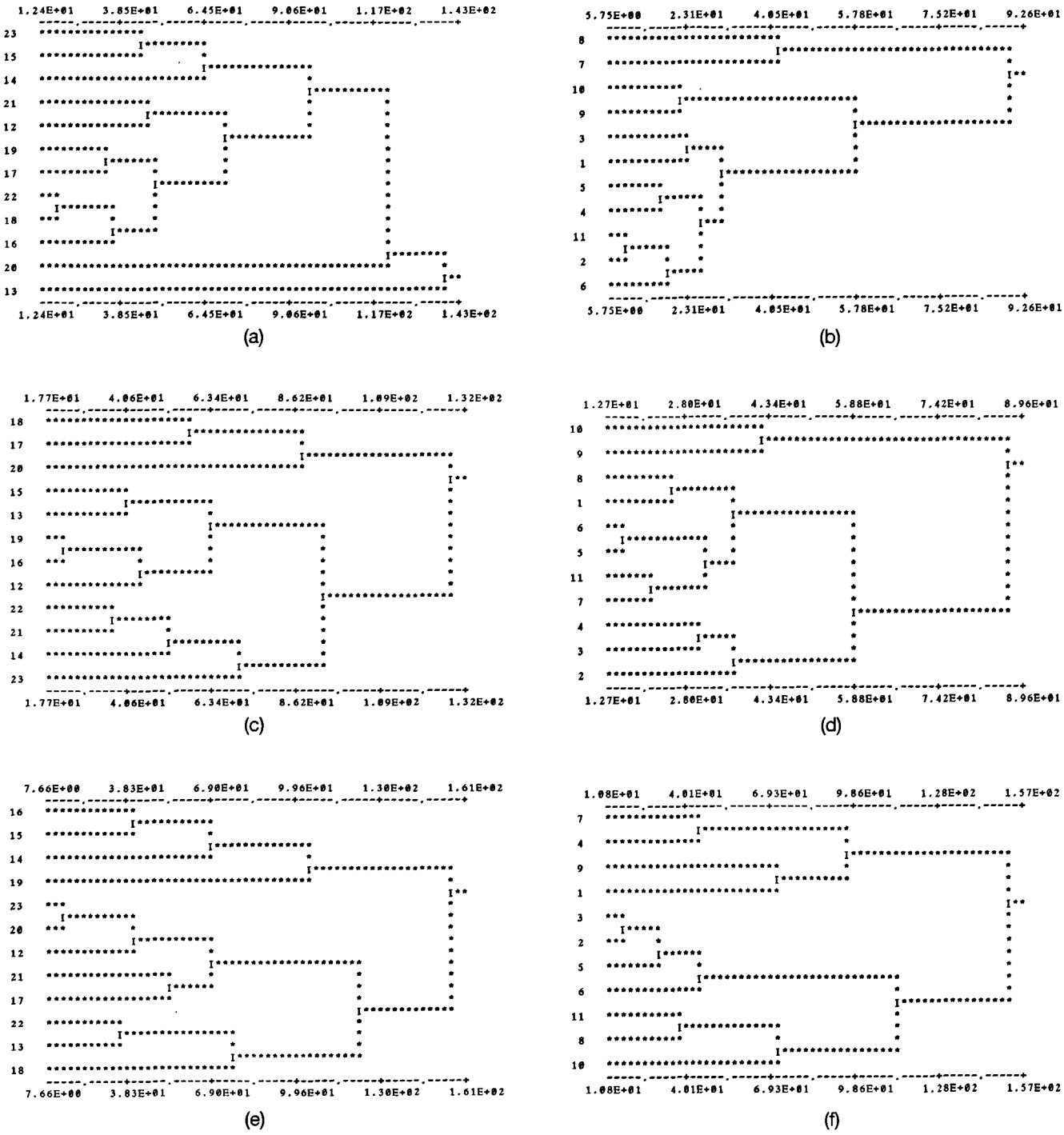


Figure 5

Dendrograms obtained for samples (1-11) in the Gulf of Salerno (b,d,f) and for samples (12-23) in the Gulf of Naples (a,c,e) in the three cruises.

By contrast, the classification procedure evidenced only two groups in each of the two gulfs (Fig. 5e, f). During this cruise there was strong dominance by a few species that masked the different abundance patterns of minor species, as shown in Appendix A. By means of the ordination in the reduced space (in this case I and II principal axes represent about 90% of the variance), the three homogeneous subsets pointed out by the homogeneity test positioned along the II principal axis. This show a gradient that clarifies better the complex pattern in the Gulf of Salerno presented in Figure 4.

The water column was characterized by a sharp thermocline at about 20 m depth, with very different surface chlorophyll *a* values in each area, in terms of both mean concentration and spatial distribution pattern (Tab. 1).

DISCUSSION

Applied to copepod community data, the statistical method, based on non-parametric maximum entropy tech-

niques, revealed significant differences between the pelagic systems within the area studied.

