

11. Annex 6 – Taxon Group Composition, Diversity, Biomass and Production of the Benthic Infaunal Invertebrate Community

11.1. Introduction

The infauna (endofauna) are the component of the benthic invertebrate community that spend the majority of their lifecycle living within the seafloor. They form a major component of the North Sea fauna and previous studies of these animals have described the distribution of a number of characteristics of the community, such as species diversity and species relative abundance, with interpretations of the physical and biological factors affecting their distribution (for examples see Basford *et al.*, 1990; Duineveld *et al.*, 1991; Heip & Craeymeersch, 1995; Kroncke, 1995; Kunitzer *et al.*, 1992). Based on the findings of these studies, the major factors affecting the distribution of infaunal invertebrate communities within the North Sea are sediment composition, depth, food availability and water temperature. This leads, at the coarsest level, to a division of northern taxa that extend south to the northern margins of the Dogger Bank; and southern taxa that extend north to the 100m depth contour. There is an area of overlap and variability around the 70m depth contour in the central North Sea. Temporal variability at smaller scales has been attributed to a number of potential driving factors including eutrophication and temperature effects (particularly in the shallower areas of the North Sea), fisheries disturbance and localised changes in availability of food resources (see reviews in Clark & Frid, 2001; Kroncke & Bergfeld, 2001).

It was considered essential to include the infaunal community in the MAFCONS survey data collection because of its contribution to secondary production available to the rest of the demersal community (larger epifaunal invertebrates and the invertebrate feeding demersal fish). Infaunal production is calculated here and used in tests of Huston's model linking both diversity of demersal fish and the larger epifaunal invertebrate assemblages to secondary production and fisheries disturbance (Chapter 2). At the same time some broad descriptions of distributions of key taxa and diversity and composition of these are described in terms of the North Sea system.

11.1.1. The community described

In attempting to describe the infaunal community in terms of its composition, diversity and productivity, it is important to take account of the restrictions that the sampling procedure has on the community being represented. This is not the absolute infaunal community, but that which has been sampled by the gear and retained in the handling process. As discussed in Annexes 4 and 5, no sampling gear ever samples all the individuals present. However, infauna are sampled using a Van Veen grab and this can be described as a quantitative sampler for those infaunal animals that live within the depth range that it samples. We acknowledge that certain animals living below the depth of sediment sampled (some of high biomass and thus high contribution to production) will not be sampled well by this sampling apparatus. Also, those highly mobile animals living in contact with the seafloor (hyperbenthos) will also be poorly represented because they can move out of the way of the grab before it makes contact. The community described is a macrofaunal assemblage of animals large enough to be retained in a 1mm sieve.

11.1.2. Productivity

Traditional methods for calculating secondary production from the benthos have been applied to single animals or populations based on the change in body mass or growth over time. However, the methods used to calculate this generally involve the destruction of samples and require intensive sampling of the same population to account for changes over time. Methods include those based on cohort analysis, size class based methods and the relationship between productivity and mortality (Cushman *et al.*, 1978; Wildish & Peer, 1981; Crisp, 1984; Morin *et al.*, 1987). None of these methods are practical when trying to quantify secondary production at the community level. In the MAFCONS project, assessments of the secondary production from the infaunal and epifaunal benthos at between 100 and 150 stations per year over two years have been undertaken.

Over the last 20 years, efforts have turned towards parameterising empirical models that can be used to estimate secondary production (for review see Brey, 2002). These models describe the relationships between easily measured parameters such as biomass, individual body mass and water temperature with production (P) or the production/biomass (P/B) ratio for individual populations. Empirical relationships between these parameters are calculated using the combined published results of the traditional studies as described above. It is then possible to predict P or the P/B ratio for new sampled populations just using data for the easily measured parameters such as biomass and temperature. All of these approaches depend more or less directly on the negative exponential relationship between metabolic rate and body mass. A detailed review of the empirical models that have been developed is given in Chapter 10.

In all cases, models are based on data for individual species populations. Thus production is calculated for each species making up a community and all species totals are then summed to give total community production. Where species level data do not exist, the variability around mean individual weight will be likely to increase as taxonomic resolution decreases and this may affect the validity of using the empirical models that include mean individual weight as a parameter. However, here the infaunal data have been size structured to reduce the variability around the mean individual weight per taxon using a stacked sieve method (see Edgar, 1990a) and error associated with individual taxa relationships is reduced when applied to the entire community (Brey, 2002; Edgar, 1990b). In this project we examined the methods available for estimating secondary productivity from the infauna. The infauna include both colonial and individual based populations of animals. Due to this it was necessary to combine two methods, one based on biomass (for colonial animals), and one based on average mean weight per sieve size class.

11.2. Methods

11.2.1. Data set

Five 0.1 m² Van Veen grabs were taken at each MAFCONS station sampled, close to the track of the main demersal fish-sampling trawl. Overall 1250 Van Veen grab samples were taken across the North Sea, from 250 stations (120 in 2003 and 130 in 2004) but it was only possible to process the samples from 200 of these stations (105 in 2003, 95 in 2004; red stations in Figure 11.2.1.1.). Sampling was undertaken between July and September in each year. Bottom water temperature data, necessary for the production calculations, were recorded using a CTD at the time of sampling.

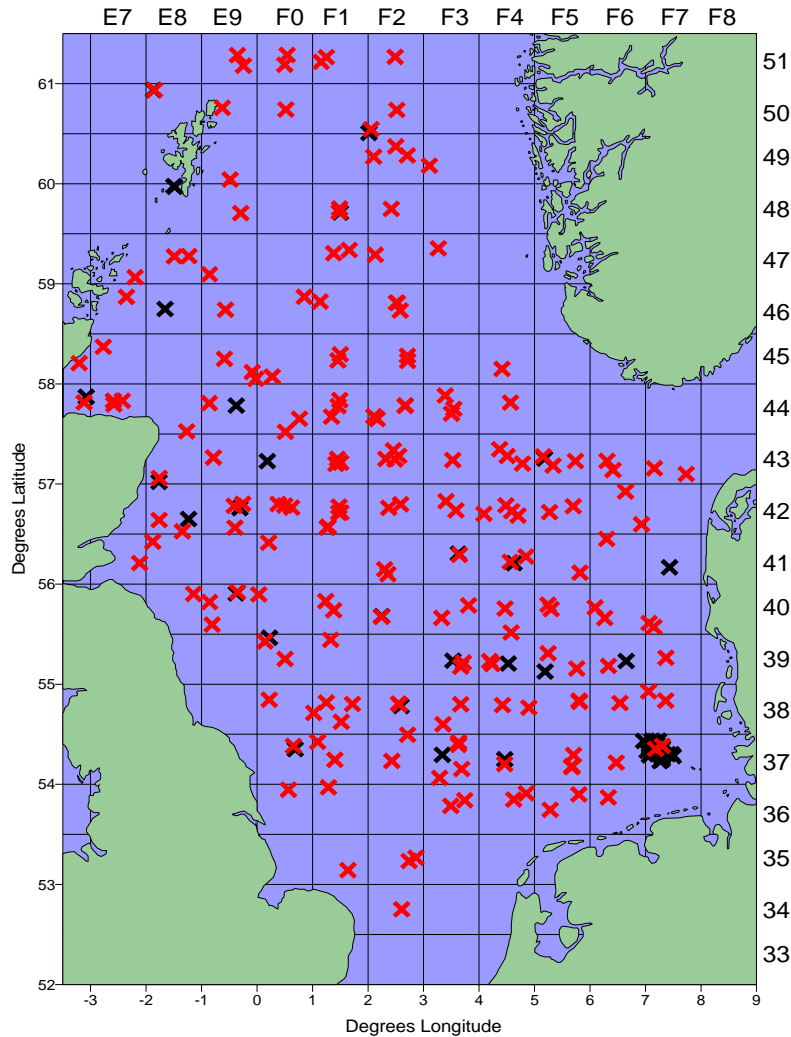


Figure 11.2.1.1. All 250 stations sampled for infauna with Van Veen grabs (5 taken at each station) during the 2003 and 2004 MAFCONS surveys. Red stations indicate the 200 stations it was possible to process and analyse in this report.

11.2.1.1. *Sample treatment.*

Infaunal samples were washed through a stack of sieves (0.5mm, 1mm, 2mm and 4mm) and all material preserved before processing in the laboratory. Total abundance and total biomass of animals in the 1-4mm sieves were recorded for animals sorted to one of 73 possible taxon groups (Appendix 1). The criteria used to determine the taxon groups were; (1) The ease to separate out animals into these groups during the sorting process (i.e. no requirement for use of keys; obvious at first sight); (2) the likelihood of the groups within Phyla having different morphologies and different behaviours in the sieving process. Samples were also identified and enumerated at the species level (where possible) but the species level data are not considered further here. A detailed description of the sample processing is given in the MAFCONS methods manual (Chapter 6).

11.2.1.2. *Data standardisation*

It was assumed that catchability of the gear was consistent for the assemblage found within the depth range sampled by the Van Veen grab. However, it is acknowledged that depth range sampled varies dependent on sediment type of the sample location. Those species living outside of the sampled depth range are not covered in this assemblage and it is accepted that this will have implications for total biomass, productivity and diversity of the communities described. We also recognise that the volume of sediment sampled by each individual grab varied around a mean of 10 litres. Unfortunately it was not possible to standardise abundance and biomass data to account for this variation in volume sampled, because several sets of stations did not have a recorded volume per sample.

For all taxon groups where all or a high percentage of records had no abundance value, abundance data were converted to presence/absence codes and could not be used for abundance weighted analyses. These taxon groups included: Bryozoa, Foraminifera, Hexacorallia, Hydrozoa, Octocorallia and Porifera.

11.2.2. Distribution of total abundance and biomass

For each station, total abundance (N) (not including colonial species) and total biomass (B) (including all species except a small number of encrusting species that could not be weighed) were standardised to numbers per m^2 by working up the individual $0.1m^2$ grab sample data to numbers per metre squared and then calculating the mean of all five grab samples per station. Univariate indices of total abundance and total biomass were calculated for each station as point estimates for each year. Both years were subsequently combined and average density and biomass (N and B per m^2) calculated for each ICES rectangle using all stations sampled in a particular rectangle. Distributions of the 12 dominant taxa based on total abundance across the survey (none-colonial taxon groups), and the 12 dominant taxa based on biomass (including colonial taxon groups) were plotted for the combined surveys.

