Benthic offshore surveys of proposed dredge spoil disposal sites off Otago Peninsula

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August 2008

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Benthic offshore surveys of proposed dredge spoil disposal sites off Otago Peninsula

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Executive Summary

Port Otago Ltd wishes to prepare Port Chalmers for the next generation of container ships that will come into New Zealand. To accommodate these large vessels, the Port Company proposes dredging the approaches to Port Chalmers and the berth areas, involving the dredging and disposal of the dredge material. Two areas have been mooted as potential disposal sites, both north-east of Taiaroa Head, in approximately 30 m water depth.

An earlier scoping study recommended that preliminary studies determine whether the proposed disposal sites possessed species or assemblages of unique or particular biological interest, and provide a baseline with which to compare future effects after disposal had taken place. The present study of the benthic fauna of Blueskin Bay is designed to addresses these objectives (note that the term "Blueskin Bay" is used to refer to the entire area sampled, from the sheltered interior of the bay to offshore areas in up to 30 m depth). A two-pronged approach was used: preliminary qualitative surveys using sidescan sonar transects (in April 2008, swath width 60 m) and video splashcam drops, to determine major habitat boundaries (if any) and the presence of major epifaunal habitats, followed by a benthic grab survey (May 2008), designed to give quantitative estimates of the relative density and species richness of macrobenthic infauna. Extra attention was given to the two potential disposal areas ("Boxes A and B").

Because no obvious patterns in large-scale distributions of epifauna were apparent from the sidescan and splashcam survey, the quantitative grab survey for macrofauna was stratified by depth. Three replicate grabs (0.05 m^2 bite area) were taken at each of 32 stations throughout Blueskin Bay. Samples were analysed for sediment grain-size, organic-matter content and fauna.

The sidescan survey showed that the preferred dredge disposal site (Box A) was generally turbid, dominated by fine sand, and possessed little epifauna. The alternative disposal site (Box B) possessed high densities of a large tubeworm and other epifauna (including the knobbed whelk, *Austrofusus glans*, and the ostrich-foot shell, *Struthiolaria papillosa*), despite having a similar sediment to Box A. Horse mussels (*Atrina zelandica*) appeared to occur in patches northwest of Box A, though no definitive images were obtainable due to poor water visibility in the area. Many of the offshore sites at depths > 27 m possessed fine sand habitats with patchy beds of tubeworms. Apart from one site where the substratum was formed by coarse sand and shell gravel, the sediments of the wider area were fine sands, apparently grading into siltier sand closer to Taiaroa Head. Occasional patches of shell fragments were found throughout the surveyed area.

Grab samples confirmed that the sediments of Blueskin Bay were dominated by fine sands, as might be expected in an area subject to frequent episodes of high wave action. Silt (and hence "mud" content) formed a generally low percentage of the sediment, with a correspondingly low organic content. There was no distinct pattern in sediment structure with depth. Highest concentrations of

organic content occurred in the centre of the bay, and silt was similarly distributed. Very fine sands dominated the area north of Box A. Fine sand dominated sediments in shallower parts of the bay and the area east of Taiaroa Head, forming over 85% of the total sediment in inner Blueskin Bay and up to 90% elsewhere. Medium sand was uncommon in the bay proper, and occurred as a significant fraction only east of Taiaroa Head, where tidal currents tend to be strong and the depth profile is much steeper than elsewhere.

Faunal densities were lowest in inner Blueskin Bay and highest in the series of stations just north of the Otago Harbour entrance (including Box A). Average density across all samples was 160.5 (± 80.0 s.d.) animals per grab. Species richness ranged from 10 to 39, with an average of 24.5 (± 6.2 s.d.) taxa per sample. The most species-rich area was also that which contained the highest densities, and the most species-poor area was off Taiaroa Head. The high infaunal abundance and diversity in the area including Box A contrasts with the low abundance and diversity of epifauna in Box A relative to Box B.

The faunal assemblage was numerically dominated by the gastropod (snail) *Antisolarium egenum*, followed by three polychaete worms and the ubiquitous bivalve *Nucula nitidula*. nMDS ordination (a visual method of representing faunal similarities among samples) showed that groupings of samples apparently reflected effects of depth and type of sediment on the fauna.

Canonical correlation analysis (CAP, a method of identifying relationships between multivariate data – in this case, the types and abundances of faunal species in each sample - and environmental variables that may explain patterns in the fauna) confirmed that faunal distributions are driven by both depth and sediment variability, although they did not explain all the variation in the data. For example, worms in the polychaete genus *Aricidea* and the Families Cirratulidae and Scalibregmatidae, and an unidentified cumacean (a small crustacean), occurred in their highest densities in the very fine sand/silt basin in the middle of the bay. Conversely, the snails *Antisolarium egenum* and *Zethalia zelandica*, and the polychaete worm *Armandia maculata* were all associated with shallow, inner bay regions. Amphipoda (small crustaceans) and Tellinidae A (a bivalve) characterised coarser, deeper habitats.

Multivariate analysis of variance did not suggest that the infaunas of the proposed disposal sites are different from immediately surrounding areas (i.e., within ca. 4 km). Comparison of the results of the present study with those of previous studies in the same area suggests that the fauna recorded in the present study is typical of the nearshore sand zone that occurs in water depths of ca 30 m off this part of the Otago coast.

It is recommended that once a disposal site has been decided, a targeted monitoring programme be designed to determine:

- the recolonisation rate of macrobenthic infauna after spoil disposal in the main disposal area;

- changes in the composition of the assemblage relative to pre-disposal baselines and unimpacted control sites;

- the extent of movement of dredge spoil in space and time;

- the effects of sediment deposition at varying intensities (i.e., varying distances from the disposal site, measured with sediment traps and/or sediment profiling) on assemblage composition; and

- the recolonisation time of assemblages under varying sedimentation scenarios.

1. Introduction

Port Otago Ltd (the Port Company) wishes to prepare Port Chalmers for the next generation of container ships that will come into New Zealand. These will be considerably larger than existing ships with proposed drafts of up to 14.5 m. To accommodate these large vessels, the Port Company proposes dredging the approaches to Port Chalmers and the berth area by deepening the channel. Disposal of the dredged material is likely to be at sea. Two areas have been mooted as potential disposal sites (Box A and Box B in Figure 1). Both areas are north-east of Taiaroa Head, in approximately 30 m water depth.

Existing ecological information and scoping of assessments likely to be required as part of this process were summarised by James et al. (2007), who pointed to a lack of information on the composition and dynamics of shelf benthos of Otago. James et al. (2007) also listed the potential effects of dredging and spoil disposal, the most severe of which was the smothering of biological communities in the disposal area. It was recommended that preliminary studies determine whether the proposed disposal sites possessed species or assemblages of unique or particular biological interest, as well as providing a baseline with which to compare future effects after disposal had taken place.

Exploratory surveys of benthos and environmental impact studies have differing aims and require different survey designs. The current study was designed to characterise the benthic communities of the offshore area north and east of Otago Peninsula to inform the placement of dredge disposal sites. A two-pronged approach was used: preliminary qualitative surveys using sidescan sonar transects and video splashcam drops, to determine major habitat boundaries (if any) and the presence of major epifaunal habitats, followed by a benthic grab survey, designed to give quantitative estimates of the relative density and species richness of macrobenthic infauna. Extra attention was given to two survey "Boxes" that had been designated as potential spoil disposal sites.

The main aims of this study are thus to explore 1) the spatial distribution of macrofaunal assemblages in relation to the proposed dredge spoil disposal sites, and 2) attempt to understand what factors may be driving the current distributions of animals, with a view to predicting what the likely consequences of spoil disposal may be.

2. Materials and methods

2.1 Sidescan sonar and splashcam

Sidescan sonar tows were done from the 7 m NIWA research vessel *Icarus* in April 2008. Sample sites were randomly allocated throughout the study area, except for three transects run in parallel through each of the two "Boxes" (Figure 2). Each tow was 60 m wide by 500 m in length, except for the Box tows, which were circa 2000 m in length. Tows were positioned by GPS, and subsequently resurveyed using a "splashcam". This is a video camera suspended from a cable that is lowered to the sea floor at regular points along the sidescan transect, serving both to validate and supplement the sidescan data. Positions of sidescan/splashcam transects are plotted in Figure 2.

2.2 Grab survey

Given that no obvious patterns in large-scale distributions of epifauna were apparent from the sidescan and splashcam survey (see Results, Section 3.1), the quantitative grab survey for macrofauna was stratified by depth. Three replicate grabs were taken at each of 32 stations (Figure 1) throughout Blueskin Bay between 13 May and 15 May 2008, using the *FV Triton*. One station planned in the original design (number 16) was omitted due to time and weather constraints.

Grabs were taken using a spring-loaded and weighted 229 × 229 mm ponar grab (bite area ca 0.05 m^2, bite depth ca. 5 cm). A change from the originally intended 0.25 m^2 Van Veen grab was necessitated by the well consolidated nature of the sediments and high fine sand fraction in the survey area (see Results).

Three cores were subsampled from each grab. These were analysed to obtain:

- % organic content: samples were dried to constant weight, and then incinerated at 500˚C. The loss on ignition (LOI) represents the proportion of total organic matter present in the sample.

- Sediment grain size structure: samples were dried to constant weight, wet sieved through a series of 6 sieves (Table 1), then each fraction dried and re-weighed, giving the proportion (by weight) of each sediment size fraction in the samples.

- The third core was sent to Canterbury University for sediment rollability analysis (to be reported elsewhere).

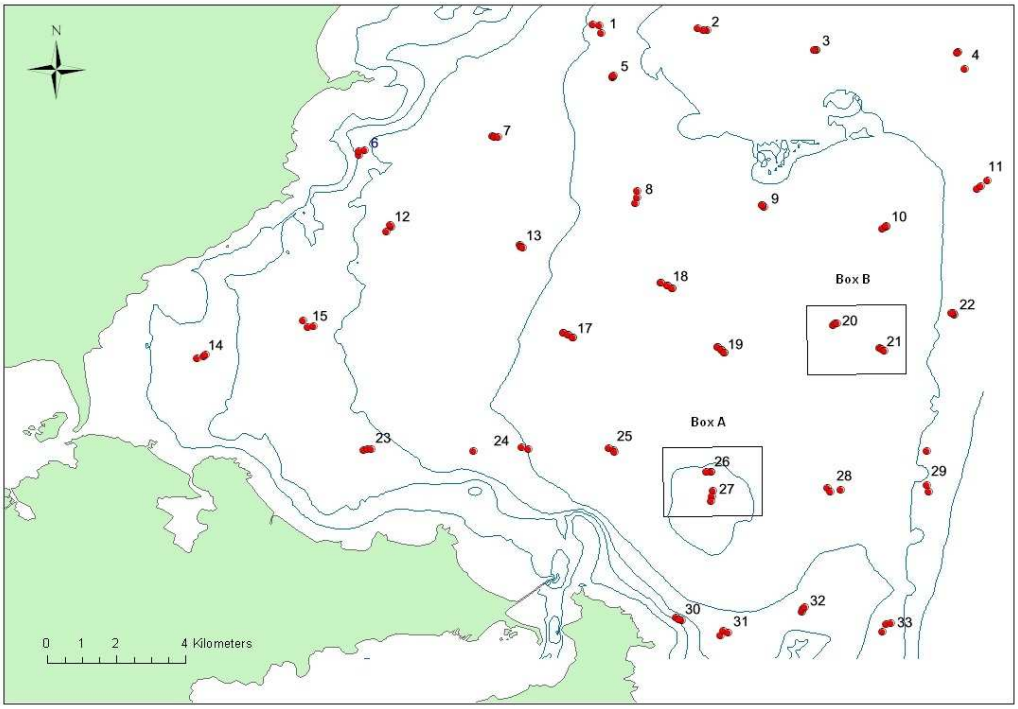

Figure 1: Map of the Blueskin Bay area showing the positions of replicate grab samples taken 13-15 May, 2008. Box A and Box B are the two potential dredge disposal sites. Station numbers are those referred to for spatial analysis purposes in the Results. Depth contours are at 5 m intervals from 10 m to 30 m.

Table 1: Sediment grain size classifications referred to in this report, and their size ranges.