We used the statistic H to quantify the shifts in the species compositions and we compared it with the diversity index. We showed that the latter was not able to discriminate among subgroups characterizing different spatial and temporal patterns. Comparing the homogeneous patterns with clusters for each cruise we note that:

(i) if few species were dominant (for example in June), the clustering was not able to distinguish among subgroups which differed in the abundances of minor species;

(ii) if an area was characterized by a uniform pattern with some singularities (for example the Gulf of Salerno in November) the clustering did not show the isolated sample but linked it to other stations;

(iii) if an area was characterized by a fragmented pattern (for example the Gulf of Naples) the cluster, minimizing the differences among samples, defined large subgroups which masked the changes in contiguous sub-areas.

Furthermore the ordination of homogeneous subsets along the principal axes (PCA) shows better the presence of possible gradients.

The homogeneity test characterized the habitats in each situation, pointing out either the maximum number of homogeneous samples or the maximum number of different sub-areas. In this way, it can guide further research aimed at differentiating the targets.

In this analysis, the Gulf of Salerno appeared as a homogeneous area with uniform spatial patterns in copepod assemblages. A slight increase in chlorophyll *a* values from November to June was recorded, although the gulf remained largely indistinguishable from the external oligotrophic Tyrrhenian waters. A previous study carried out in this environment showed it to be a spatially homogeneous system without areas of nutrient enrichment (internal report). The coastal influence was limited to a narrow littoral area smoothly merging into the open sea waters. Marked gradients in chlorophyll *a* and in other environmental parameters were not observed in the stratified season.

The present analysis of copepod communities confirmed the strong spatial homogeneity of the Gulf of Salerno through the seasons, even when the more stable hydrological features and local circulation of the water masses should favour the differentiation of habitats together with the development of the populations.

By contrast, the Gulf of Naples appeared to be fragmented into different subsystems with boundaries moving according to the season. The results therefore suggest a more diversified zooplankton community, probably coupled to a more varied local hydrography and somewhat more complex interactions between environmental factors. For example, in June, one homogeneous group (stations 12, 19) was defined by the presence of *Acartia clausi*, a typical neritic species. This was probably due to the proximity of the sampling sites to Capri and Ischia islands, since the values of the hydrographic parameters recorded at those stations were closer to those of coastal waters (*e.g.* lower salinity values, with 0.1 PSU differences with the other two stations 17 and 18, located at the gulf entrance. The overall salinity range measured at all stations in the gulf was about 0.2 PSU). It could also in all likelihood be due to the position of stations 12 and 19, which lie within the shelf break whereas 17 and 18 are in a canyon area. Most probably, the nutrient richness resulted from land runoff, which contributes to the pelagic structures observed in the Gulf of Naples. In this gulf, several distribution patterns of primary producers and physical chemical parameters, recorded on various scales in space and time, have been reported by other authors (Ribera d'Alcala' *et al.*, 1989; Zingone *et al.*, 1990).

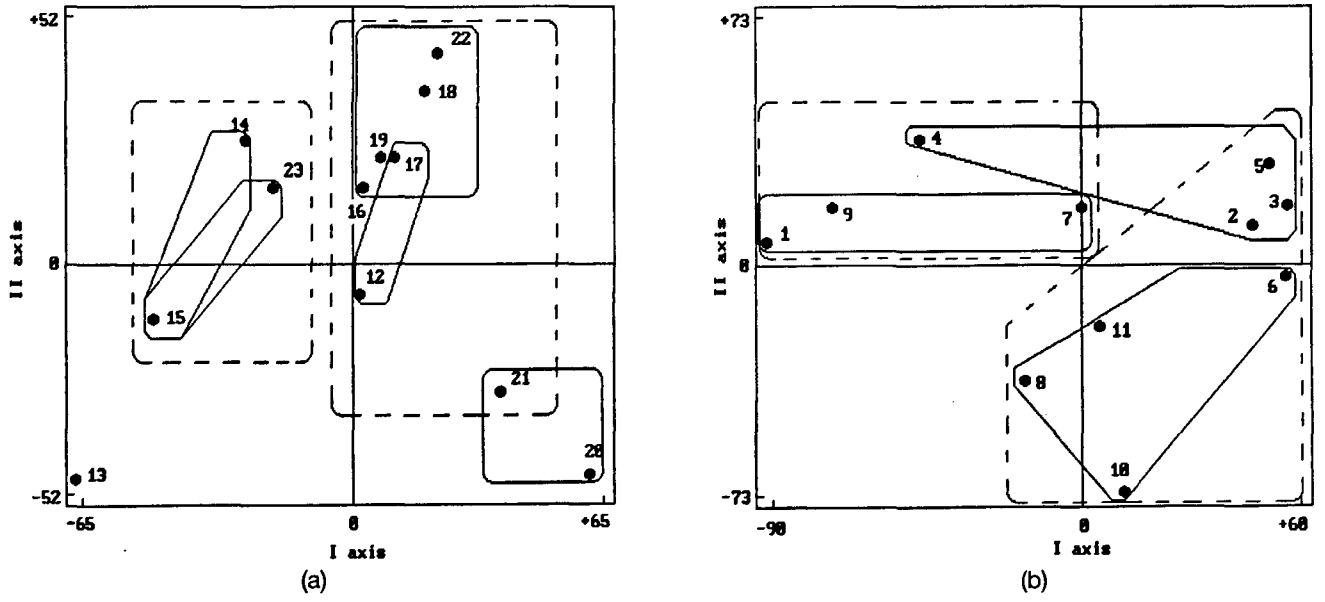


Figure 6

Ordination in reduced space where the solid lines show the homogeneous groups and the dashed lines the clusters for: a) Gulf of Naples in November; b) Gulf of Salerno in June.