11.2.3. Distribution of communities based on relative abundance of taxon groups (community composition)

Firstly, taxon groups were standardised within Phyla to exclude multiple taxonomic levels that could potentially cover the same animals. Inclusion of multiple taxonomic level groups could obscure true variation in community composition. The common taxonomic level varied between Phyla; in some cases all data were recorded at the Phyla level, but in most cases data were organised at the Order or Class level (See 'Community Analysis Group' list in Appendix 1). In order to enable full analysis where only presence/absence data were available, the fauna were subdivided into two groups – all infauna (including colonial species – presence/absence analysis) and non-colonial taxa only (where taxon abundance (N , m^2) for each station was used as the basic input data). A Bray-Curtis similarity matrix comparing the similarity between the infauna community taxon compositions present in all pairs of ICES rectangle, was constructed for the combined surveys after first pooling the entire sample data collected for each ICES rectangle. The Bray-Curtis similarity matrices were then subjected to hierarchical group-average clustering to identify the groups of ICES rectangles with similar taxon compositions. All abundance data were root transformed to down-weight the effect of the most abundant taxa on the Bray-Curtis similarity indices. All analyses were performed using the *PRIMER*© software (Clarke & Warwick 2001).

11.2.4. Distribution of taxon group diversity

11.2.4.1. *Diversity metrics*

Species (taxon group here) diversity conceptually consists of two different aspects of species relative abundance; the actual number of species included in any particular sample, and the evenness of the distribution of individuals between the species encountered. Here we use three different metrics each differing in the extent to which they are influenced by one or other of these two aspects of species diversity (eg Southwood, 1978): Hill's N_0 , total number of species (species richness); Hill's N_1 , an index the number of species present, defined as the exponential of H' , where H' is the Shannon-Wiener diversity index; and Hill's N_2 an index that is predominantly influenced by the abundance of the dominant species defined as the reciprocal of D , where D is Simpson's dominance index. Hill's N_1 is therefore computed as:

$$N_1 = e^{-\sum_{s=1}^S p_s * \ln(p_s)} \quad 11.2.4.1.1$$

and Hill's N_2 as:

$$N_2 = \frac{1}{\sum_{s=1}^S p_s^2} \quad 11.2.4.2.2$$

where p_s is the proportion of the total number of individuals contained in the sample in question contributed by each of the S species recorded in the sample (Magurran, 1988). N_1 is more sensitive to the number of species recorded in the sample, where as N_2 is more sensitive to the evenness of the distribution of individuals between species.

Taxon group richness (Hill's N_0) was calculated using all taxa, whilst Hill's N_1 and N_2 indices were calculated using only the non-colonial taxon group data, as they require the individual taxon abundance values. Groupings of data were standardised to the same taxon level within Phyla as described in 11.2.4 (see PRIMER Group list in Appendix 1). All diversity metrics were determined using the *PRIMER*© software package (Clarke & Warwick 2001).

11.2.5. Secondary production

Total community production per day (g AFDM per m²) was estimated using an empirical model based on the relationship between daily production, mean individual body mass and water temperature following the method of Edgar (1990a). As secondary production from the MAFCONS surveys is based on data only collected at one time of year, it was not possible to use any of the empirical models that also take annual variation in biomass and temperature into account. Jennings *et al.* (2001) published an empirical relationship between P/B and individual weight but this did not take into account the additional variability associated with temperature and as the MAFCONS project is interested in spatial patterns at the scale of the North Sea, where variation in bottom temperature is considerable, it was considered imperative that temperature be taken into account. It should be noted, however, that given that the MAFCONS survey data were collected during the summer months, biomasses and associated productions are likely to be at the peak of annual cycles.

11.2.5.1. *Edgar's (1990) model*

Edgar's (1990) model for benthic infauna invertebrate secondary production relates production to both organism dry-weight biomass and water temperature as:

$$\text{Log}P = -2.46 + 0.79\text{Log}B + 1.05\text{Log}T \quad 11.2.5.1.1$$

where P is the daily production ($\mu\text{gAFDM}\cdot\text{day}^{-1}$), B is the mean individual ash free dry body mass (μgAFDM) and T is the bottom water temperature ($^{\circ}\text{C}$). Edgar's model was developed using a dataset of actual data for all of these parameters from studies of 41 macrobenthic species in environments that covered the temperature range found in the MAFCONS survey (6-18.5 $^{\circ}\text{C}$). On examining this relationship, Edgar found that models for mollusca and crustacea separated from other infauna and other epifauna. Thus all the taxa in the infaunal database were assigned to one of these four groups before the empirical relationships for each one were applied (Infauna group relationship given in equation 11.2.5.1.). If some of the taxon groups were known to include both epifaunal and infaunal species, it was assumed that, as these data were collected with an infaunal sampler, the infaunal species within that taxon group would be prevalent. If there were no infaunal species known within a taxon group, this was assigned as epifaunal ('Edgar Group' in Appendix 1).

11.2.5.1.1. Converting wet mass to ash free dry mass

Using Edgar's method, all wet mass (WM) biomass values need to be converted to ash free dry mass (AFDM). Brey (2002) has a table of wet mass to ash free dry mass (WM>AFDM) conversion factors for invertebrates and fish at the level of taxonomic resolution for which there are sufficient data to assign a value. All conversion factors are based on calculations of the difference between wet mass and ash free dry mass for a number of examples for each group (a full reference list can be obtained from the author). Each taxon group in the infaunal database was assigned to a corresponding Brey group, but where no corresponding link to a Brey group was available; a number of steps were followed. If no alternative source of conversion factor was available, but it was agreed that a taxon resembled a group with a Brey conversion factor, based on its behaviour in the ashing and drying procedure, this alternative group's conversion factor was used. For 'Other organic matter', where fragments of biomass were found in a sample but it was not possible to assign them to any taxonomic group, the WM>AFDM conversion was a mean of the Mollusca, Echinodermata, Annelida and Crustacea values (see Appendix 1 for assigned Brey groups).

11.2.5.2. *Production analysis steps*

11.2.5.2.1. Taxa with total abundance and biomass data

For Edgar's model both the total number of individuals and total ash free dry mass (biomass) are required to calculate the mean individual weight required by the empirical relationship. This was calculated for each taxon group within the individual sieve sizes of each replicate sample. Daily production was then calculated using mean individual weight and water temperatures taken from the environmental data recorded at each station. Total daily production per taxon was calculated by multiplying individual daily production per sieve size class by the total number of individuals within that sieve size and then summing all production across sieve sizes.

11.2.5.2.2. Taxa with only biomass data

For a number (or all) of the records for some taxon groups, biomass data were available but abundance data were not. This occurred either because animals were colonial (and thus it was not possible to count the number of individuals), or where individual animals were fragmented. In these cases it was not possible to account for production directly by applying Edgar's model. However, where biomass data were available but no abundance data were given, it was still possible to assign total production using production-biomass (P/B) ratios. A P/B ratio was assigned to the taxon group following the steps described below and then biomass multiplied by the ratio to give total production. Three different steps were followed to assign P/B ratios to taxa with only biomass data. Firstly, where a P/B ratio was available for that taxon group within the same sieve size based on survey level data, this was used. Secondly, where no P/B ratio for the specific taxon group was available, but there were data for other taxa within the same Phylum, a Phyla level P/B ratio specific to the sieve size was assigned. Finally, where no P/B ratios were available for a Phylum (e.g. Bryozoa), the average of all P/B ratios from within the same sample and sieve size was assigned.

11.2.5.2.3. Taxa with only presence/absence data

It was not possible to estimate production attributable to these taxa because there was no measurement of individual weight or total biomass.

11.2.5.3. *Total daily community production*

Once total daily production had been calculated for each taxon group within a sieve fraction following the methods described above, total community production was calculated by summing across all taxa within a sample. Station specific production was calculated for the individual survey years by calculating the mean production per station across the five replicate grab samples. ICES rectangle level data were then produced by averaging stations within individual rectangles across the two years sampled.

11.3. Results

11.3.1. Distribution of abundance and biomass

From the 200 stations sampled and processed over the two years of surveys undertaken by the MAFCONS project, a total of 73 taxon groups were recorded from the Van Veen grab samples covering 23 different Phyla (Appendix 1). Of these 73 taxon groups, the 12 dominant taxa based on abundance (none-colonial taxa only) made up 85% of the total abundance across the whole survey, whilst the 12 dominant taxa based on biomass made up 88% of the total biomass across the whole survey. Spatial variation in mean total density is shown in Figure 11.3.1.1 and whilst highest abundances are mainly located in the southern North Sea, distribution of high biomass areas is more variable. The spatial distributions of the key taxon groups based on abundance and biomass (Figures 11.3.1.2 and 11.3.1.2) illustrate a number of different patterns in terms of dominance. Some taxa were particularly dominant in small areas and rare elsewhere (e.g. Phoronida and Echinoidea) whilst others were more dominant in a particular area of the North Sea (e.g. Scaphopoda, Echinoidea and Nematoda in the northern North Sea and Pelecypoda, Asteroidea and Ophiuroidea in the southern North Sea) and some were fairly ubiquitous in their distributions (e.g. the Polychaete groups). Examination of the influence of environmental factors on these distributions is not implicitly

undertaken here. However, given the well described differences in terms of depth, temperature and hydrography in the southern and northern North Sea, it is clear that some of these taxon groups may be more sensitive to these drivers than others.