Sediment classification	Grain size range
Silt and clay	< 63 μm
Very fine sand	125-63 μm
Fine sand	250-125 μm
Medium sand	500-250 μm
Coarse sand	1.0-0.5 mm
Very coarse sand	2.0-1.0 mm
Gravel	> 2.0 mm

After coring, the samples were preserved in 5% formalin at sea. In the laboratory, the samples were weighed as a very coarse measure of quantity (given varying water content and sediment density). Samples varied between 1.1 and 6.0 kg. Several litres of fresh water were added to each sample to dilute the fixative and suspend delicate animals. This supernatant was then poured into a pre-wetted 1.0 × 1.0 mm aperture mesh sieve. This process was repeated. The sieve residue was gently washed into a small pottle with 70% isopropyl alcohol. The sediment was then placed in a plastic tray, more water added, and the sample agitated to suspend any remaining non-mineralised organisms. The process was repeated and animals again washed into a small pottle. Finally the whole sample was sieved. Coarse material such as shell fragments were washed into a separate pottle.

Samples were manually sorted to the lowest readily identifiable taxon in small aliquots using a Leica MZ7.5 stereomicroscope. Each sample was preserved for subsequent taxonomic analysis and for reference purposes, to ensure taxonomic continuity with future surveys.

All data were entered into Excel spreadsheets, and are maintained and regularly backed up on NIWA's network drives.

2.3 Data analyses

Since the analysis of animal assemblages is by nature multivariate (we are dealing with multiple samples containing multiple species that vary considerably), we must use multivariate statistical techniques to reduce the complexity of the dataset such that patterns in distribution and abundance are discernible. Such techniques are even more invaluable when we have (as in this study) a set of explanatory variables that may account for some of the variation seen in the species data – in this case depth, sediment organic content, and a suite of measures of sediment grain size.

In the report, relationships between macrofaunal samples are visualised using MDS (multidimensional scaling, e.g., Clarke 1993) and cluster analysis. Relationships between macrofauna and the environmental variables are determined using a canonical correlation technique in CAP (canonical analysis of principal coordinates, Anderson & Willis 2003). A brief explanation of how these analyses work is given in Appendix I.

The distributions of individual species of interest were mapped in ArcMap GIS to inform interpretation of the formal statistical analyses. Prediction maps of the various species distributions were created using Ordinary Kriging function in Geostatistical Analyst extension of ArcMap 9.2 (ESRI).

3. Results

3.1 Sidescan sonar and splashcam

Preliminary surveys of the greater Blueskin Bay area using sidescan sonar transects, validated by splashcam imaging, were completed 7-10 April 2008. The preferred dredge disposal site (Box A) was generally turbid, dominated by fine sand, and possessed little epifauna. The alternative disposal site (Box B) possessed high densities of a large tubeworm and other epifauna (including the knobbed whelk, *Austrofusus glans*, and the ostrich-foot shell, *Struthiolaria papillosa*), despite having a fundamentally similar sediment structure. Horse mussels (*Atrina zelandica*) appeared to occur in patches northwest of Box A, though no definitive images were obtainable due to poor water visibility in the area (e.g., Figures 3 and 4). Many of the offshore sites at depths > 27 m possessed fine sand habitats with patchy beds of tubeworms (Figures 5 and 6). Apart from one site where the substratum was formed by coarse sand and shell gravel (see Figures 7 and 8), the sediments of the wider area were fine sand that appeared to grade into siltier sand closer to Taiaroa Head. Occasional patches of shell fragments were found throughout the surveyed area.

Major boundaries in biogenic habitat structure occurred only between areas possessing high densities of tubeworms and those without (estimated boundary is shown on Figure 2).

No features constituting rare species or habitats of ecological importance at regional scales were identified within or near the proposed disposal sites at Box A or Box B.

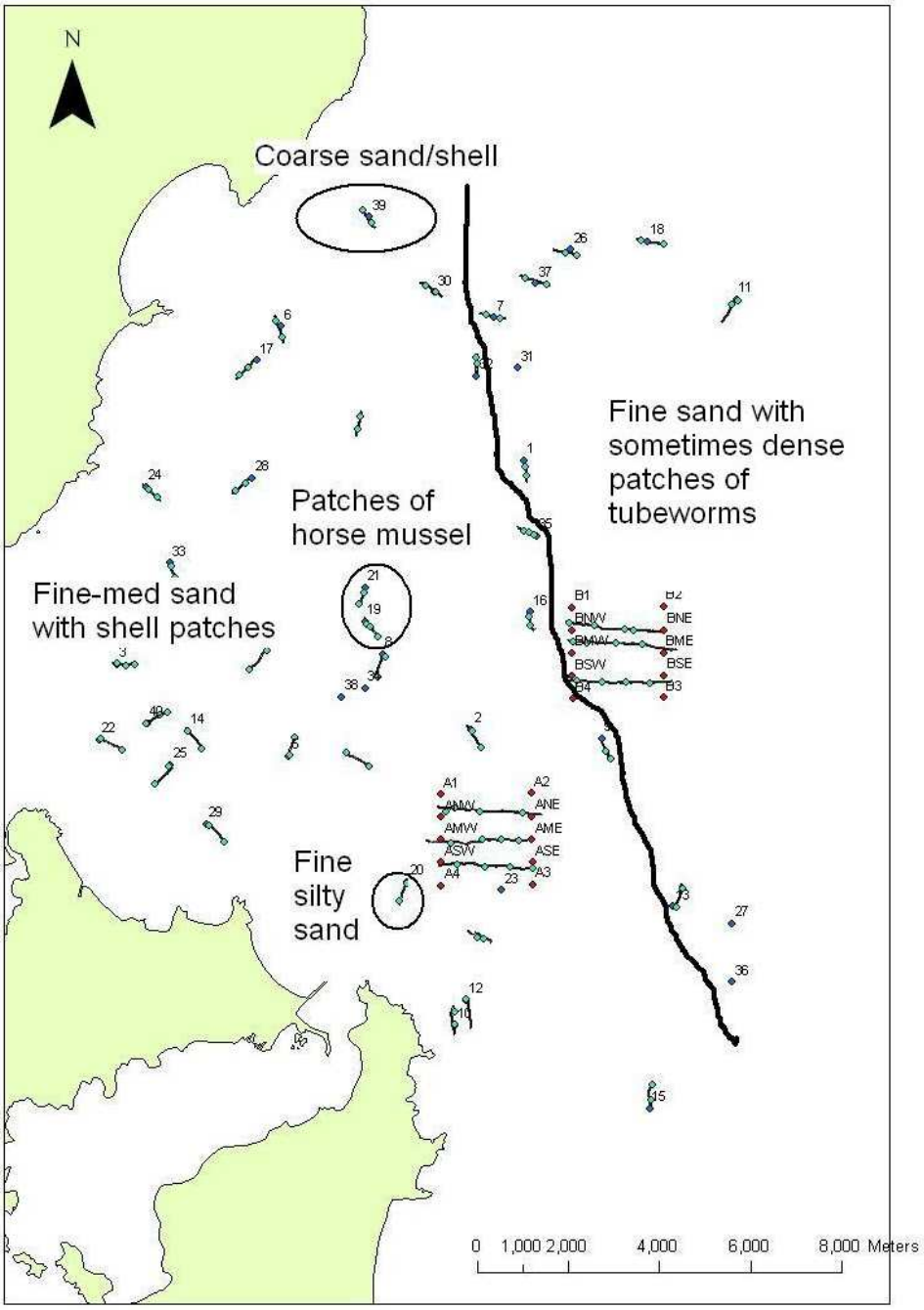

Figure 2: Map of the area showing positions of sidescan and splashcam transects 7-10 April 2008. The bold line separates areas dominated by patches of a large tube-dwelling polychaete worm (identification pending) in deeper water from areas where they are relatively rare.

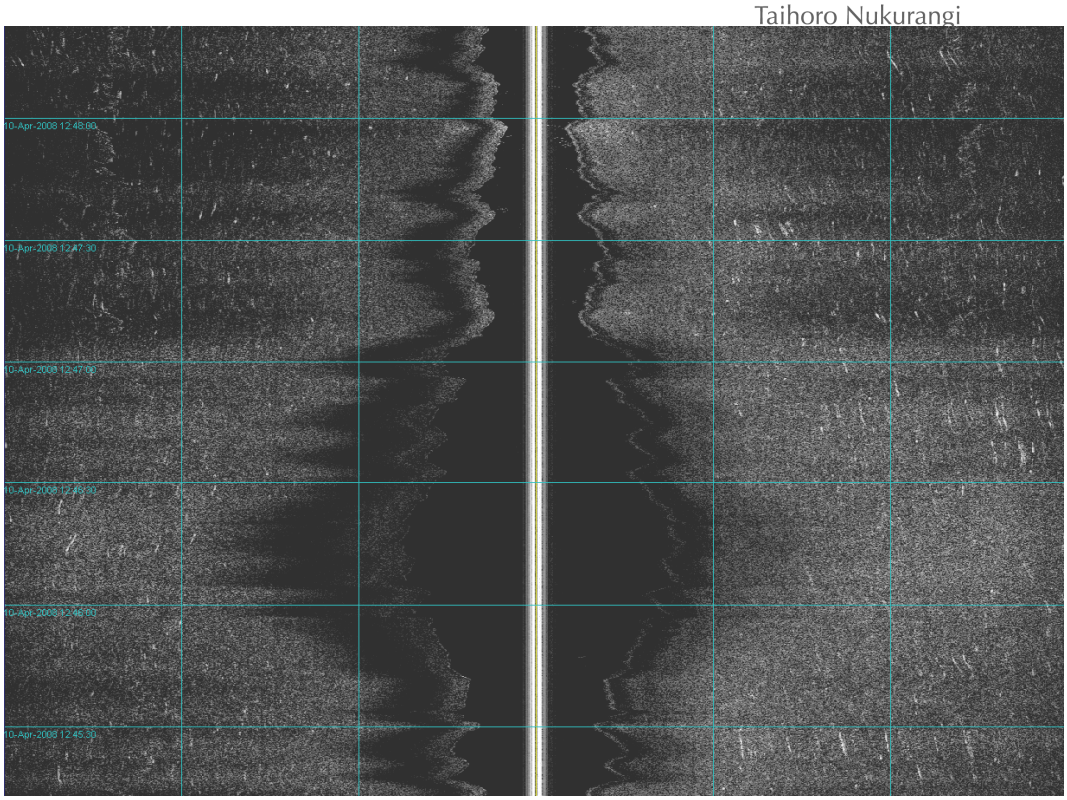

Figure 3: Sidescan image from Site 19 (in Figure 1), showing reflective material consistent with scattered horse mussels. Width of trace is 60 m.

Figure 4: Splashcam screenshot of horse mussels (*Atrina zelandica*) fouled with algae. Water clarity tends to be low in these areas because of suspended sediment.

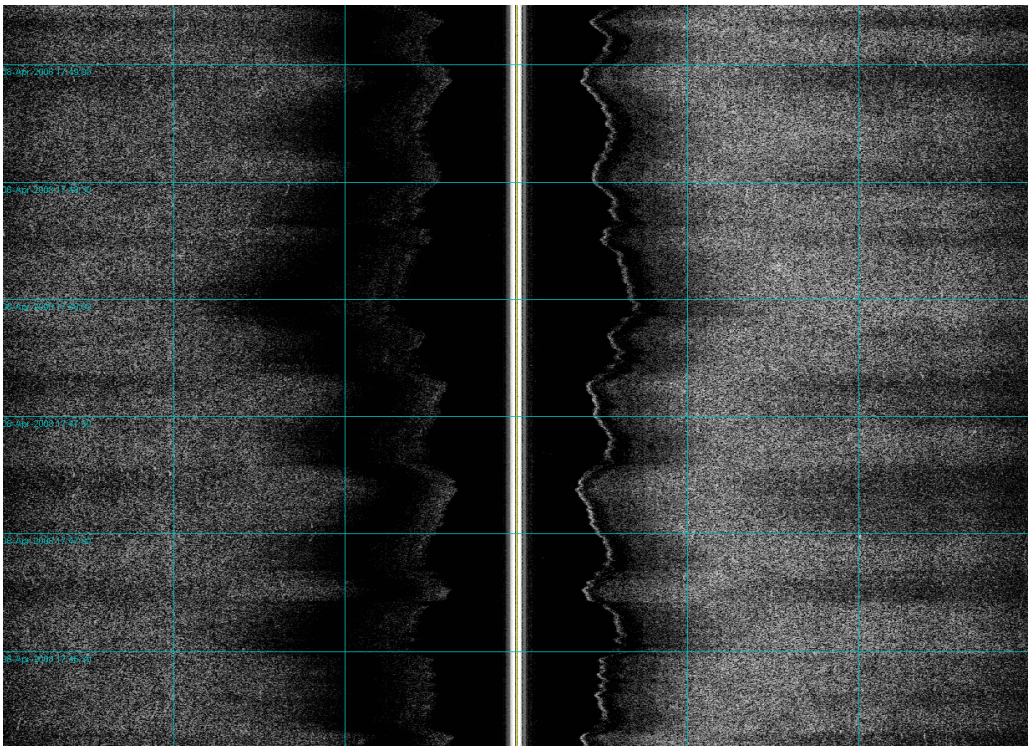

Figure 5: Site 28 (refer Figure 1), showing featureless fine sand.