The present analysis clearly demonstrated the peculiarity of the easternmost inshore area of the Gulf of Naples and the area off Cuma, where most of the domestic and industrial sewage from Naples is discharged. This should confirm the existence of particular ecological features affecting zooplankton communities in these areas. The subsystems were distinguished by the higher relative importance of some neritic copepod species such as *Paracalanus parvus, Calocalanus styliremis, Paracalanus nanus*, which appear to benefit from the enrichment of these waters.

In the summer of 1983, generally the season of lower phytoplankton abundance in temperate seas, high numbers of phytoplankton were found in surface waters in this coastal area and in the harbour entrance (Zingone *et al.*, 1990). Moreover, in these areas, even in periods of low chlorophyll *a* values, dissolved and particulate organic matter or detritus could be immediately available for copepods as supplementary food energy (Lenz, 1977). The nutritive value of detritus may be enhanced by adsorption of dissolved matter on to inorganic particles or by colonization by microorganisms with high protein content.

As a consequence of the above observations, the analysis gives rise to a number of suggestions concerning the influence of environmental stress, such as pollution, on spatial differentiation in zooplankton communities, even if the impact of pollution on the planktonic system depends on the hydrology of the examined area (as shown by Siokou-Frangou *et al.*, 1990 in the Saronikos Gulf, Greece). In different Mediterranean regions, Patriti (1984) recorded a clear decrease in zooplankton numbers at heavily polluted stations, whereas Siokou-Frangou and Papathanassiou (1991) reported that total zooplankton abundances changed at the polluted stations according to the sampling period.

The responses of coastal zooplankton species to environments with differences in trophic features, and the quantitative development of their populations, are difficult to predict. Most species exhibit a complex pattern, involving different reproduction strategies, feeding behaviours, chemo- and mechanoreception that interact to determine zooplankton community composition (Paffenhöfer and Streams, 1988).

Sullivan *et al.* (1985) observed that populations of dominant coastal copepods showed no immediate increase after artificial nutrient enrichment, but did so during the second and third years of the study. The lack of a rapid population response suggests that factors other than food supply can operate to control copepod standing stocks in the field. Among these factors there may be external causes, such as predation, or events related to the biology of the species, such as egg-hatching success (Ianora *et al.*, 1992).

There is no a single response for planktonic organisms faced with environmental stress. In copepods, similar taxa (*e.g.* congeneric species) often exhibit different patterns of distribution, abundance and behaviour in different neritic environments (Checkley *et al.*, 1992). Symptoms of stress can often be detected in deviations in reproduction cycles, or in morphological, histological or biochemical abnormalities within populations and organisms (Rapport *et al.*, 1985).

In this paper, we limited the analysis to classification and to the description of homogeneous groups based on species composition. The small differences in copepod assemblages characterizing each homogeneous area defined by the analysis were statistically significant. Although they were not immediately related to precise ecological factors, these differences indicated changes in species composition that were characteristic for each homogeneous group and did not depend on intrinsic fluctuations. Such changes could be early indicators of stress, showing when initially homogeneous areas begin to differentiate due to forcing factors, before modifications in the environmental parameters become detectable by analytical instruments.

The method is not able to explain the structure extracted from the basic data. Other multivariate techniques can be utilized to interpret this structure either by the inner descriptors or by information from outside data matrix.

Further, the results of the present study suggest that a careful monitoring could be carried out at smaller spatial and temporal scales in more specific regions, in order to follow more closely the pelagic system dynamics. In this way, a more focused data set on environmental and biological parameters could help in the closer indentification of habitats and relate community structures to ecological features in marine regions. A better prediction of the kinds of stresses that will cause the most serious modifications of productive and diverse temperate coastal areas may help to avoid them (Suchanek, 1994).

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APPENDIX A

NOVEMBER 1986

HS A: *Clausocalanus furcatus* (29.4 %)
Clausocalanus paululus (14.5 %)
Calocalanus styliremis (9.7 %)
Oncaea media (7.5 %)
Farranula rostrata (6.9 %)
Paracalanus nanus (5.9 %)
Oithona plumifera (5.3 %)
Corycaeus giesbrechti (2.9 %)
Clausocalanus arcuicornis (2.3 %)
Oithona longispina (2.0 %)

HS B: *Clausocalanus furcatus* (25.4 %)
Paracalanus parvus (9.0 %)
Paracalanus nanus (8.2 %)
Farranula rostrata (8.2 %)