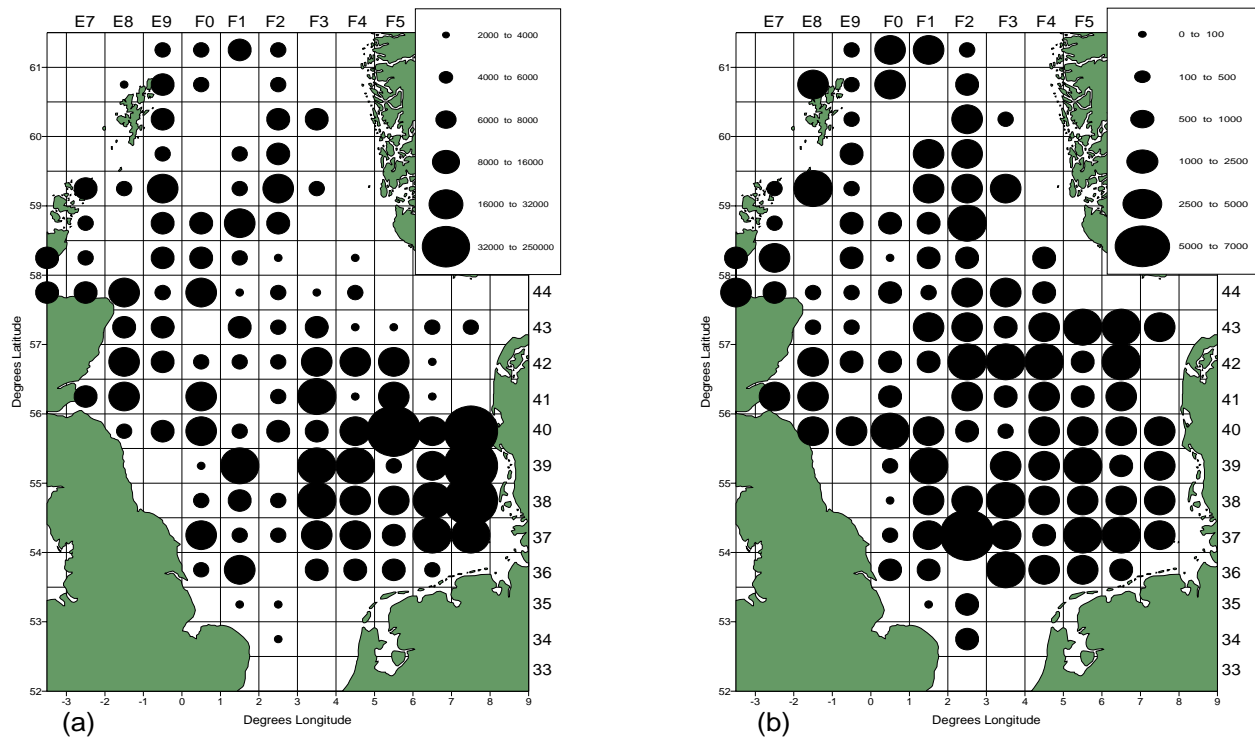


Figure 11.3.1.1. Spatial variation in mean density of the infaunal community based on (a) abundance ($N. m^{-2}$) (non-colonial taxa only) and (b) biomass ($g \text{ wet weight. } m^{-2}$) (all taxa).

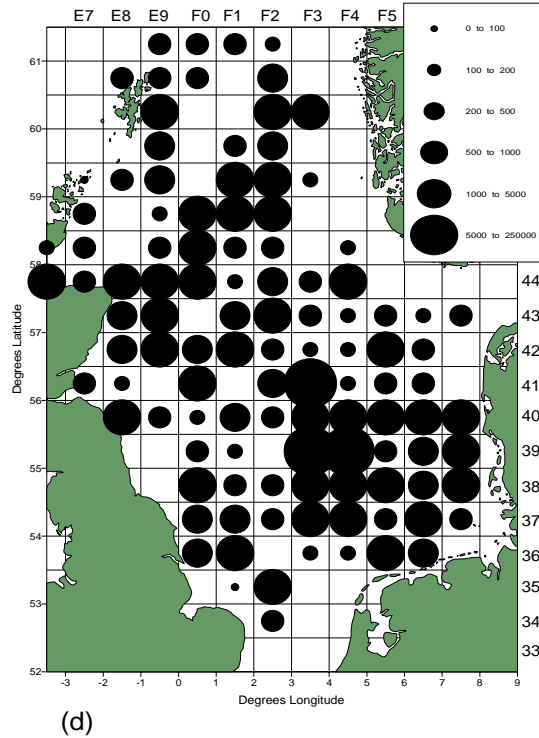
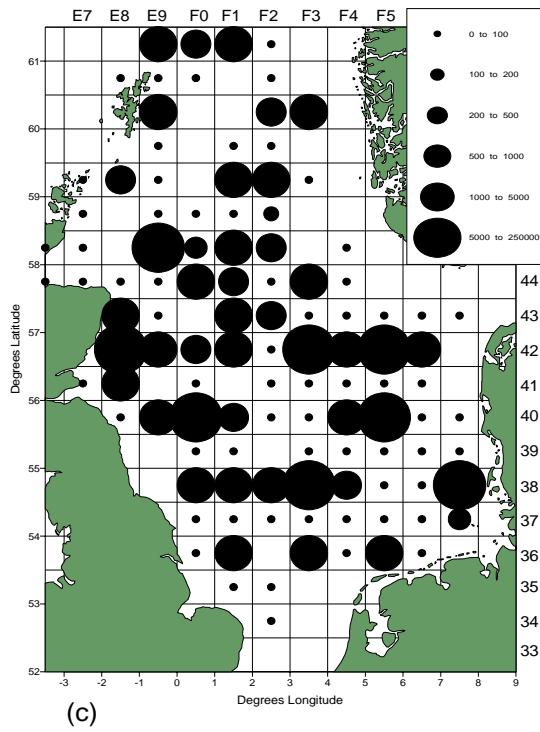
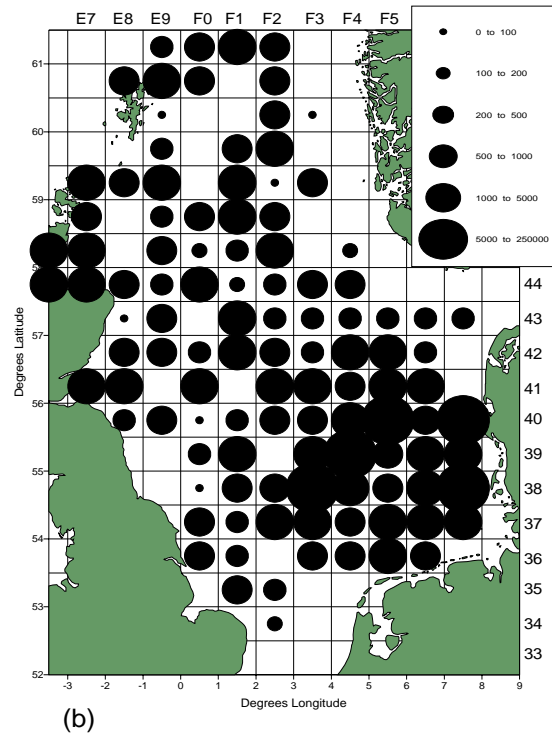
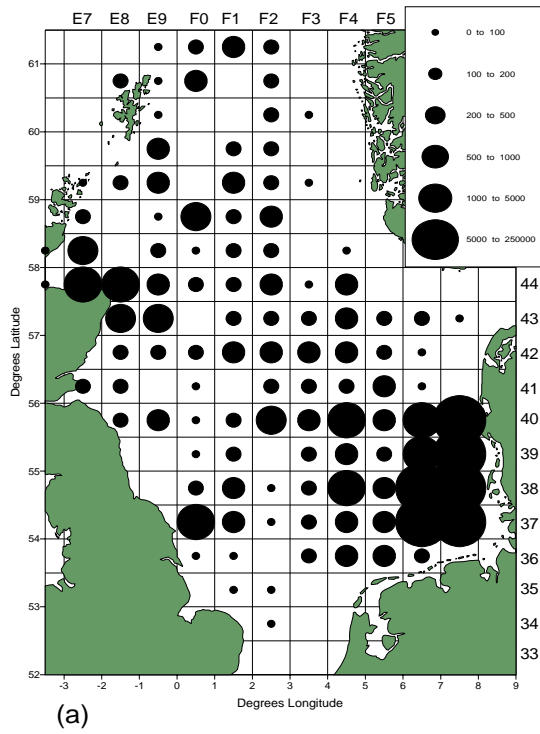


Figure 11.3.1.2. Spatial variation in mean density ($N. m^{-2}$) of the dominant taxon groups based on abundance: (a) Phoronida, (b) Polychaeta sedentaria, (c) Polychaeta, (d) Spatangoida.