Figure 6: Splashcam screenshot of fine sand with low densities of large tubeworms.

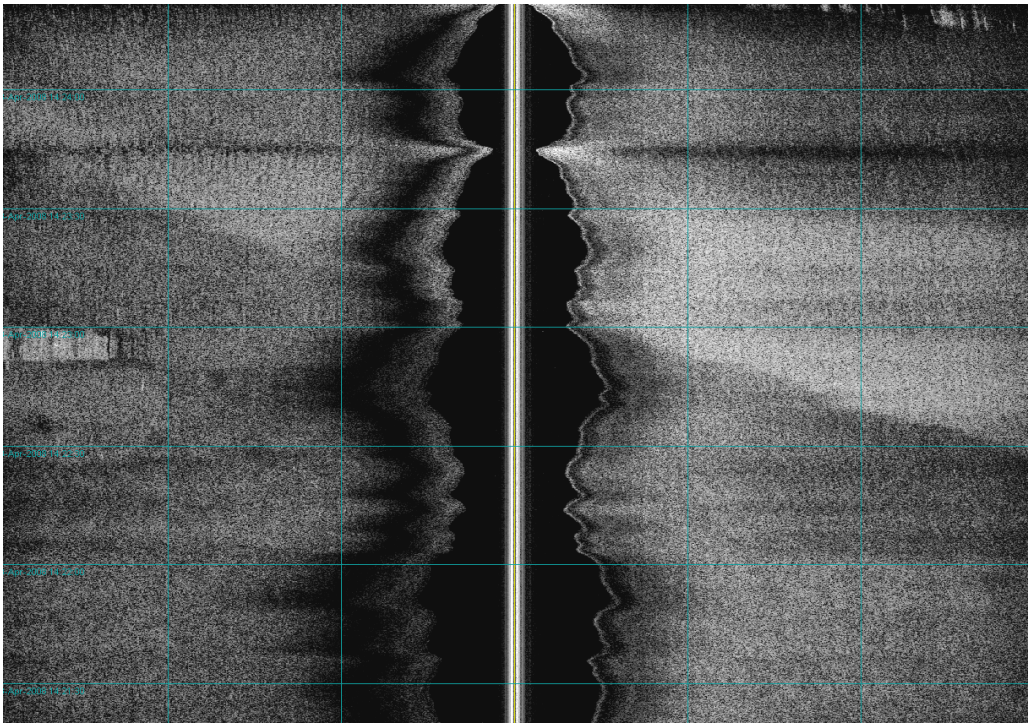

Figure 7: Site 39, showing fine sand interspersed with coarser sand (lighter area) that shows mega-ripples with wavelengths just less than 1 m.

Figure 8: Splashcam screenshot of rippled coarse sand and shell gravel (Site 39).

3.2 Quantitative grab survey

3.2.1 Sediment characteristics

The sediments of Blueskin Bay were generally well consolidated and dominated by fine sands (Table 2), as might be expected in an area subject to frequent episodes of high wave action. Silt (and hence "mud" content) formed a generally low percentage of the sediment, with a concomitantly low organic content (Table 2: muddy sediments typically have an organic content of 5-10% dry weight). Organic content (expressed here as LOI) is generally well correlated with silt content, as was the case here (Figure 9) – coarser sediments do not hold organic material well, as a rule. There were few other correlations between variables, except that fine sand and very fine sand were inversely correlated (Figure 9). There was no distinct pattern in sediment structure with depth. Coarser fractions occurred sporadically throughout the area and generally formed less than 1% of the sediment.

Table 2: Average depth and sediment constituents over the whole survey area (organic matter and grain-size components are given as percentages of total dry weight).

Variable	Mean percent content	Std deviation
Depth	26.12	4.49
Organic matter	1.47	0.41
Silt	15.64	10.34
Very fine sand	24.64	20.49
Fine sand	56.85	24.46
Medium sand	2.39	7.52
Coarse sand	0.15	0.21
Very coarse sand	0.11	0.18
Gravel	0.19	0.41

Examination of the spatial distribution of the sediments provides clues to the patterns of correlation among different variables. Figure 10 shows that organic content occurred in highest concentrations at the centre of the bay, and that silt was similarly distributed (Figure 11). Very fine sands dominated the area north of Box A, and overlapped with the most silty areas (Figure 12). The slightly coarser fine sand had the

inverse distribution to the silt and very fine sand fractions, dominating sediments in shallower parts of the bay, and the area east of Taiaroa Head (Figure 13). Fine sand formed over 85% of the total sediment in inner Blueskin Bay (Station 14) and up to 90% elsewhere. Raw data values for the individual replicates can be found in Appendix II.

Medium sand was uncommon in the bay proper, and occurred as a significant fraction only east of Taiaroa Head – specifically at Station 33 (Figure 14), where tidal currents tend to be strong and the depth profile is much steeper than elsewhere. Gravels (including shell and detritus) did not form an important component of the sediment in any part of the study area (Figure 15).

There appears to be a large "basin" of finer sediments in the centre of Blueskin Bay, which probably reflects reduced wave action and/or tidal currents relative to the shallows and offshore areas.

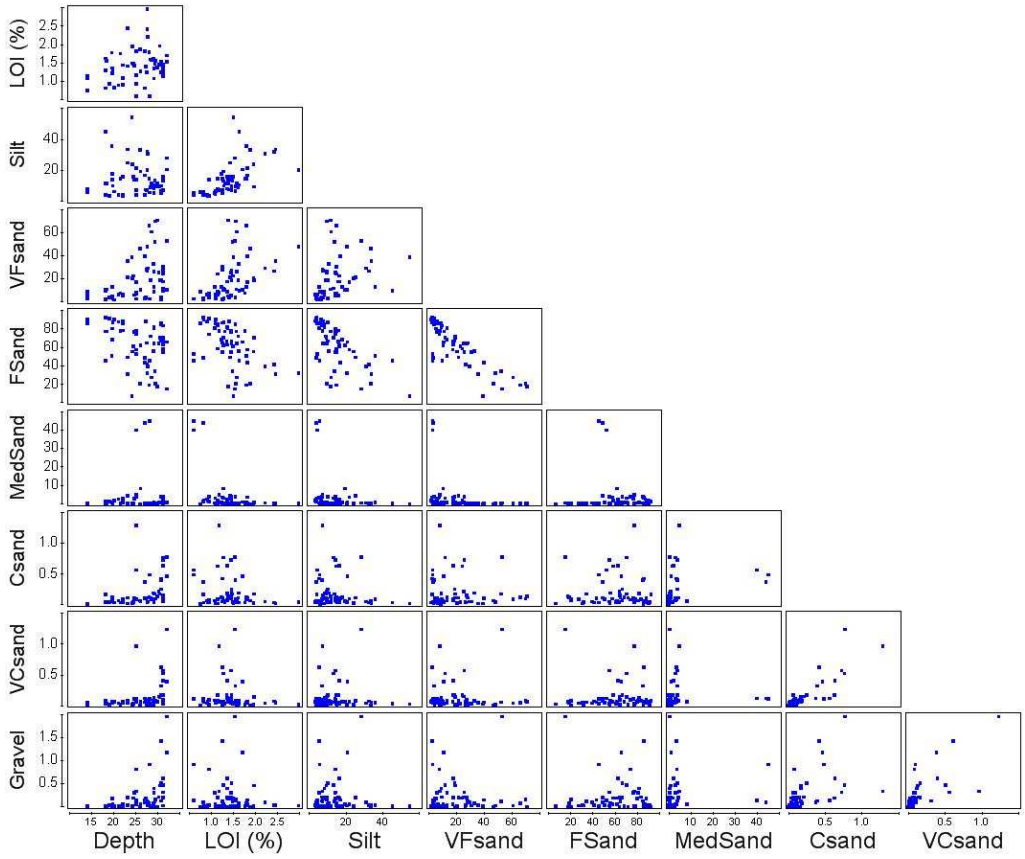

Figure 9: Draftsman plot showing relationships between the measured sediment variables and water depth.

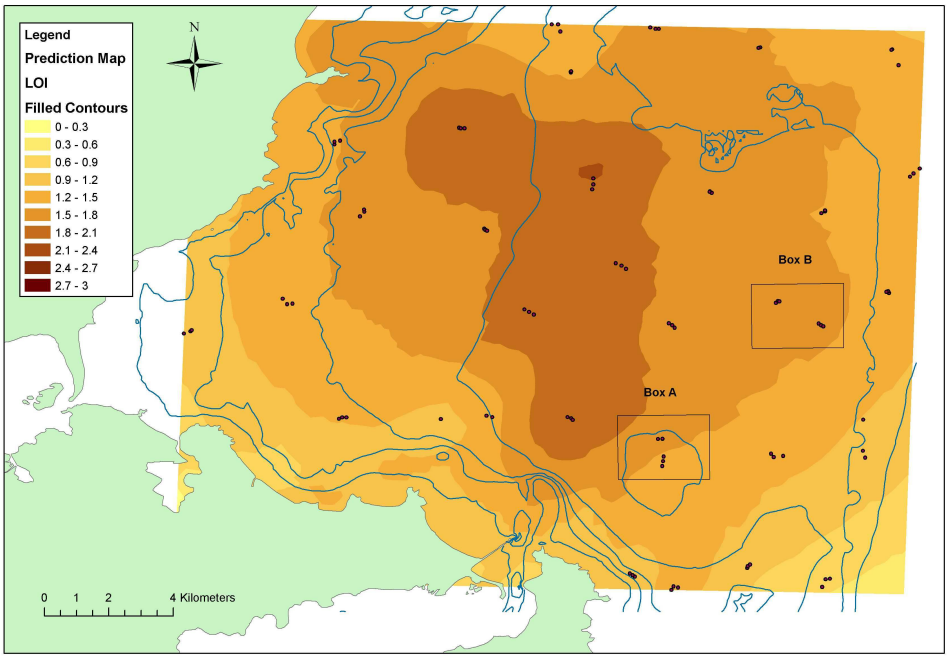

Figure 10: Distribution of organic content (% loss-on-ignition) in the sediments of Blueskin Bay. Black dots are the positions of individual replicate grabs (refer to Figure 1 for station names).

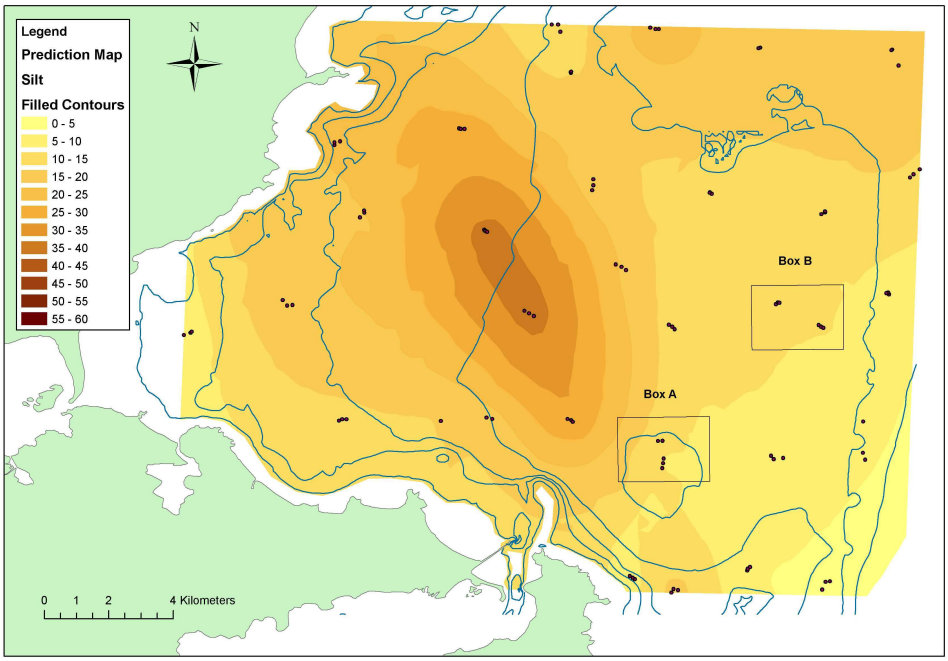

Figure 11: Distribution of silt (grain size < 63 µm) content (%) in the sediments of Blueskin Bay.