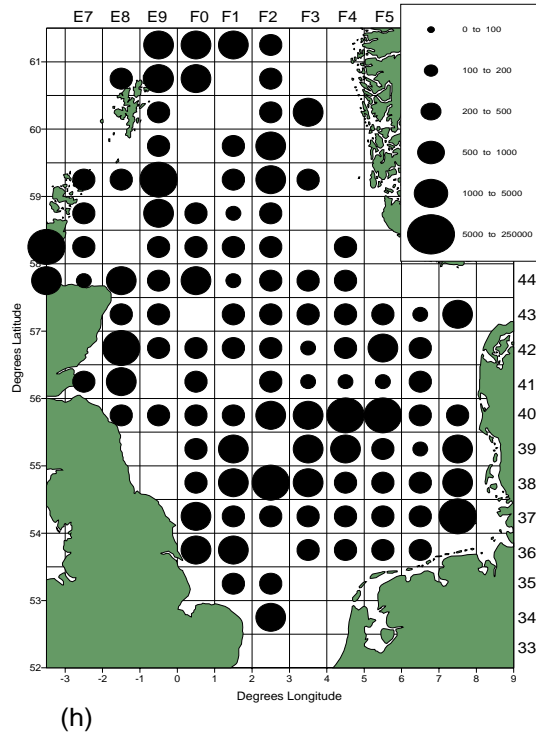
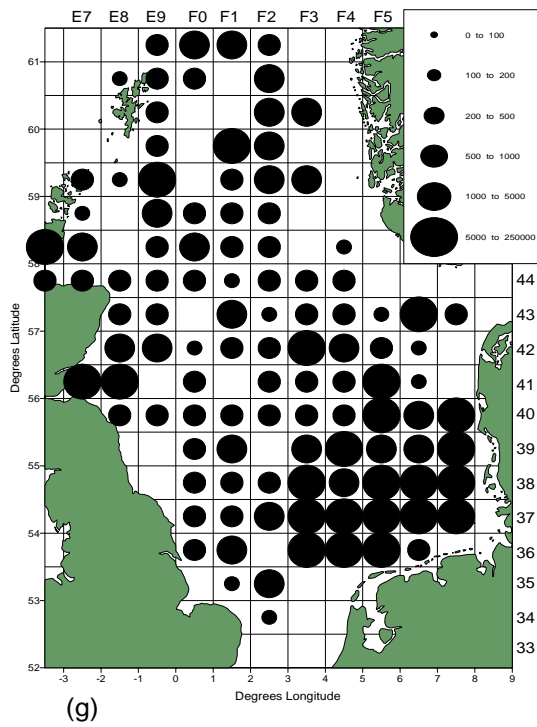
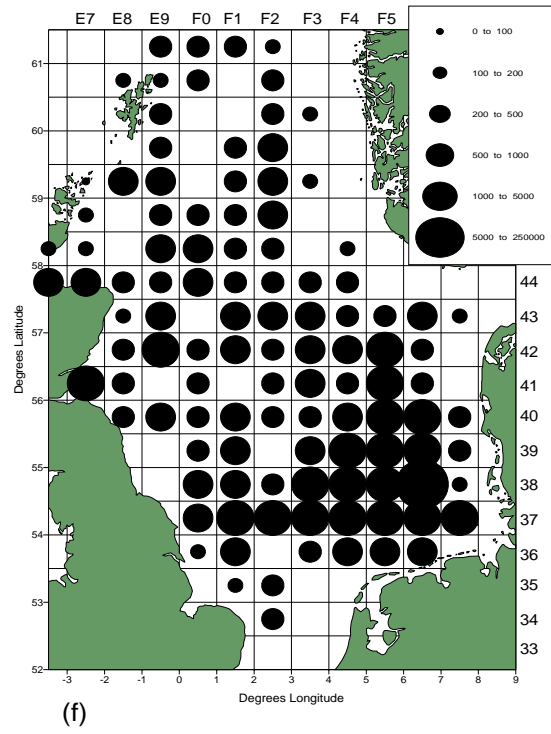
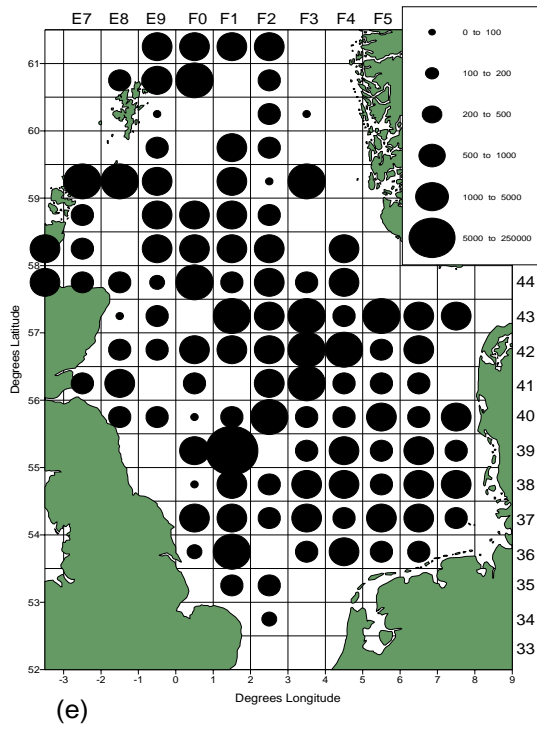


Figure 11.3.1.2 continued. Spatial variation in mean density ($N. m^{-2}$) of the dominant taxon groups based on abundance: (e) Polychaeta errantia, (f) Ophiuroidea, (g) Pelecypoda, (h) Amphipoda.

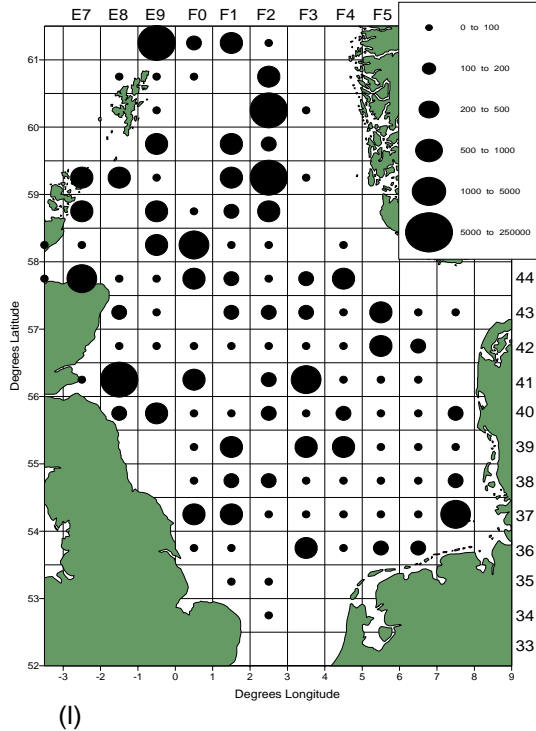
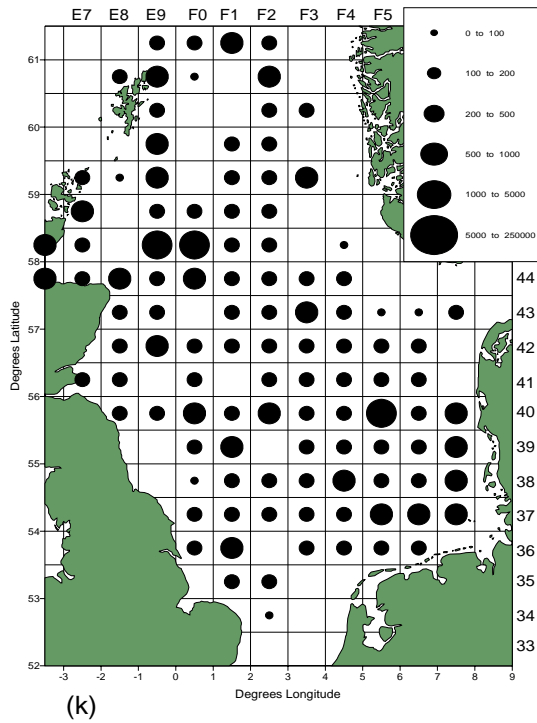
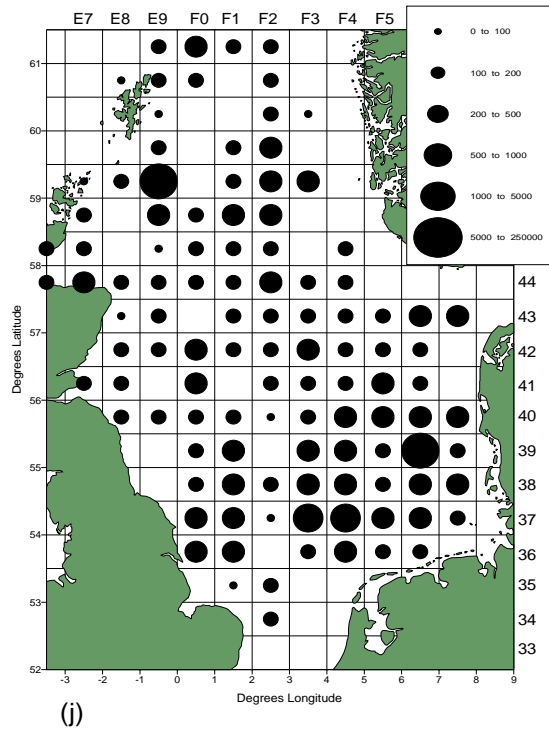
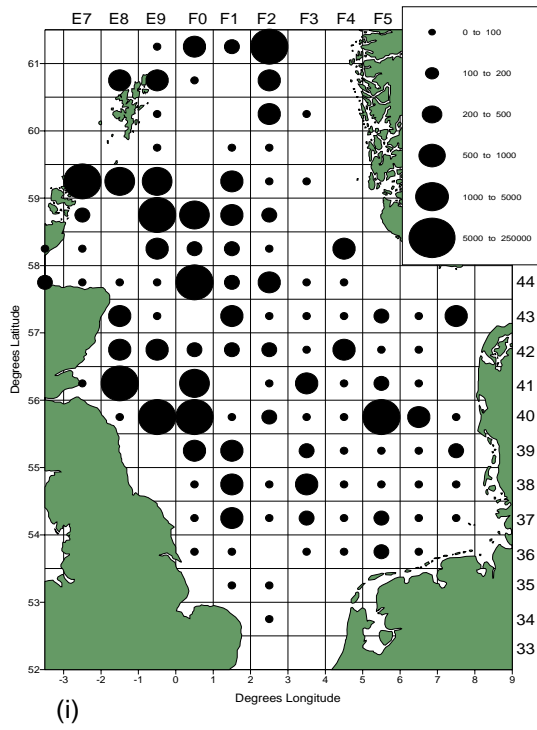
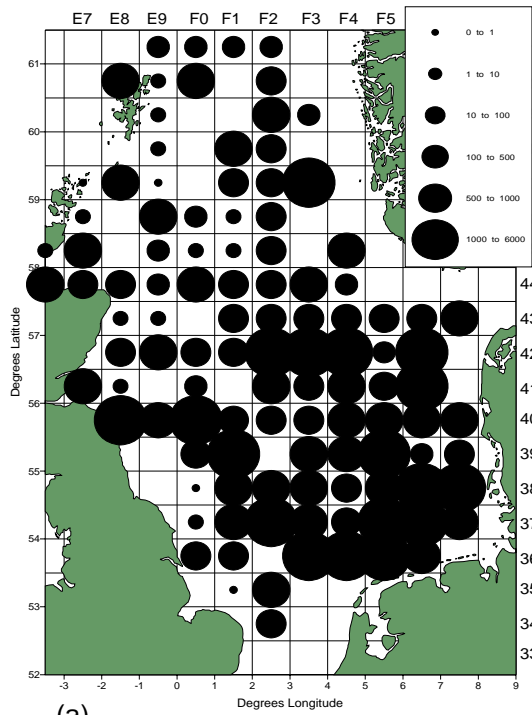
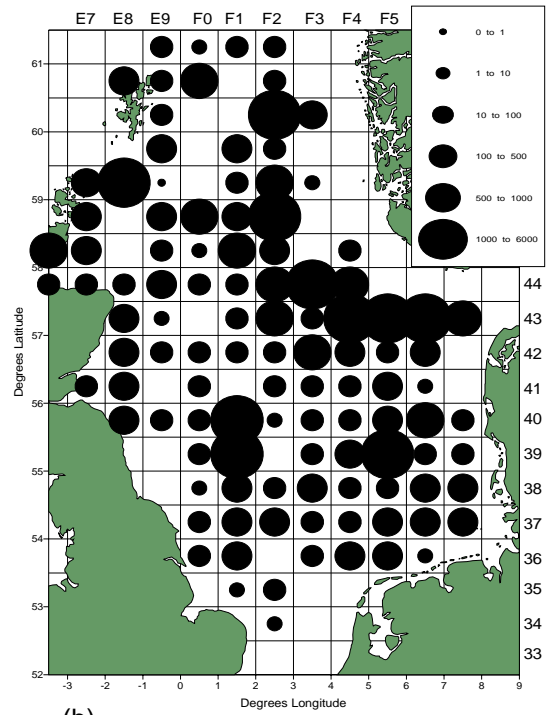