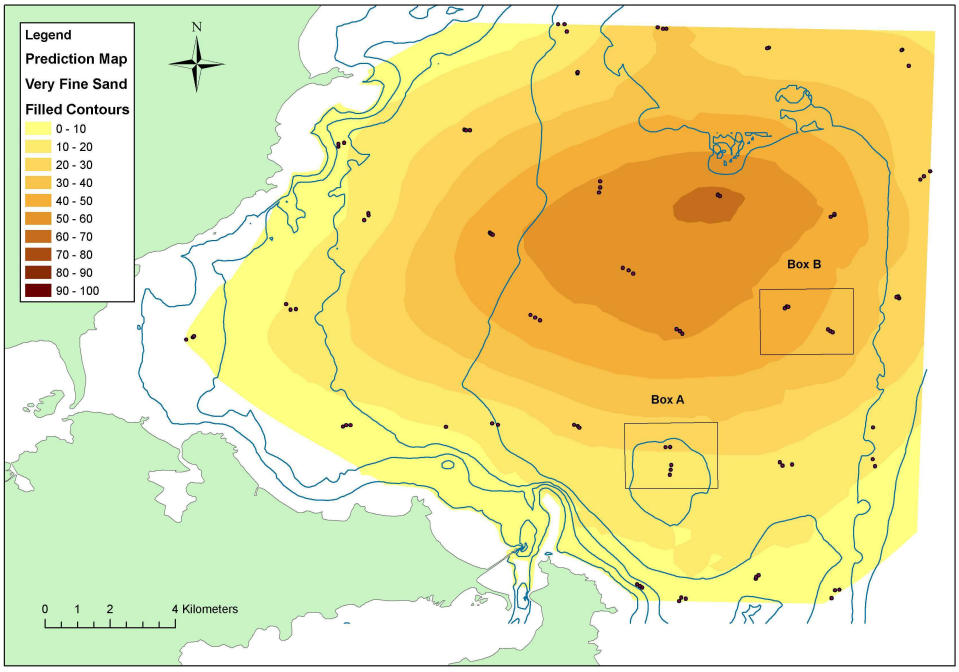

Figure 12: Distribution of very fine sand (grain size 63-125 µm) content (%) in the sediments of Blueskin Bay.

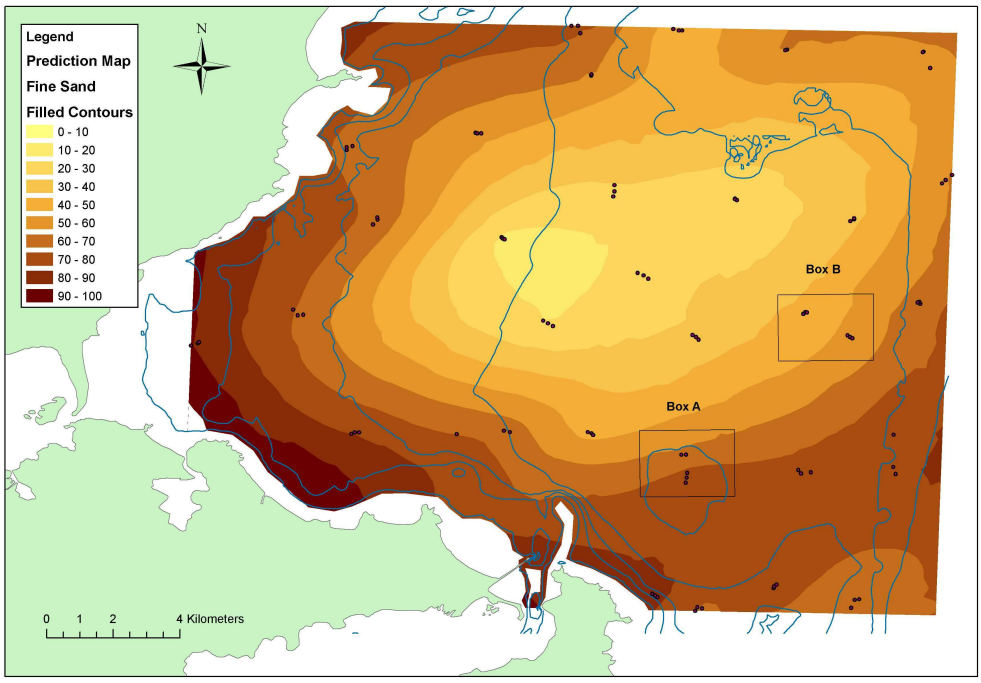

Figure 13: Distribution of fine sand (grain size 125-250 µm) content (%) in the sediments of Blueskin Bay.

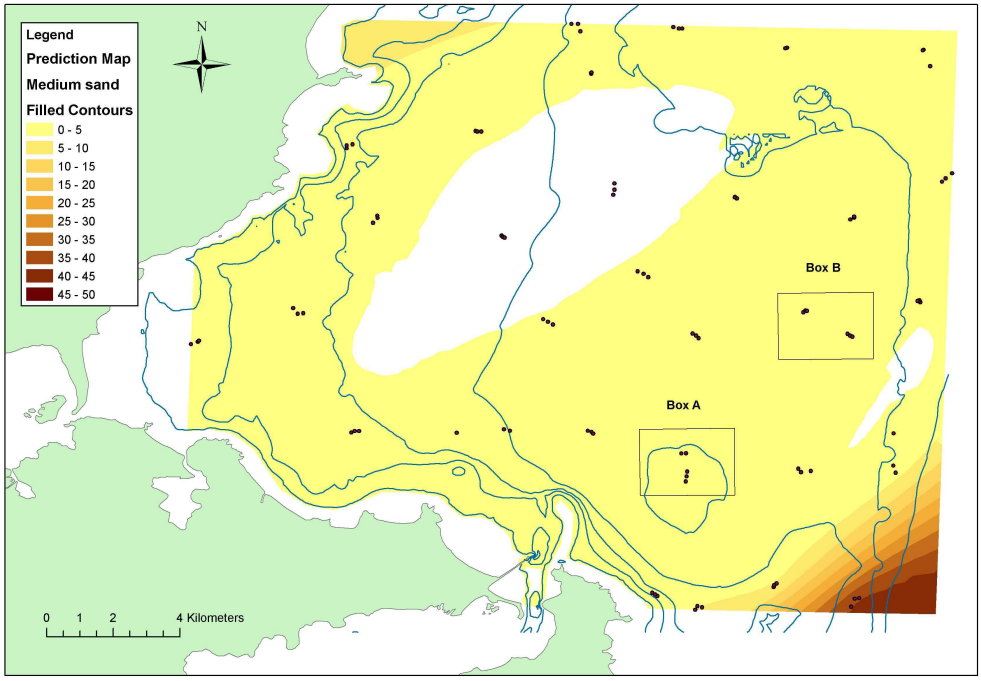

Figure 14: Distribution of medium sand (grain size 250-500 μm) content (%) in the sediments of Blueskin Bay.

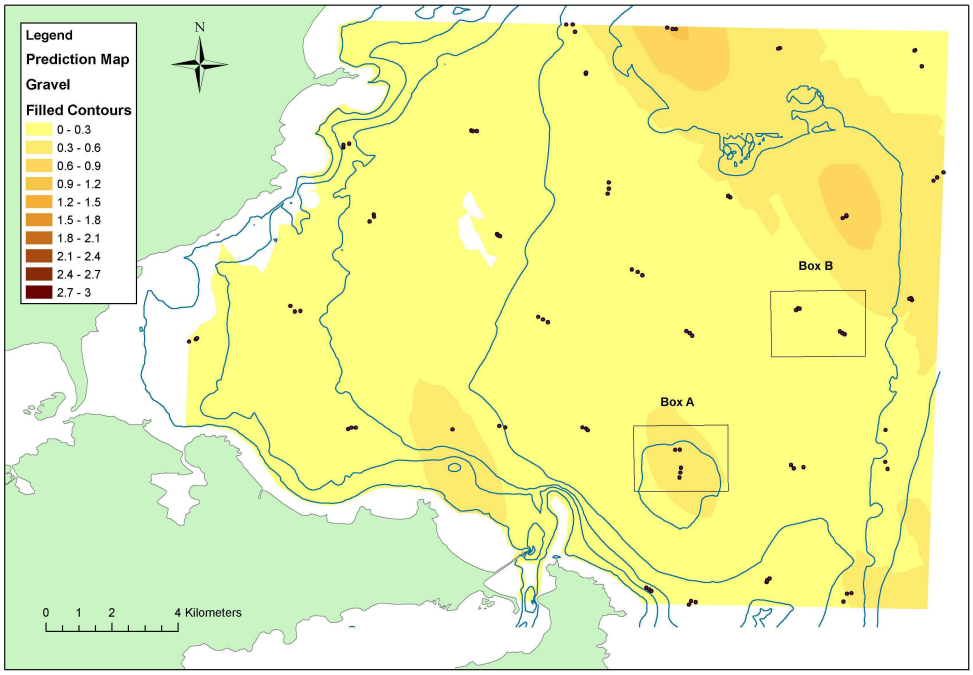

Figure 15: Distribution of gravel (grain size >2.0 mm) content (%) in the sediments of Blueskin Bay.

3.2.2 Macrofauna

A total of 15 409 individual animals in 120 taxa were recovered from the 96 grab samples. The lowest number of individuals in a single replicate grab was 40 at Station 14, inner Blueskin Bay, which was the area of lowest density. The highest individual grab density occurred at Station 26 (403 individuals), and the highest density of animals overall was found in the series of stations just north of the Otago Harbour entrance (Stations 23-27, including Stations 26 and 27 in Box A). Average density was 160.5 ± 80.0 s.d. animals per grab. Species richness ranged from 10 to 39, with an average of 24.5 (± 6.2 s.d.) taxa per sample. The most species-rich area was also that which contained the highest densities (Stations 23-27), and the most species-poor area was Station 14 and Stations 32-33 (off Taiaroa Head, see Figure 16). Species richness estimates made here are likely to be underestimates, since many taxa were identified only to Family level. The most species-rich area was found north of the harbour entrance (Figure 17). The most abundant taxa in the survey are listed, with their total abundances, in Table 3. The assemblage was numerically dominated by the gastropod (snail) *Antisolarium egenum*, followed by three polychaete worms and the ubiquitous bivalve *Nucula nitidula*.

To gain an understanding of the relationships among samples, as well as variability within sites, we performed a multidimensional scaling ordination. This places the samples in two-dimensional space reflecting the degree of similarity between each pair of samples (further explanation in Appendix I). Different replicates from the same station tended to be closely related (Figure 17), but there were clear differences between stations that appear to reflect the effects both of depth and the dominant sediment type. For example, Stations 14, 31, and 32 appear at the lower right of the plot (all dominated by fine sand, even though their depths differ), whereas samples from the deeper sites of northern Blueskin Bay cluster towards the top left of the plot. These patterns indicate some structure in the assemblages. A cluster analysis was then performed to visualise major groupings in the samples (Figure 18). The first major division (to the left of the plot) separates Stations 29, 31, 32 and 2 replicates of Station 14 from the rest. The large numbers of divisions between 40% and 60% similarity on the y-axis indicate considerable variability, even within stations, but it may also be seen that Station 21 (in Box B) has a somewhat different faunal assemblage than other stations.

To explain these patterns in the context of depth and the sediment structure, we conducted a canonical correlation analysis (CAP, Anderson & Willis 2003 and see Appendix 1). This analysis attempts to find the best means of fitting the observed assemblage structure to the environmental variables. It also enables identification of the individual species likely to be responsible for the observed patterns.

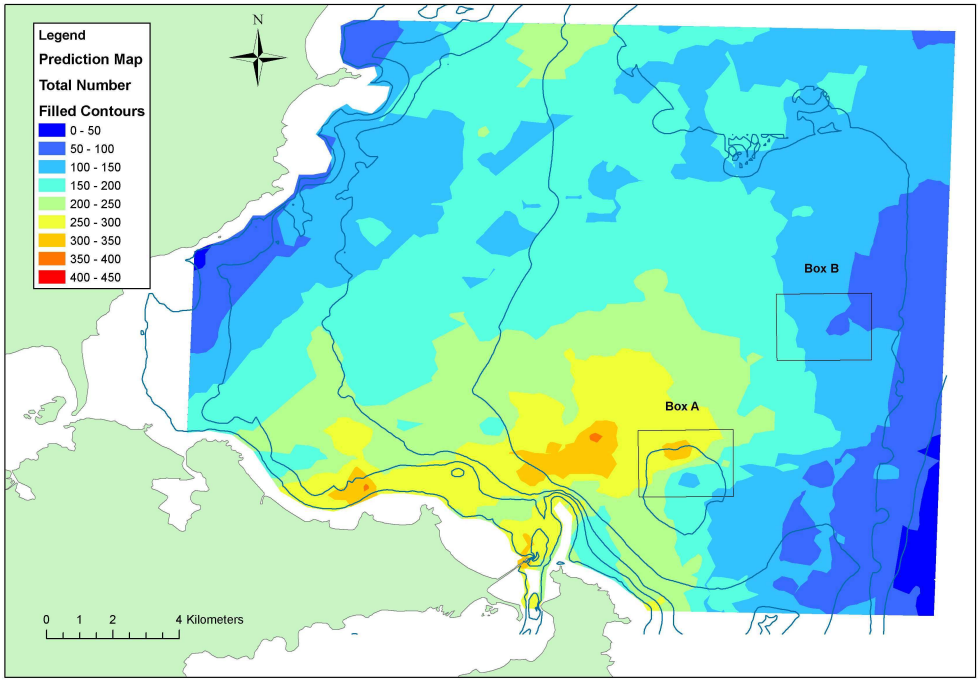

Figure 16: Distribution of macrofaunal density (total number of individuals of all species) in the Blueskin Bay area.

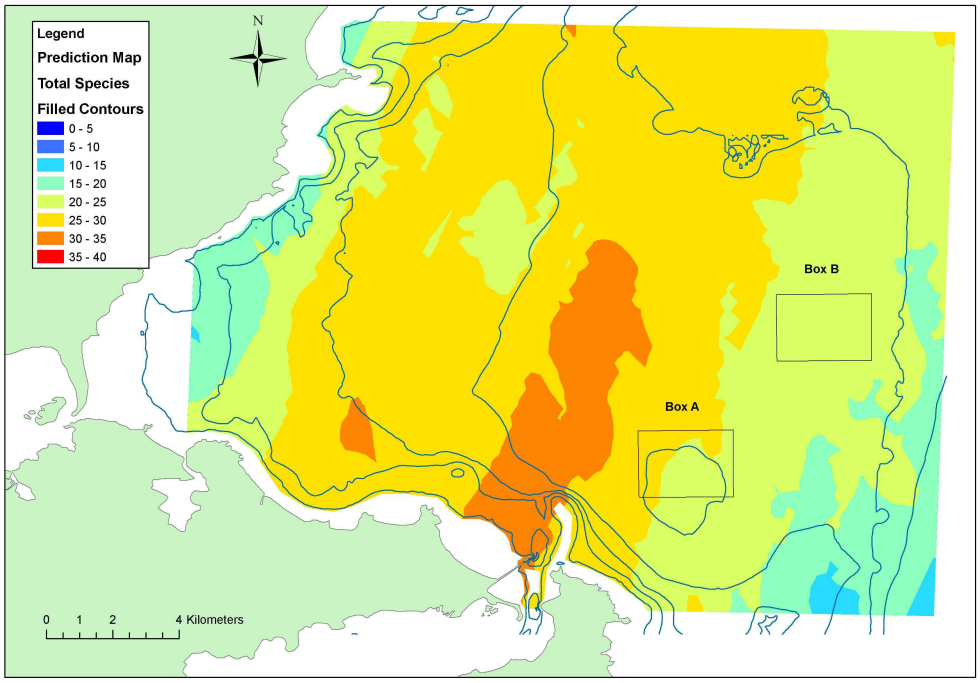

Figure 17: Distribution of species richness (number of taxa) in the Blueskin Bay area.

Table 3: The top 20 most abundant macrofaunal species taken in grab samples in Blueskin Bay, May 2008 (numbers are totals across all samples from all stations).

Phylum	Group	Taxon	Number of individuals
Mollusca	Gastropoda	*Antisolarium egenum*	4916
Annelida	Polychaeta	Cirratulidae sp.	1396
Annelida	Polychaeta	*Aglaophamus* sp. A	1073
Annelida	Polychaeta	*Spiophanes cf bombyx*	935
Mollusca	Bivalvia	*Nucula nitidula*	914
Arthropoda	Amphipoda	Phoxocephalidae sp.	570
Mollusca	Bivalvia	*Tawera spissa*	431
Annelida	Polychaeta	Terebellidae	385
Arthropoda	Amphipoda	Lysianassidae sp.	339
Annelida	Polychaeta	*Owenia* sp.	293
Arthropoda	Amphipoda	Haustoriidae	293
Arthropoda	Cumacea	Cumacea B	275
Arthropoda	Amphipoda	Amphipoda	273
Annelida	Polychaeta	Ampharetidae	236
Annelida	Polychaeta	Spionidae unident.	233
Annelida	Polychaeta	*Heteromastus cf. filiformis*	223
Annelida	Polychaeta	Scalibregmatidae A	202
Annelida	Polychaeta	Prionospio spp.	180
Annelida	Polychaeta	Magelona sp.	166
Arthropoda		Tanaidacea	160

The CAP analysis confirmed that faunal distributions are driven by both depth and sediment variability, although the model did not explain all the variation in the data. Deep sites tended to occur together at the lower left of the plot (Figure 20), and shallower ones to the top right. Stations with a higher fraction of coarser sediments were ordinated to the right (i.e., were positively correlated with the first canonical axis, CAP1) whereas those with higher silt and fine sand content were plotted to the

left (negatively correlated with CAP1). However, those with higher silt content were also positively correlated with CAP2, emphasising that sometimes complex interactions of sediment type and depth explain the distribution of infauna. Unsurprisingly, given their known correlation, organic content and silt effects were plotted in the same direction in the ordination.

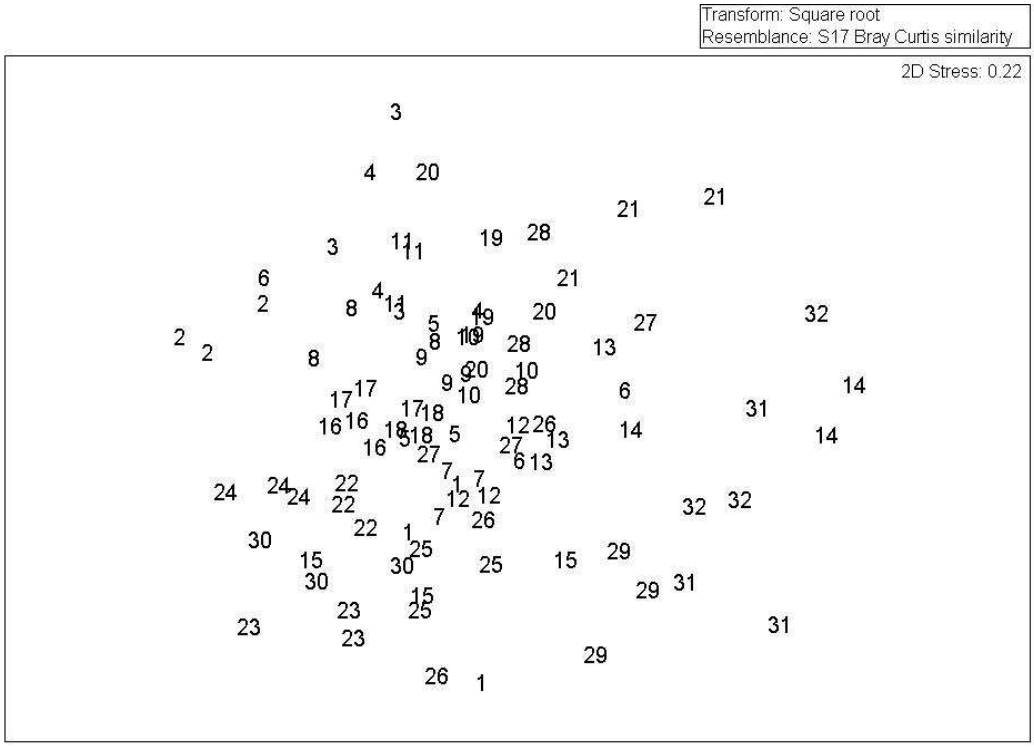

Figure 18: Multidimensional scaling (MDS) ordination of macrofaunal samples taken in Blueskin Bay, May 2008. Labels are Station numbers. Data were 4^{th}-root transformed and ordination is based on Bray-Curtis similarities.

Individual species that are strongly correlated with CAP1 then might be expected to be those that occur in shallower water and coarser sediments, and those negatively correlated with CAP1 in deeper water and finer sediments. These species are listed in Table 4. Referring to the species distribution plots given in Appendix III, we find that, for example, unidentified species of polychaete worms in the Families Cirratulidae and Scalibregmatidae, *Aricidea* sp. (another polychaete worm) and Cumacea B (a small crustacean), occurred in their highest densities in the very fine sand/silt basin in the middle of the bay (refer Figure 12 - this is most marked in Cirratulidae). Conversely, the snail *Zethalia zelandica*, the polychaete worm *Armandia maculata*, and snail *Antisolarium egenum* were all associated with shallow, inner bay regions.

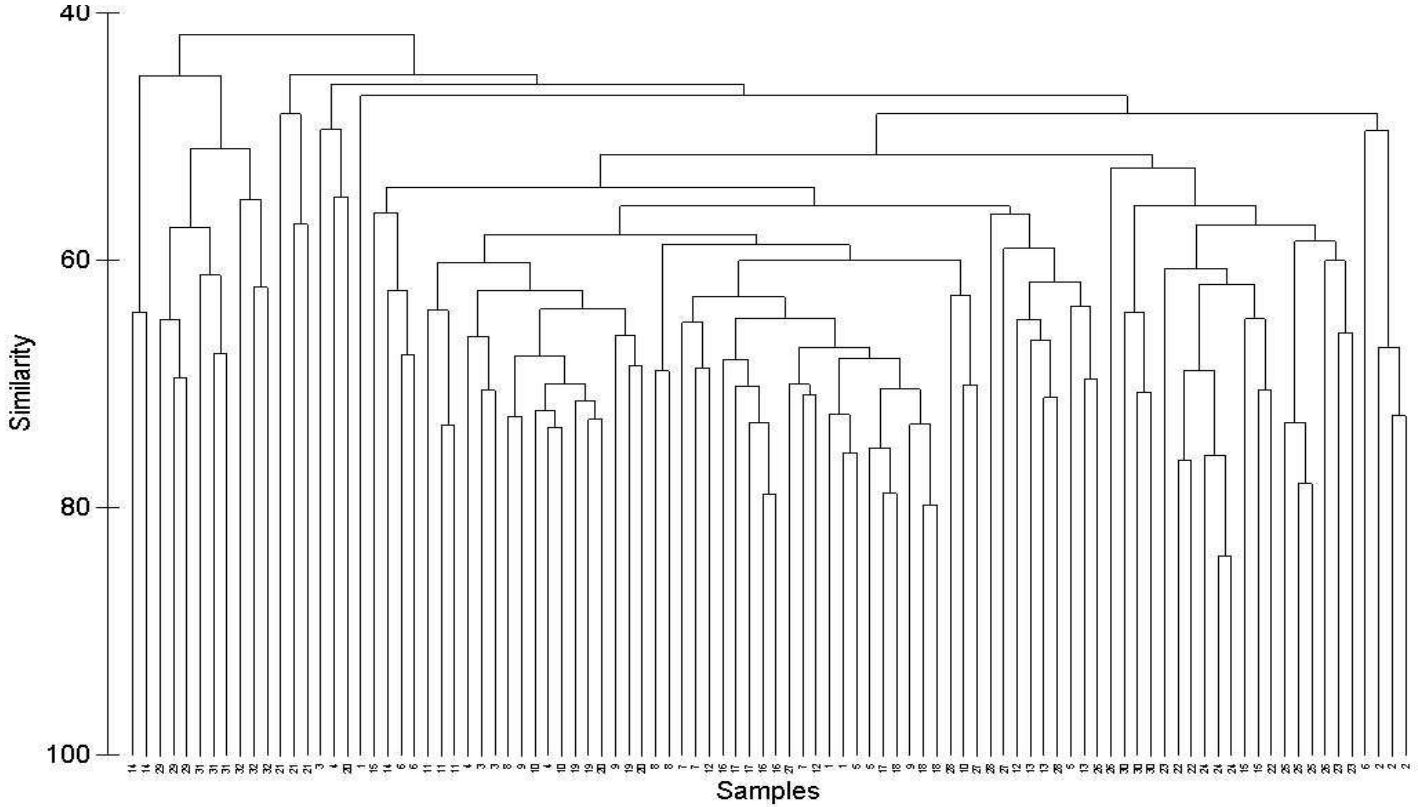

Figure 19: Cluster dendrogram (on Bray-Curtis similarities calculated from 4th root-transformed data) of relationships between macrofaunal grab samples in Blueskin Bay.