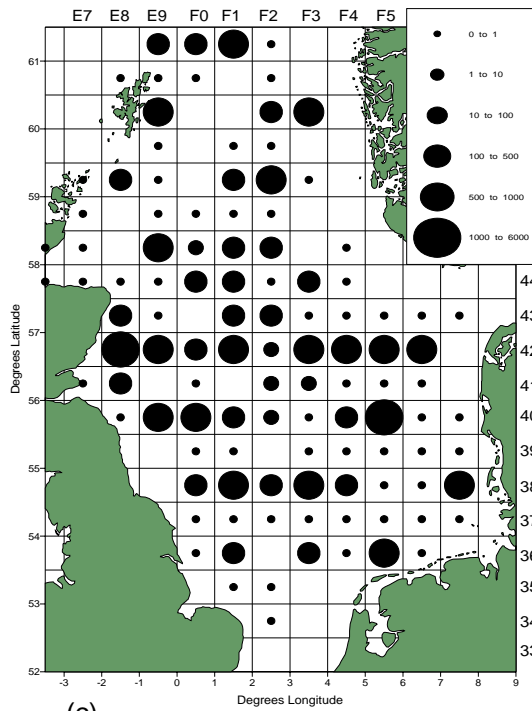
Figure 11.3.1.2 continued. Spatial variation in mean density ($N. m^{-2}$) of the dominant taxon groups based on abundance: (i) Nematoda, (j) Gastropoda, (k) Cumacea, (l) Echinoida.



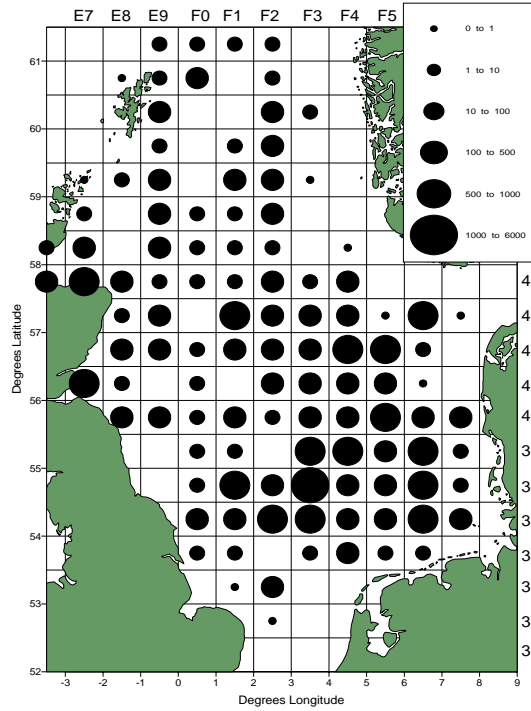
(a)



(b)



(c)



(d)

Figure 11.3.1.3. Spatial variation in mean density (g WW. m^{-2}) of the dominant taxon groups based on biomass: (a) Spatangoida, (b) Pelecypoda, (c) Polychaeta, (d) Ophiuroidea.

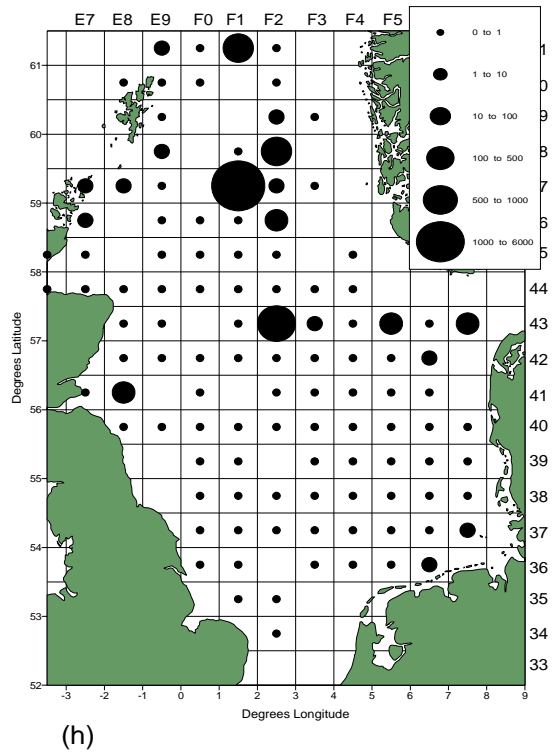
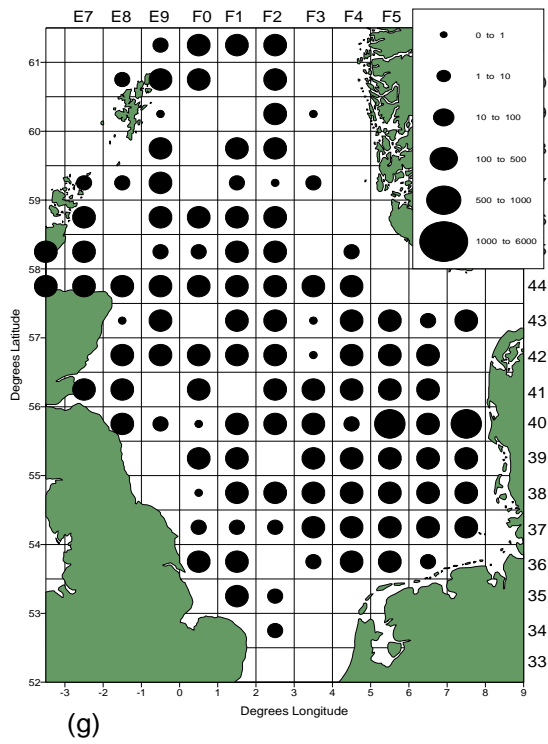
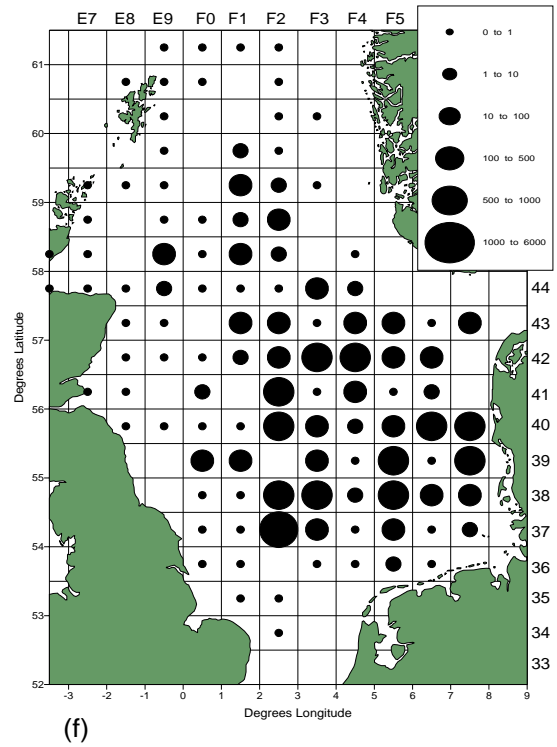
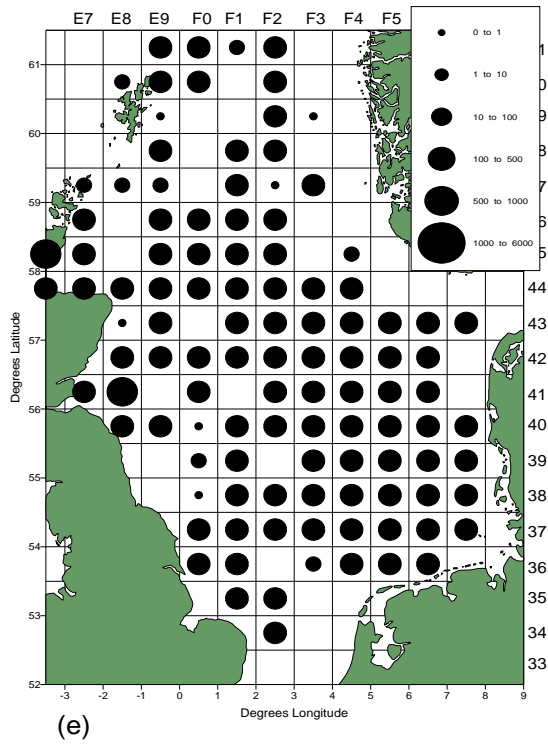


Figure 11.3.1.3 continued. Spatial variation in mean density (g WW. m^{-2}) of the dominant taxon groups based on biomass: (e) *Polychaeta errantia*, (f) *Asteroidea*, (g) *Polychaeta sedentaria*, (h) *Echinoida*.