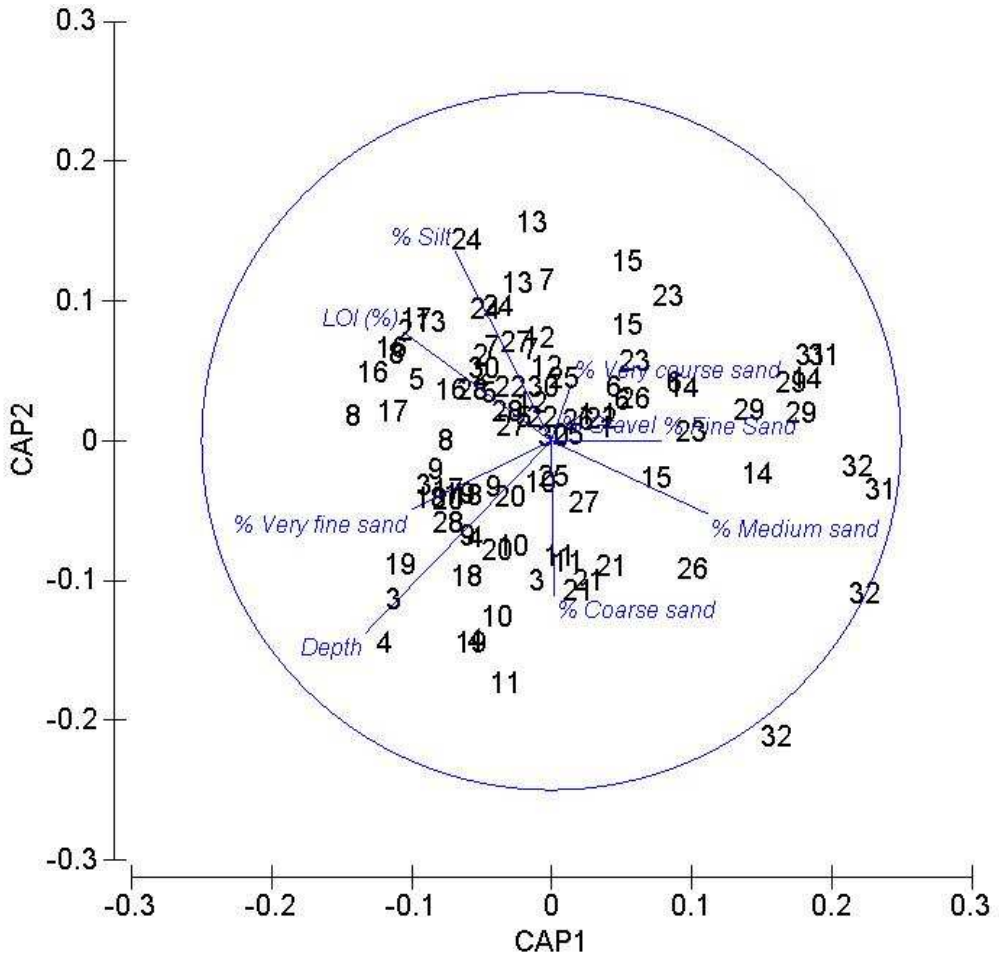

Figure 20: Canonical correlation analysis (using CAP) of macrofauna with normalised environmental variables. Correlation coefficients of assemblage structure with CAP axes, $\delta^1 = 0.72$, $\delta^2 = 0.52$. The superimposed biplots indicates the degree of correlation of the environmental variables with the canonical axes.

On the second canonical axis (CAP2), we might expect negatively correlated species to characterise coarser, deeper habitats. Of those species listed (Table 5) the distribution plots of Amphipoda (small crustaceans) and Tellinidae A (a bivalve) in Appendix 3 most clearly follow this pattern. Positively correlated species with CAP2 will tend to occupy the shallow habitats that are relatively silty. Terebellidae (a family of polychaete worms), *Antisolarium egenum*, Ampharetidae (a family of polychaete worms), *Owenia* (a polychaete worm), and Ophiuroidea (brittle stars) all clearly follow this pattern. What is perhaps more interesting about this group is that they appear to reflect a dependence upon nutrient or fine sediment outflow from Otago Harbour, as their densities increase toward the harbour entrance. All are deposit feeders, which tends to support the idea that they benefit from material of harbour or terrestrial origin. If the presence of deposit feeders was dependent solely on silt

content in the sediment, then we may expect that similar assemblages would be found in the centre of the bay where the highest silt content was found (Figure 11).

The high infaunal abundance and diversity in the area of Box A contrasts with the low abundance and diversity of epifauna in Box A relative to Box B, referred to in Section 3.1. This was primarily due to high numbers of the snail *Antisolarium egenum* found in Box A. Total counts of the most common taxa in Boxes A and B are summarised in Appendix IV.

Table 4: Species responsible for separation of stations along the first canonical axis (CAP1) of Figure 18. Only the 10 most correlated species are shown.

Negative correlation with CAP1		**Positive correlation with CAP1**	
Cirratulidae sp.	-0.7235	*Zethalia zelandica*	0.6429
Cumacea B	-0.6575	*Armandia maculata*	0.3059
Aricidea sp.	-0.5871	*Antisolarium egenum*	0.2752
Scalibregmatidae A	-0.5839		
Phoxocephalidae sp.	-0.5443		
Spiophanes cf bombyx	-0.5376		
Magelona sp.	-0.5290		
Tanaidacea	-0.4155		
Ampharetidae	-0.3919		
Lumbrineridae sp.	-0.3886		

Table 5: Species responsible for separation of stations along the second canonical axis (CAP2) of Figure 18. Only the 10 most correlated species are shown.

Negative correlation with CAP2		Positive correlation with CAP2	
Aricidea sp.	-0.4199	Terebellidae	0.5572
Amphipoda	-0.3273	*Antisolarium egenum*	0.5197
Tanaidacea	-0.2801	Ampharetidae	0.4978
Tellinidae A	-0.2668	Ophiuroidea	0.4606
Tawera spissa	-0.2525	*Aglaophamus sp. A*	0.4312
		Paphies subtriangulata	0.3951
		Glyceridae spp.	0.3938
		Goniadidae	0.3774
		Lumbrineridae sp.	0.3710
		Heteromastus cf. filiformis	0.3612

As an extremely simple test of whether the two proposed spoil disposal sites (Box A and Box B) differed from the surrounding area, we conducted a multivariate analysis of variance using the PERMANOVA technique (Anderson 2001). This one-way test compared the assemblages of Boxes A and B with those of the surrounding area (Stations 10, 19, 25 and 28). Both tests returned non-significant results (Table 6), indicating that, at the local scale, the designated areas are not unique. This result reinforces the conclusions drawn from the larger-scale species mapping above.

Table 6: Results of PERMANOVA comparing assemblages of potential dredge disposal sites with nearby areas.

Box A:

Source	df	SS	MS	Pseudo-F	P
Treat	1	1279.2	1279.2	1.4202	0.151
Residual	10	9007.0	900.7		
Total	11	10286.0			

Box B:

Source	df	SS	MS	Pseudo-F	P
Treat	1	1081.0	1081.0	1.2087	0.242
Residual	10	8943.8	894.4		
Total	11	10025.0			

4. Discussion

This survey has shown that neither of the proposed dredge disposal sites possesses communities that are unique or sensitive within the context of the greater Blueskin Bay area and that would be endangered at larger scales by sediment input. Mapping of environmental variables and species distributions in GIS supports statistical analyses showing that nearshore habitats of Blueskin Bay are composed of well-sorted sands, sometimes dominated by one grain size class, whereas deeper habitats in the centre of the bay have significantly higher proportions of silt and fine sands. This "basin" of finer sediments has consequences for community structure (Gray 1974) that interact with depth to form different assemblages in different parts of the bay. In addition, there appears to be a significant influence of nutrient input from Otago Harbour that supports higher densities of some species in the shallower zones near the harbour entrance.

Comparison of the results of the present study with those of previous studies in the same area (Rainer 1981, Probert & Wilson 1984, Probert 1990 and Paavo & Probert 2005) suggests that the fauna recorded in the present study is typical of the nearshore sand zone that occurs in water depths of ca 30 m off this part of the Otago coast (Probert 1990). Rainer's (1981) study included 5 stations in Blueskin Bay in 10-30 m water depth. Sediments at these stations were fine sand, with some shell in places and slightly muddy at the site furthest inside the bay (close to station 15 of the present study). The most abundant infaunal species recorded by Rainer, such as the gastropods *Zethalia zelandica* and *Antisolarium egenum*, and cirratulid and megalonid polychaetes, included several taxa that were predominant in the present study. *Antisolarium egenum* was also characteristic of the well-sorted fine sand at stations along a line running south from Taiaroa Head and in water depths of 14-25 m in the study by Probert & Wilson (1984). Probert's study (1990) included stations just north of the harbour entrance (the Hayward Point dredge disposal site) and along a transect running northeast from Taiaroa Head (including the area in and around Box A). *A. egenum* was again abundant at several of these stations, with average densities at sites deeper than 15 m being very similar to those recorded in the present study (341 0.1 m^{-2} vs 320 0.1 m^{-2}, respectively) and representing more than 80% of total individuals. As in the present study, nethtyid (including *Aglaophamus* sp.) and spionid polychaetes were relatively abundant. *Z.* (*Umbonium*) *zelandica* was abundant at all stations.

The coastal fine-sand habitat is an extensive feature of this part of the Otago coast (most of the modern sand deriving from the Clutha River). In a local sense, therefore, the proposed disposal sites do not appear to be unusual or of particular ecological

importance relative to the areas around them. The calcareous bryozoans characteristic of the middle and outer continental shelf in this part of the coast (Probert & Wilson 1984) do not extend into the present study area.

Probert & Wilson (1984) noted that "although the inshore sand fauna off the Otago Peninsula has similarities with comparably located faunas elsewhere in the world (including New Zealand: McKnight 1969), notably in the amphipod and polychaete components, it differs significantly in that gastropods rather than bivalves largely comprise the mollusc component". Neither of the dominant gastropods in the present study area (*Antisolarium egenum* and *Zethalia zelandica*) are restricted to this part of the coast and both are abundant in sandy or silty-sandy sediments all around New Zealand. The same is also true of the commonest members of the fauna that were identified to species (Table 3). Without knowing their precise identities, we cannot comment on the distribution and relative abundance of the other taxa in Table 3, but all belong to taxa that are, in general terms, widely distributed.

Movement of sediments from dredge spoil placed at either of Box A or Box B will likely smother the assemblages of the area. Resuspension and deposition of finer sediments in small quantities into the basin area in the centre of the bay is unlikely to have long-term consequences, as this area already possesses an assemblage adapted for silty environments. Sediment structures in shallower areas inside Blueskin Bay and off Taiaroa Head indicate that these areas are subject to either or both of high wave energy and tidal currents that are likely to resuspend and transport any finer sediments from dredge spoil out of the area. Potential effects will be expanded on in another report in preparation and once we have modelling and sediment transport information available.

It is recommended that once a disposal site has been decided, a targeted monitoring programme be designed to determine:

1. the recolonisation rate of macrobenthic infauna after spoil disposal in the main disposal area to inform the likely effects of future disposal from maintenance dredging;

2. changes in the composition of the assemblage relative to pre-disposal baseline studies and unimpacted control sites;

3. the extent of movement of dredge spoil in space and time;

4. the effects of sediment deposition at varying intensities (i.e., varying distances from the disposal site, utilising direct measures of sedimentation rates from sediment traps and/or sediment profiling) on assemblage composition; and

5. the recolonisation time of assemblages under varying sedimentation scenarios.

Specific, targeted sampling designs are required to unequivocally detect changes accounting for the natural spatial variability detailed in the report (Morrisey et al. 1992). This design should be implemented prior to initial disposal taking place, and monitoring conducted on a regular basis.

5. Acknowledgements

In Dunedin, thanks to Neil McDonald, Kevin Templeton, Michelle Taiaroa, and Bill Dickson for their hospitality and kind assistance in the field. Thanks to Megan Carter and Phoebe van der Pol for work on sediment analyses, and Michael Stevenson for help with generating stations for the sidescan survey. Catherine Chague-Goff (NIWA Christchurch) organised the organic content analysis. Don Morrisey substantially improved the text of the report.

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7. Appendix I – Guide to multivariate statistical methods

This Appendix provides some background to the statistical procedures used in this report.

When a number of organisms of different species are sampled simultaneously in response to a particular sampling program or experimental design, multivariate statistical methods are required to analyse the data. In particular, each species or taxonomic group is considered a separate variable and these variables are inter-related (i.e., they are not independent). Each variable is also generally considered a dimension. We will have, in this study, obtained counts of several such variables at once from a pooled group of benthic grab samples at each site. This we refer to as an assemblage or community. In the present and future studies, we may wish to know how the entire suite of variables has responded (a) at differing proximities from the sediment disposal site, (b) to different depths, and (c) to environmental variables (such as sediment chemistry or structure).

To do this, two methods of multivariate analysis are required. These included: (a) *ordination* (to visualize patterns and reduce dimensionality), and (b) *hypothesis-testing methods* (to rigorously test explicit models and ideas). In general, all of the multivariate methods we used here begin with the calculation of a measure of distance or dissimilarity between every pair of sites or replicates on the basis of the composition and relative abundance of the species that were found within them.

7.1 Distance and Dissimilarity Measures

The distance between any two observations (e.g., grabs or sites) can be calculated simply as the straight-line distance in Euclidean space, as follows:

$$d_{12} = \sqrt{\sum_{k=1}^{p} (y_{1k} - y_{2k})^2}$$

where d_{12} is the Euclidean distance between cores (or sites) 1 and 2, y_{ik} is the measure for variable k in core (or site) i, and there are $k = 1,\ldots, p$ variables in the data matrix. This distance measure is generally appropriate to use with quantitative environmental data (such as grain sizes of sediments). It is, however, sensitive to differences in scale or units among the variables. Thus, before calculating the Euclidean distance, one generally standardizes each variable to z-scores (also called normalisation), as follows:

$$y'_{ik} = \frac{y_{ik} - \bar{y}_k}{\sqrt{\frac{1}{N-1}\sum_{i=1}^{N}(y_{ik} - \bar{y}_k)^2}} = \frac{y_{ik} - mean(y)_k}{sd(y)_k}$$

where $\bar{y}_k = mean(y)_k = \frac{1}{N}\sum_{i=1}^{N} y_{ik}$ is the mean of variable *k* (the average of a total of *N* cores) and $sd(y)_k = \sqrt{\frac{1}{N-1}\sum_{i=1}^{N}(y_{ik} - \bar{y}_k)^2}$ is the standard deviation of variable *k*.

Ecologists generally do not use the Euclidean distance, however, for counts of species abundances (e.g., Clarke 1993). One reason for this is that it treats the value of zero like any other value on the number line. As a consequence, Euclidean distance will have a tendency to make two cores that both lack some species to be more similar to one another than if they both had that species, just in different relative abundances. This is not ecologically very meaningful. For species data, a value of zero is more appropriately thought of, in general, as a lack of any information. A measure that reflects differences in composition as well as differences in relative abundances of species (or taxa) is more commonly used for species data. Currently, the most commonly used measure for this is the Bray-Curtis measure of dissimilarity (Bray and Curtis 1957), which is defined as:

$$d_{12} = \frac{\sum_{k=1}^{p}|y_{1k} - y_{2k}|}{\sum_{k=1}^{p}(y_{1k} + y_{2k})}$$

The Bray-Curtis measure varies between 0 and 1.0. The closer to 1.0 the measure is, the more dissimilar those two cores (or sites) are in terms of their composition and relative abundance of species (the measure is sometimes reversed so that values closer to 1.0 are regarded as more similar – the software package PRIMER does this). This measure, when multiplied by 100, is also referred to as the "percentage difference" between two communities. Although this measure treats zeros in an ecologically meaningful way, it is like the Euclidean distance measure in that it is sensitive to differences in scale among the variables. If one or more of the species is extremely abundant, it will tend to dominate the measure. Thus, the data are generally transformed before calculating the Bray-Curtis measure, in order to even up the relative importance (contribution) of different species. A transformation to square roots, ln(y + 1) or to fourth roots is generally appropriate, depending on the differences in scale among variables (Clarke and Green 1988, Clarke 1993). For this investigation, we fourth-root transformed the species data and then calculated Bray-Curtis dissimilarities among all pairs of observations (either cores or sites) as a starting point for multivariate analyses of the species data.

For more information on measures of distance and dissimilarity, see Faith et al. (1987) and Legendre and Legendre (1998).

7.2 Principal Component Analysis (PCA)

Principal component analysis (PCA) is an ordination method that is useful for reducing the number of variables (and thus the number of dimensions) in a multivariate system. To explain how PCA works, consider a system with two variables, as shown in Figure A1. Imagine that we wish to reduce the dimensionality from 2 dimensions down to 1 dimension. For every site, we have two values, one along each dimension, which places the site as a point in the two-dimensional multivariate (in this case bivariate) space.

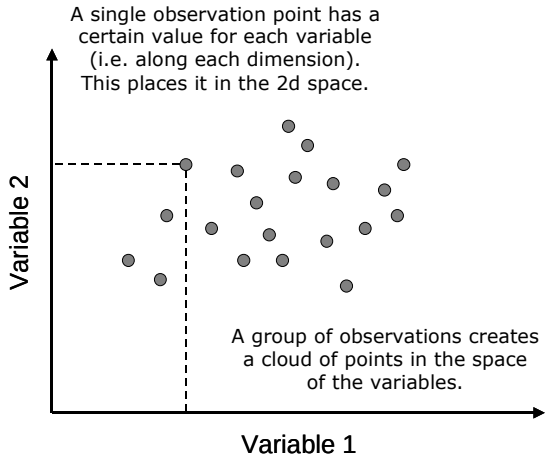

Figure A1: A set of observations (e.g., sites) as points in bivariate space.

Next, draw an axis through the cloud of points in such a way as to maximise the variation of points along it (Figure A2). This is exactly the same as drawing an axis in such a way so as to minimise the sum of squared Euclidean distances from the points to the new axis. The axis is called the first principal component and the values along the axis for the points are called principal component scores (PC scores).

We can repeat this procedure to obtain more PC axes, where in each case we are looking for an axis that maximises variation through the cloud, but subsequent axes are constrained to be completely uncorrelated with previous PC axes. Thus, different components of variation (different directions and therefore different aspects of the data cloud) are described by different individual PC axes. There will be the same number of PC axes as there were original variables in the analysis. Thus, to be useful for reducing dimensions, a large proportion of the variation in the original data needs to

be described well by just the first few PC axes. This happens (i.e., the PCA is most successful for reducing dimensionality) when there is a reasonable amount of correlation among the original variables.

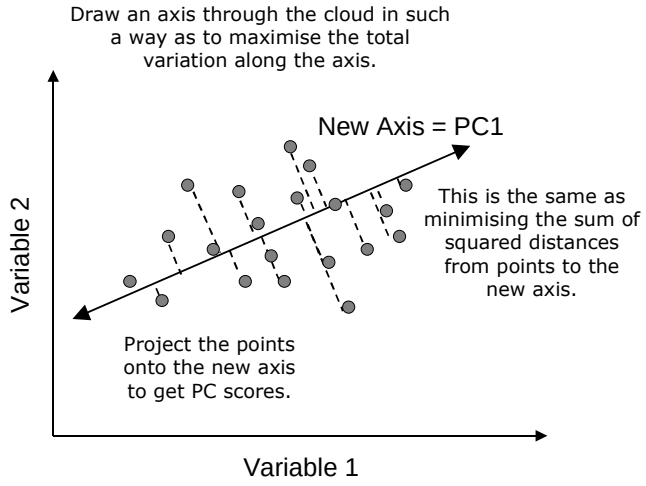

Figure A2: Drawing of the first principal component axis through a cloud of points in bivariate space. The two variables have a positive correlation in this hypothetical example, so the PC axis will explain a reasonably large proportion of the total variation.

How can the PC axes be interpreted? Well, the PC scores are new variables that are linear combinations of the original variables that can be plotted in an ordination diagram or used for subsequent analyses. For example, to get the score for site one along PC axis one, one would calculate:

$$Score_1 = \beta_1 y'_{11} + \beta_2 y'_{12} + ... + \beta_k y'_{1k} + ... + \beta_p y'_{1p}$$

where y'_{11}, y'_{12}, …, y'_{1k}, …, y'_{1p} are the normalized values for variables 1 through *p* at the original site 1 and β_1, β_2, …, β_k, …, β_p are the weights for variables 1 through *p* for principal component axis 1. When the variables are normalized like this for the analysis, the relative sizes of the weights can be used to determine the relative importance of the original variables in the description of the PC axis (e.g., Table 3).

PCA intrinsically preserves Euclidean distances among the points and, therefore, is commonly used for analysis of environmental data (as opposed to species data). For more details on PCA, see Mardia et al. (1979), and Seber (1984). PCA is the Euclidean form of the general term PCO (Principal Coordinates analysis).

7.3 Non-metric Multi-dimensional Scaling (MDS)

Non-metric multi-dimensional scaling is an extremely robust method of ordination that can be done on the basis of any measure of dissimilarity (including the Bray-Curtis measure, as was used in the present investigation). The algorithm essentially attempts to plot the points (e.g., sites) on the basis of the relative dissimilarities between them in an arbitrary number of Euclidean dimensions. That is, one chooses, for example, *a priori*, to see an ordination or "map" of the sites in, say, two dimensions in Euclidean space. The algorithm starts by placing the points in a random orientation. It then iteratively moves or "jitters' the points around relative to one another so as to minimize the discrepancy between the inter-point Euclidean distances on the 2-d plot and their original Bray-Curtis dissimilarities. A measure of this discrepancy is called "stress" and the algorithm works to find a solution that minimizes stress. Several random starts are usually needed in order to obtain a global (as opposed to a local) minimum in the value of stress.

Unlike PCA, the axes produced in non-metric MDS are arbitrary and bear no known relationship to the original variables. This is why these plots do not have any labels on their axes. It also means that the axes can be rotated, inverted, expanded or contracted, without altering their meaning. Each MDS plot in the text reports a measure of stress, because stress indicates how accurately the MDS plot reflects the original relative Bray Curtis (or other) dissimilarities among the points. As a general rule of thumb, stress values less than 0.2 provide a good representation of the original dissimilarities among the points. MDS plots with stress values of 0.2 or greater are suspect in terms of their interpretability.

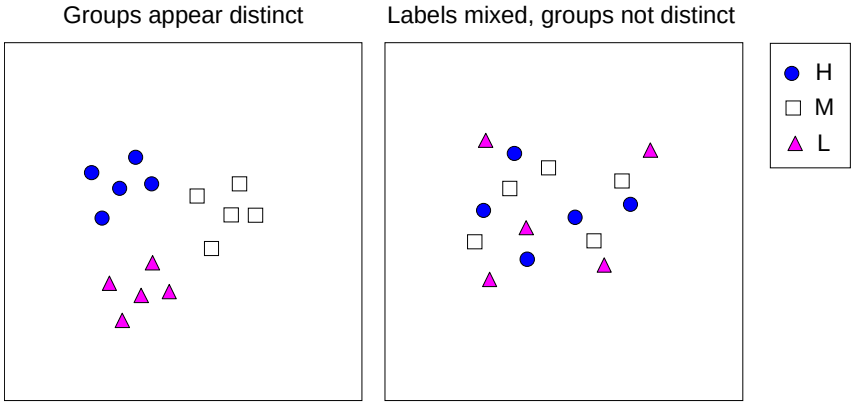

Figure A3: Examples of patterns in non-metric MDS plots that indicate either differences among assemblages (left: similar symbols are grouped together), or no clear differences (right: symbols are mixed and do not form distinct groups).

When viewing an MDS plot, the relative distances between points indicate their relative similarity with respect to the composition and abundance of assemblages. In general, the points on the plot are labelled according to their membership in groups. For example, if individual sites are subject to High, Medium or Low levels of sediment deposition, and given labels for H, M and L, respectively, in MDS plots. Of interest is to see whether the sites belonging to the same group are clustered together on the plot and are cleanly separated from other sites belonging to other groups (e.g., Figure A3). This would suggest that groups differ in their communities of organisms. On the other hand, if labels of different types are well-mixed in the diagram, this would suggest no clear differences in assemblages from different groups.

For more details on MDS, see Kruskal & Wish (1978) and Clarke (1993).