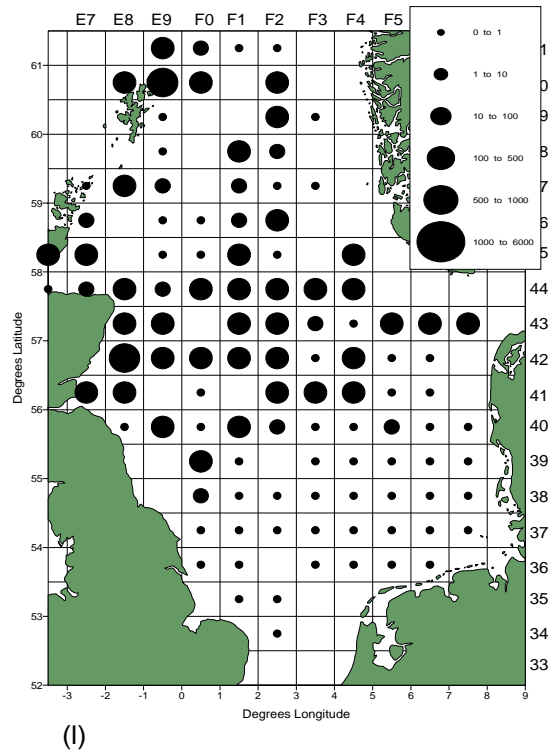
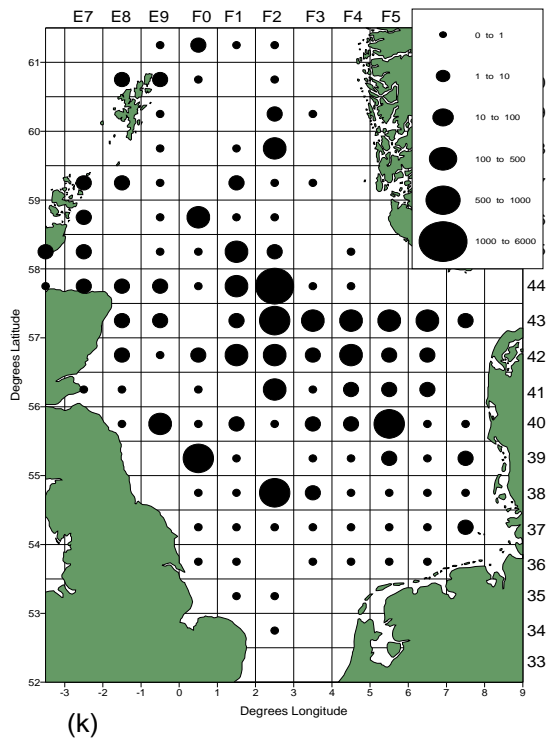
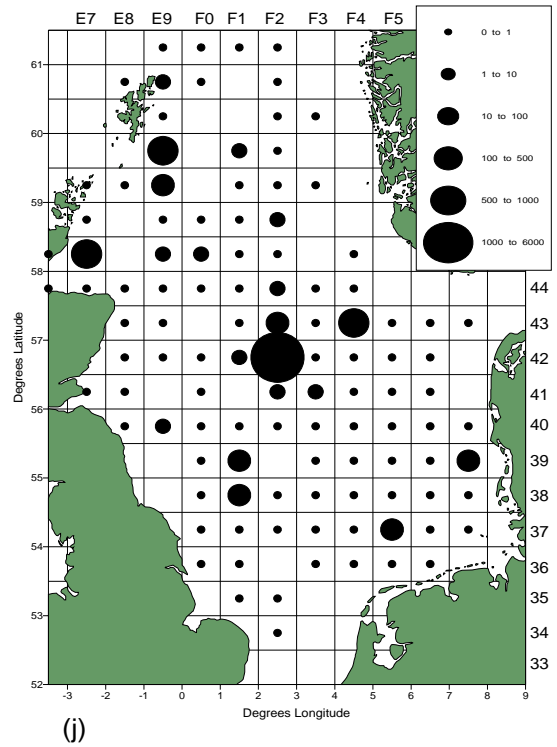
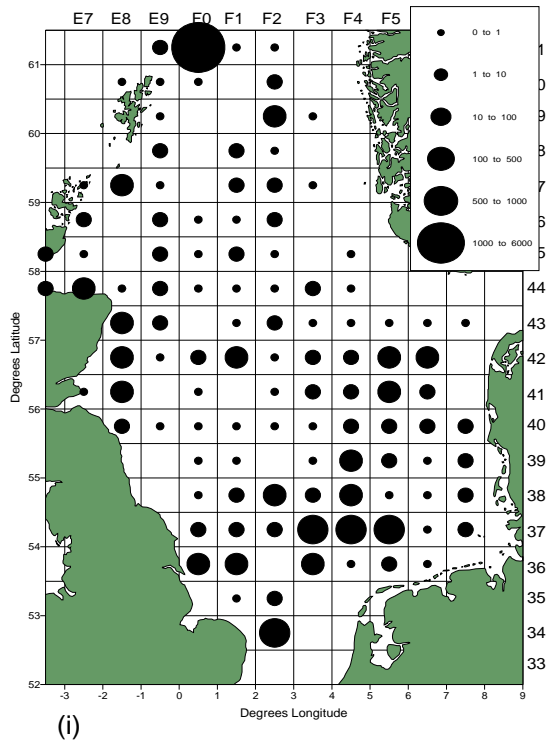


Figure 11.3.1.3 continued. Spatial variation in mean density (g WW. m^{-2}) of the dominant taxon groups based on biomass: (i) Decapoda, (j) Echinoidea, (k) Actinaria, (l) Scaphopoda.

11.3.2. Community structure based on relative abundance of taxon groups

Following hierarchical cluster analysis of the stations based on the Bray Curtis similarity in taxon group composition, two main clusters were identified in the infaunal community data that had over 65% similarity between rectangles within them (Figure 11.3.2.1. red and blue clusters). These clusters were identified independent of whether the analysis included just the abundance-weighted taxon data or the presence/absence data of all species including colonials. Infact the inclusion of colonial species appeared to have little effect in altering the clustering of contagious stations to that already shown by the abundance-weighted data (Figures 11.3.2.1. ands 11.3.2.2.). Broad distributions appeared to be show clear resemblance to the major patterns observed for both the epibenthic and demersal fish communities (Chapters 9 and 10). The outlier stations (all labeled as one cluster for convenience here in green), were found mainly around the edges of the survey area, which could reflect increased heterogeneity of environmental variables in these areas, but could equally be an artifact edge effect on the analysis. The distributions do suggest areas of increased heterogeneity in the south- and central-west North Sea and the eastern and northeastern North Sea.

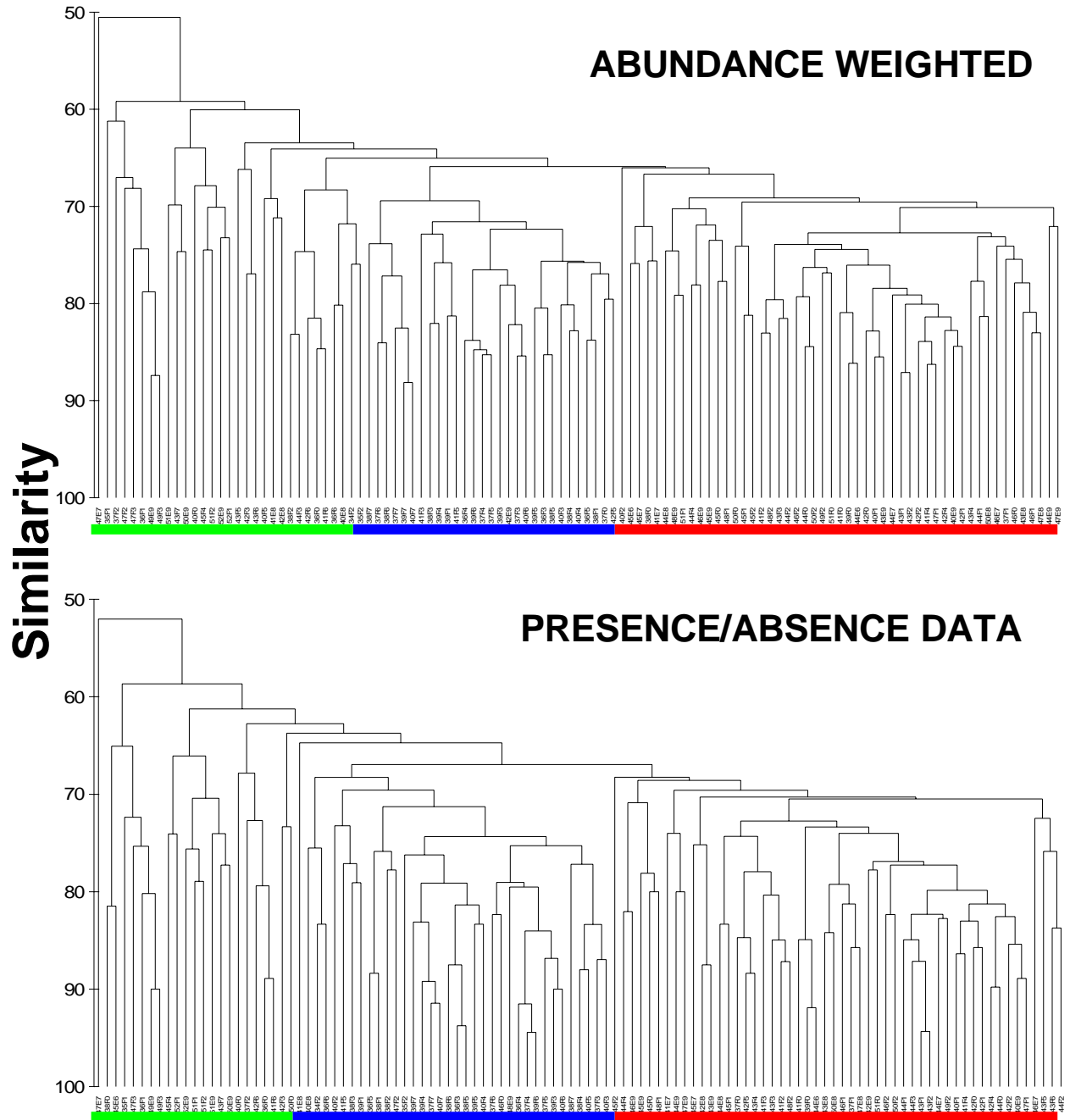


Figure 11.3.2.1. Group average cluster dendrograms of the similarity of relative infaunal taxon group densities based on mean abundance ($N. m^{-2}$) and presence-absence data for each ICES rectangle. Colour coding links to Figure 11.3.2.2.

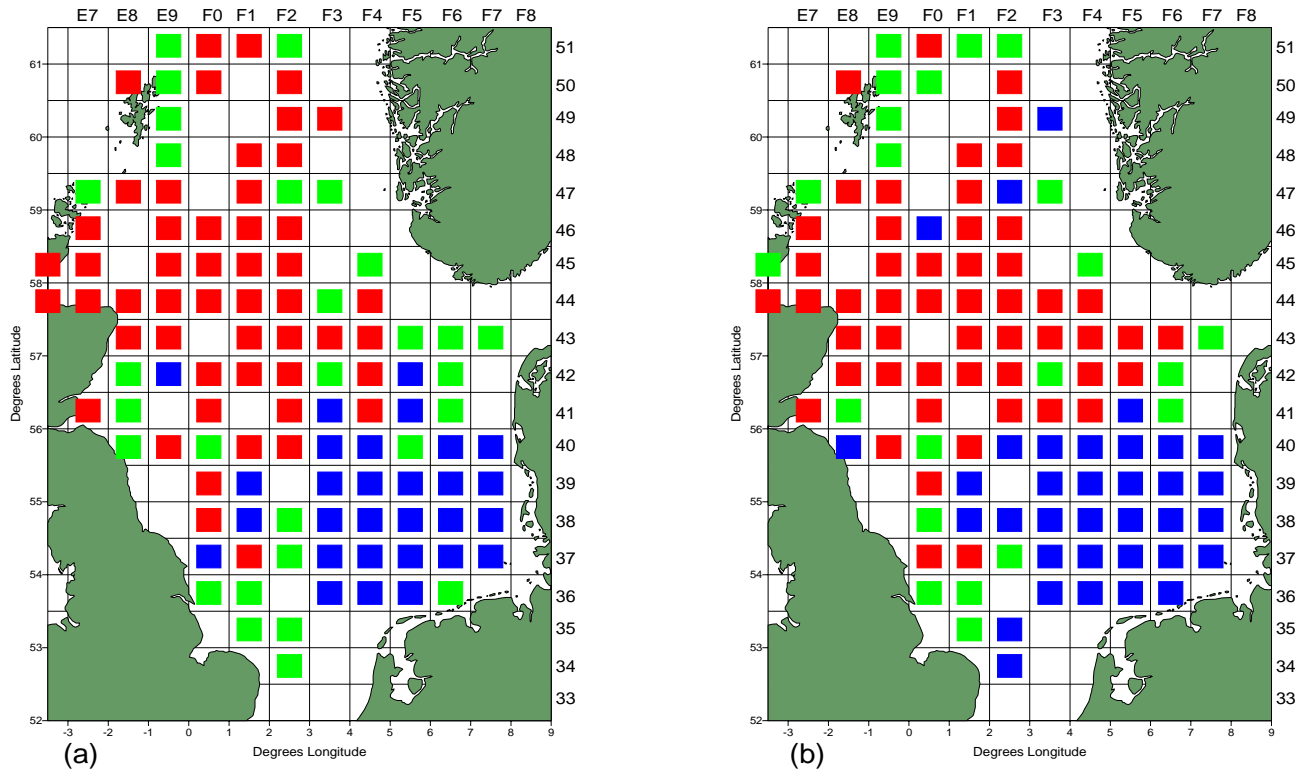


Figure 11.3.2.2. Spatial distributions of the clusters defined in Figure 11.3.2.1. based upon (a) mean abundance ($N. m^{-2}$) and (b) presence-absence data for each ICES rectangle. Colour coding links to Figure 11.3.2.1

11.3.3. Taxon group diversity

Infaunal taxon group richness varied from 8 to 32 taxa found from a potential pool of 49 taxon groups. Even at this coarse taxonomic level, where most taxon groups were not resolved further than Order or even Class and Phyla, there is some evidence of higher richness in taxonomic groups in the northern North Sea which corresponds with the overall patterns found for epibenthos in Chapter 10 (Figure 11.3.3.1 (a)). For non-colonial fauna, Hill's diversity indices $N1$ and $N2$ were also calculated, taking into account the effect of individual abundance in addition to the number of species. The general trend of higher diversity in the northern North Sea is confirmed, but both indices also indicate some relatively diverse areas in the central North Sea (Figure 11.3.3.1 (b) & (c)).

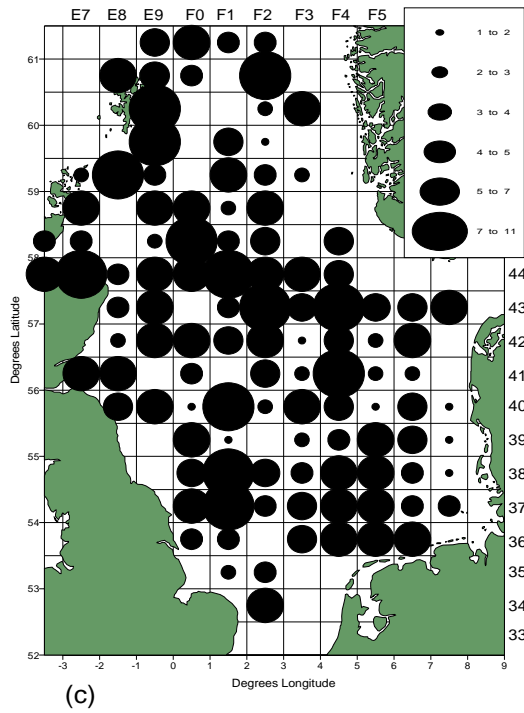
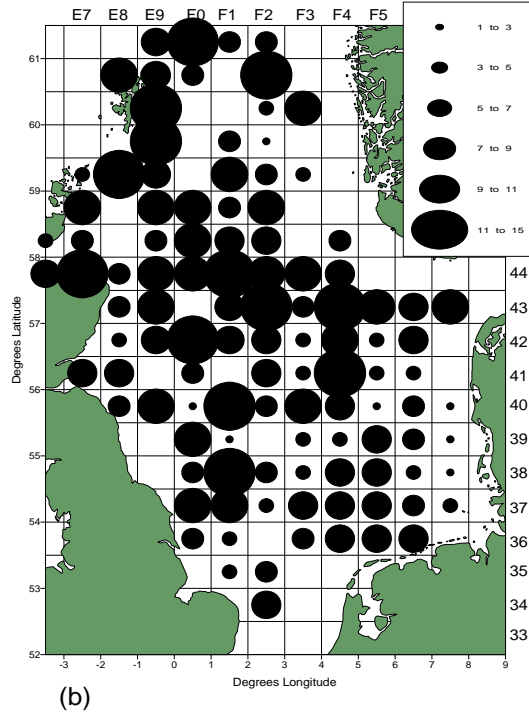
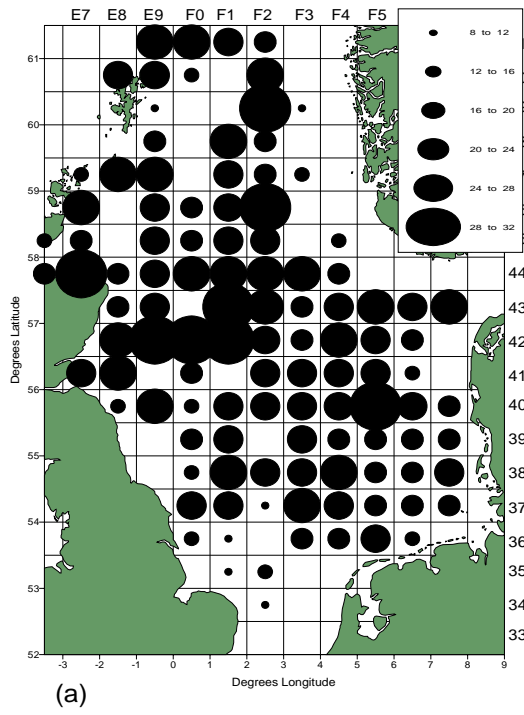


Figure 11.3.3.1. Spatial distributions of (a) species richness based on all taxa and Hill's (b) N1 and (c) N2 calculated on mean abundance ($N \cdot m^{-2}$) for each ICES rectangle.

11.3.4. Distribution of secondary production

Total infaunal community production was highest in the southern North Sea but there were also a number of smaller separate areas with comparable levels of production (Figure 11.3.4.1.). Animals found in the 4mm sieve fraction of the samples were found to contribute the most to overall production even though the smaller animals had much higher P/B ratios. In these cases the greater biomass of the larger animals outweighs the higher metabolic rates of the smaller animals in terms of actual daily production rates.

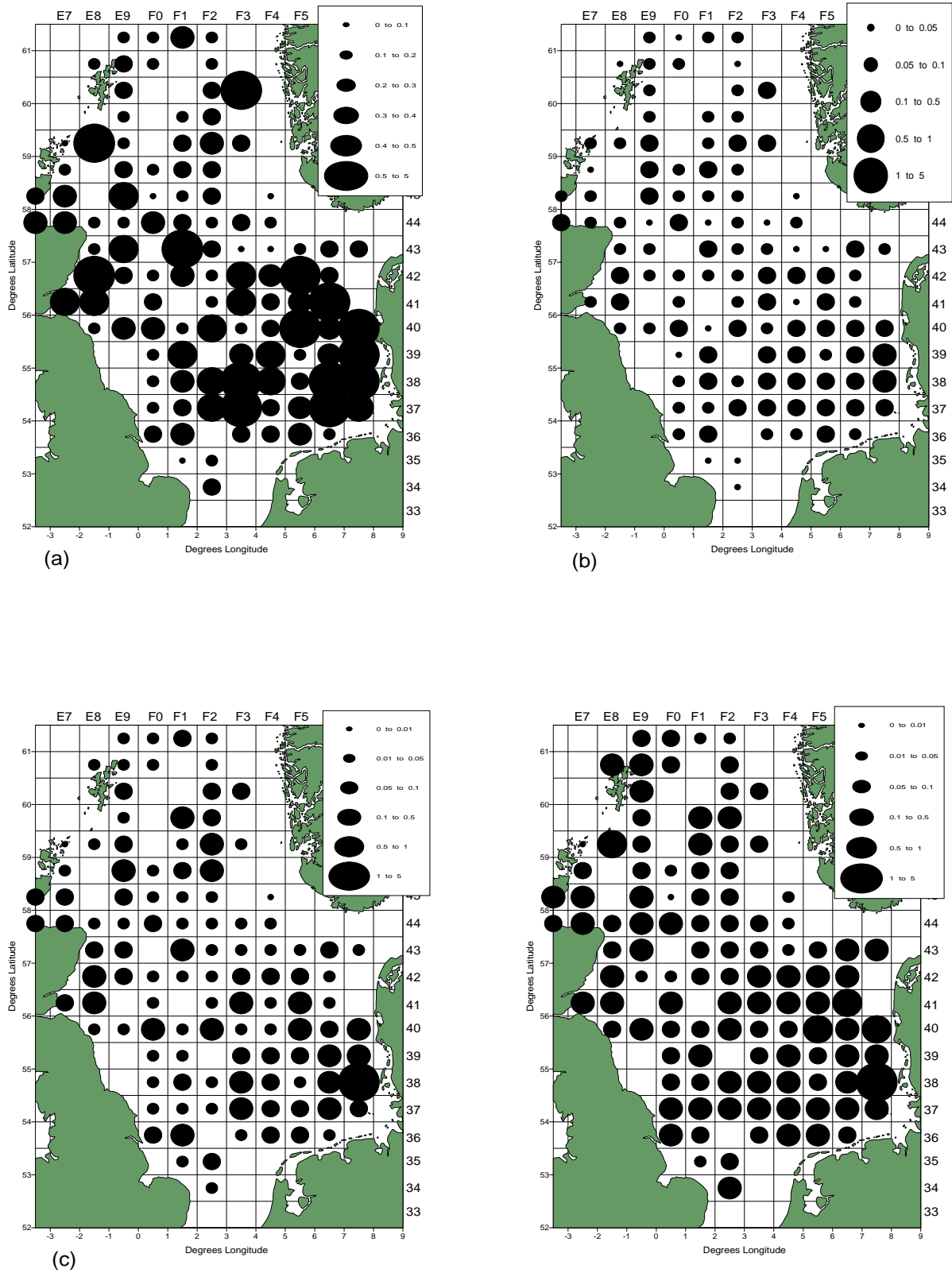


Figure 11.3.4.1. Spatial variation in daily production ($\text{g AFDM m}^{-2} \text{ day}^{-1}$) of (a) the whole infaunal community, (b) the infauna retained in a 1mm sieve, (c) 2mm sieve and (d) 4mm sieve.

11.4. References

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11.5. Appendix 1

List of Taxon groups found from 200 MAFCONS stations sampled for infauna in the North Sea in 2003 and 2004

Taxon Group	Phylum	Class	Community analysis group	Brey AFDW conversion group	Edgar productivity group
Hirudinea	Annelida	Hirudinea	Hirudinea	Annelida	Infauna
Oligochaeta	Annelida	Oligochaeta	Oligochaeta	Oligochaeta	Infauna
Polychaeta	Annelida	Polychaeta	Polychaeta	Annelida	Infauna
Polychaeta errantia	Annelida	Polychaeta	Polychaeta	Polychaeta errantia	Infauna
Polychaeta sedentaria	Annelida	Polychaeta	Polychaeta	Polychaeta sedentaria	Infauna
Insecta	Arthropoda	Insecta	!!EXCLUDE	Crustacea	Crustacea
Brachiopoda	Brachiopoda		Brachiopoda	Cnidaria	Infauna
Bryozoa	Bryozoa		Bryozoa	Bryozoa	Epifauna
Chaetognatha	Chaetognatha		Chaetognatha	Chaetognatha	Epifauna
Prostigmata	Chelicerata	Arachnida	Prostigmata	Crustacea	Crustacea
Ascidia	Chordata	Ascidiacea	Enterogona	Ascidiae	Epifauna
Tunicata	Chordata	Ascidiacea	Tunicata	Ascidiae	Epifauna
Osteichthyes	Chordata	Osteichthyes	Osteichthyes	Demersal Fish	Epifauna
Osteichthyes demersal	Chordata	Osteichthyes	Osteichthyes	Demersal Fish	Epifauna
Cephalochordata	Chordata		Cephalochordata	Ascidiae	Infauna
Tunicata	Chordata		Tunicata	Ascidiae	Epifauna
Hexacorallia	Cnidaria	Hexacorallia	Hexacorallia	Actinaria	Infauna
Actiniaria	Cnidaria	Hexacorallia	Hexacorallia	Actinaria	Infauna
Octocorallia	Cnidaria	Octocorallia	Octocorallia	Actinaria	Infauna
Pennatulidae	Cnidaria	Octocorallia	Octocorallia	Actinaria	Infauna
Cnidaria	Cnidaria		!!EXCLUDE	Actinaria	Infauna
Anthozoa	Cnidaria		!!EXCLUDE	Actinaria	Infauna
Hydrozoa	Cnidaria		Hydrozoa	Bryozoa	Epifauna
Cirripedia	Crustacea	Cirripedia	Cirripedia	Cirripedia	Crustacea
Amphipoda	Crustacea	Eumalacostraca	Amphipoda	Amphipoda	Crustacea
Caprellidae	Crustacea	Eumalacostraca	Amphipoda	Amphipoda	Crustacea
Cumacea	Crustacea	Eumalacostraca	Cumacea	Cumacea	Crustacea
Decapoda	Crustacea	Eumalacostraca	Decapoda	Decapoda	Crustacea
Pleocyemata	Crustacea	Eumalacostraca	Decapoda	Decapoda	Crustacea
Caridea	Crustacea	Eumalacostraca	Decapoda	Decapoda	Crustacea
Euphausiacea	Crustacea	Eumalacostraca	Euphausiacea	Euphausiacea	Crustacea
Isopoda	Crustacea	Eumalacostraca	Isopoda	Isopoda	Crustacea
Mysidacea	Crustacea	Eumalacostraca	Mysidacea	Crustacea	Crustacea
Tanaidacea	Crustacea	Eumalacostraca	Tanaidacea	Crustacea	Crustacea
Malacostraca	Crustacea	Malacostraca	!!EXCLUDE	Crustacea	Crustacea
Leptostraca	Crustacea	Malacostraca	Leptostraca	Crustacea	Crustacea
Copepoda	Crustacea	Maxillopoda	Copepoda	Crustacea	Crustacea
Harpacticoida	Crustacea	Maxillopoda	Copepoda	Crustacea	Crustacea
Ostracoda	Crustacea	Ostracoda	Ostracoda	Crustacea	Crustacea
Pycnogonida	Crustacea	Pycnogonida	Pycnogonida	Crustacea	Crustacea
Crustacea	Crustacea		!!EXCLUDE	Crustacea	Crustacea

Taxon Group	Phylum	Class	Community analysis group	Brey AFDW conversion group	Edgar productivity group
Ctenophora	Ctenophora		Ctenophora	Bryozoa	Epifauna
Asteroidea	Echinodermata	Asteroidea	Asteroidea	Asteroidea	Epifauna
Echinoidea	Echinodermata	Echinoidea	!!EXCLUDE	Echinoidea	Infauna
Echinoida	Echinodermata	Echinoidea	Echinoida	Echinoidea	Epifauna
Spatangoida	Echinodermata	Echinoidea	Spatangoida	Echinoidea	Infauna
Holothurioidea	Echinodermata	Holothurioidea	Holothurioidea	Holothuroidea	Infauna
Ophiuroidea	Echinodermata	Ophiuroidea	Ophiuroidea	Ophiuroidea	Infauna
Echinodermata	Echinodermata		!!EXCLUDE	Echinodermata	Infauna
Echiura	Echiura		Echiura	Priapulida	Infauna
Entoprocta	Entoprocta		Entoprocta	Bryozoa	Epifauna
Foraminifera	Foraminifera		Foraminifera	Bryozoa	Epifauna
Caudofoveata	Mollusca	Caudofoveata	Caudofoveata	Nudibranchia	Mollusca
Gastropoda	Mollusca	Gastropoda	Gastropoda	Gastropoda	Mollusca
Opisthobranchia	Mollusca	Opisthobranchia	Opisthobranchia	Nudibranchia	Mollusca
Nudibranchia	Mollusca	Opisthobranchia	Opisthobranchia	Nudibranchia	Mollusca
Pelecypoda	Mollusca	Pelecypoda	Pelecypoda	Bivalvia	Mollusca
Polyplacophora	Mollusca	Polyplacophora	Polyplacophora	Mollusca	Mollusca
Neoloricata	Mollusca	Polyplacophora	Polyplacophora	Mollusca	Mollusca
Scaphopoda	Mollusca	Scaphopoda	Scaphopoda	Gastropoda	Mollusca
Solenogastres	Mollusca	Solenogastres	Solenogastres	Nudibranchia	Mollusca
Mollusca	Mollusca		!!EXCLUDE	Mollusca	Mollusca
Nematoda	Nematoda		Nematoda	Annelida	Infauna
Cerebratulidae	Nemertea	Anopla	Nemertea	Nemertea	Infauna
Nemertea	Nemertea		Nemertea	Nemertea	Infauna
Phoronida	Phoronida		Phoronida	Oligochaeta	Infauna
Platyhelminthes	Platyhelminthes		Platyhelminthes	Nemertea	Infauna
Pogonophora	Pogonophora		Pogonophora	Oligochaeta	Infauna
Porifera	Porifera		Porifera	Porifera	Epifauna
Priapulida	Priapulida		Priapulida	Priapulida	Infauna
Sipuncula	Sipuncula		Sipuncula	Sipunculida	Infauna
Epifauna			!!EXCLUDE	Other Organic Matter	Epifauna
Other Organic Matter			!!EXCLUDE	Other Organic Matter	Infauna