7.4 Constrained Ordination

There are some situations where there are statistically significant differences in assemblages that are, nevertheless, not visible in patterns on the MDS plot. Some methods of ordination are designed to view the cloud of multivariate data in such a way that *any* differences in the assemblages that might be apparent in multivariate space can be viewed in a lower-dimensional diagram. Such methods are called "constrained" ordinations, because they use the hypothesis of interest as part of the criterion for finding an axis through the multivariate cloud for ordination. Note that PCA and non-metric MDS are both ordination methods that are "unconstrained." That is, these methods do not use any hypothesis at all, but instead use very general and "hypothesis-free" criteria (e.g., maximizing the variance of the entire data cloud along a new PC axis, or minimizing stress in the case of MDS). Such unconstrained methods may be thought of as "letting the data speak for themselves" (Clarke & Ainsworth 1993).

One method of constrained ordination is Canonical Discriminant Analysis (CDA). This method finds an axis through the cloud of points that maximizes differences between groups, where the group membership is provided by an *a priori* hypothesis. To see how CDA differs from PCA, we can consider how each of these methods would treat with the same set of two-dimensional data for which we wish to obtain a one-dimensional ordination (Figure A5).

If the direction of group differences is similar to the direction of greatest total variation, then PCA and CDA will give quite similar-looking ordination plots. This will happen, for example, if the differences among groups occur in the most abundant and variable species or taxa. If, however, the direction of group differences in

multivariate space is different to the direction of greatest total variation (i.e., Figure A4), then the CDA may uncover differences among groups that are not seen in a PCA plot. This might happen, for example, when group differences are caused by changes in the less abundant and less prominent species or taxa. An important further point is that a constrained ordination is not useful, however, for determining potential differences in *dispersion* among groups, which can generally be discerned, however, in an unconstrained plot.

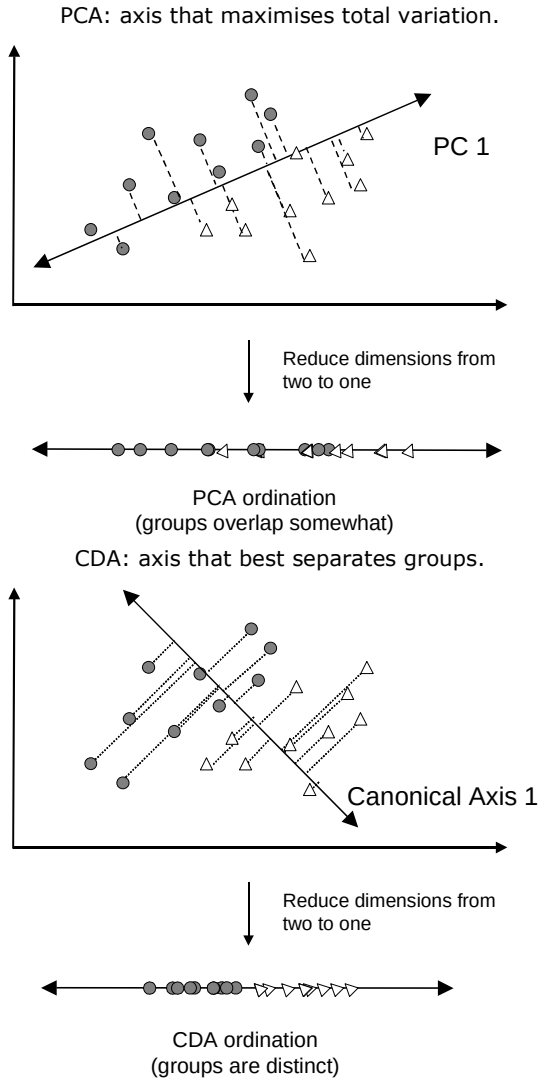

Figure A4: Contrast between an unconstrained PCA ordination and a constrained CDA ordination of the same data set. The differences arise from the fact that the PCA does not use the group membership of points to draw the axis, whereas the CDA searches for an axis that maximizes group differences.

Clearly, both an unconstrained and a constrained ordination will be useful for discovering patterns in multivariate data, in any particular situation. They just give different views of the same data cloud. For more details on CDA, see Seber (1984) and Williams (1983). CDA was not used in the present investigation, but has been described here to clarify what is meant by a constrained ordination. A more flexible and robust method of constrained ordination was used, called CAP, which stands for *Canonical Analysis of Principal Coordinates*.

7.4.1 CAP plots: Canonical Analysis of Principal Coordinates

We have seen, above, how non-metric MDS is an unconstrained ordination method that has the added advantage (over PCA) that any measure of dissimilarity can be used as the basis for the analysis. It is a particularly robust and flexible method (Minchin 1987). A constrained ordination method that can be done on the basis of any measure of dissimilarity has recently been developed and is called *Canonical Analysis of Principal Coordinates*, or CAP (Anderson & Willis 2003). It is essentially a two-step procedure that involves calculation of principal coordinates from Bray-Curtis (or some other) dissimilarities, followed by CDA on these principal coordinates. Further details are found elsewhere (Anderson & Willis 2003, Anderson & Robinson 2003).

The essential point is that CAP provides a constrained ordination of the data on the basis of any measure of dissimilarity, a kind of constrained version of MDS, if you like. In other words, CAP is to MDS what CDA is to PCA.

Allocation Success

When viewing the results of a CAP ordination, several things are reported, each with specific meaning. First, for each axis of the ordination, one is given the *squared canonical correlation* (symbolized by δ^2). This value goes from 0 to 1 and is the correlation between the group structure and the species data. The closer the value is to 1, the greater is the strength of the group effects.

Second, in the canonical ordination, one is looking for clear separation of groups of similar symbols, (as described for MDS plots, Figure A4 above). A measure of the distinctness of the groups is given by what is called the "allocation success," which is a percentage out of 100. What is allocation success? It is a measure of the probability that a new observation, when placed into the canonical ordination, will get placed into its correct group. How is allocation success determined? The method used here is called "leave-one-out classification" and proceeds as follows (e.g., Lachenbruch & Mickey 1968):

1. Remove one of the points and do the CAP analysis without it.

2. Place the point that was "left out" into the canonical space, based on its dissimilarities with all other points in the diagram.

3. Determine the group whose centroid (central location) is the closest to the point and allocate the point to this group.

4. The "true" group to which the point belongs is known: was the allocation of the point correct?

5. Repeat steps 1-4 for all of the points in the diagram and determine the proportion of the points that were correctly allocated.

If 100% of the points were correctly allocated, then the groups are extremely distinct. If, on the other hand, there are, say, three groups, then an allocation success of 30% would be no better than random. An analogous measure for determining the distinctness of the groups, called "misclassification error," is simply 100 minus the allocation success. For more information concerning methods of calculating misclassification error, see Seber (1984).

Correlations of Species with Canonical Axes

Although CAP is a very robust procedure, it has the same slight drawback that MDS has in that the axes it produces for the ordination have no known relationship to the original variables. A natural question to ask is, "Which of the original variables contribute to group differences?" In the case of PCA, one can use the weights to determine the importance of the original variables directly. However, in CAP, one can get at this question by calculating, after the fact, the simple correlation of each original variable with the canonical axes. For example, consider the CDA diagram on the left-hand side of Figure A4 and imagine that the triangles represent, say, samples taken at 100 m distance from the disposal site and the circles represent, say, samples taken 500 m from the disposal site. A species that has a strong positive correlation with the first canonical axis would, therefore, be associated with "100 m" situations, while a species that has a strong negative correlation would be associated with situations of "500 m." The sizes of correlations of individual species with canonical axes can be used as a way of deciding which species to examine more closely in univariate analyses.

7.5 References for Appendix I

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8. Appendix II – Sediment variables raw data

Refer to Figure 1 for Station positions. All data are percentages by dry weight. LOI = loss on ignition, a measure of total organic content in the sediment, Silt = sediment with particle size < 63 μm, VFine sand = particle size 63-125 μm, Fine sand = particle size 125-250 μm, Med sand = particle size 250-500 μm, Coarse sand = particle size 0.5-1.0 mm, VCoarse sand = particle size 1.0-2.0 mm, gravel = particle size > 2mm.

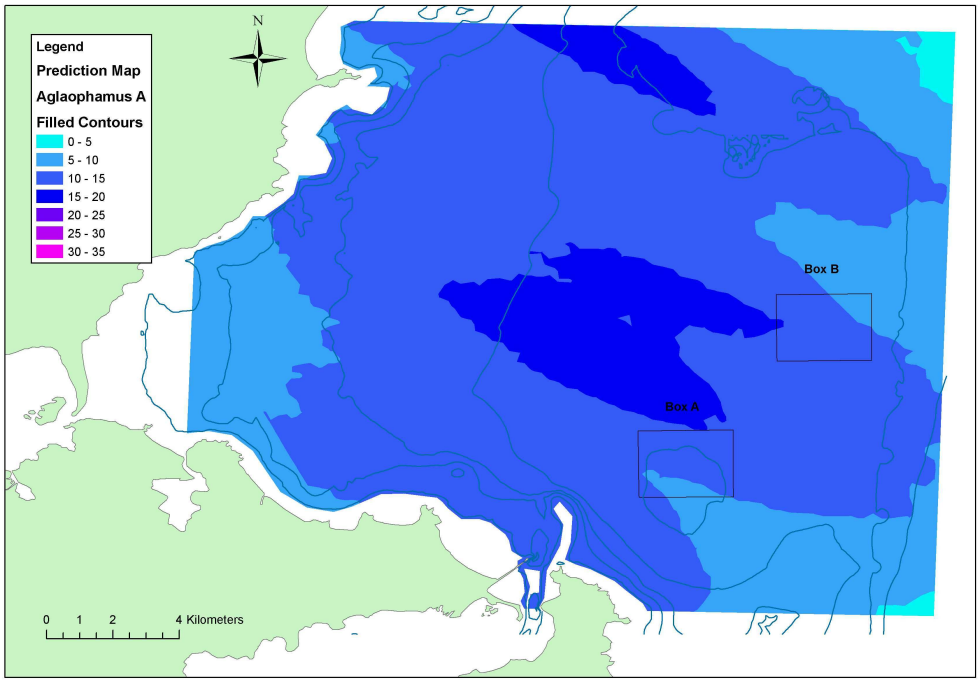
ID	Station	Repl.	LOI (%)	Silt	VFine sand	Fine sand	Med sand	Coarse sand	VCoarse sand	Gravel
1	1	1	1.17	7.14	7.96	77.33	4.99	1.28	0.96	0.33
2	1	2	1.12	14.06	4.25	73.66	7.08	0.42	0.29	0.24
3	1	3	1.50	7.89	2.69	87.32	1.25	0.54	0.17	0.13
4	2	1	1.52	28.16	52.63	14.76	0.49	0.77	1.23	1.96
5	2	2	1.70	20.59	10.54	65.73	1.12	0.47	0.38	1.17
6	2	3	1.68	24.68	57.06	16.90	0.59	0.14	0.20	0.44
7	3	1	1.58	11.90	13.27	73.90	0.49	0.13	0.21	0.10
8	3	2	1.34	15.62	17.43	66.37	0.15	0.07	0.17	0.19
9	3	3	1.79	18.99	15.70	64.94	0.22	0.07	0.06	0.03
10	4	1	1.64	30.54	25.03	43.44	0.68	0.16	0.09	0.07
11	4	2	1.13	14.81	24.13	58.37	1.71	0.63	0.16	0.19
12	4	3	1.25	14.62	30.47	54.53	0.28	0.05	0.02	0.02
13	5	1	1.44	15.17	19.58	64.89	0.20	0.05	0.03	0.10
14	5	2	1.19	11.90	20.07	67.81	0.15	0.04	0.02	0.02
15	5	3	1.48	16.06	22.60	60.95	0.13	0.04	0.03	0.19
16	6	1	1.29	11.59	10.87	77.08	0.38	0.04	0.02	0.01
17	6	2	1.62	45.09	9.52	45.08	0.25	0.03	0.02	0.01
18	6	3	1.55	11.60	10.87	77.08	0.37	0.04	0.02	0.01
19	7	1	2.44	33.65	35.42	30.65	0.19	0.01	0.04	0.03
20	7	2	2.11	22.92	10.87	65.89	0.27	0.03	0.02	0.00
21	7	3	1.94	24.19	20.43	55.15	0.18	0.02	0.01	0.01
22	8	1	2.96	20.44	47.76	31.58	0.14	0.04	0.01	0.02
23	8	2	1.65	13.29	53.56	32.85	0.16	0.04	0.06	0.05
24	8	3	1.61	17.02	54.56	28.20	0.13	0.04	0.03	0.02
25	9	1	1.62	14.05	54.16	31.23	0.28	0.08	0.03	0.18
26	9	2	1.34	9.41	77.74	12.50	0.20	0.12	0.02	0.02
27	9	3	1.38	11.69	70.78	17.14	0.20	0.14	0.05	0.00
28	10	1	1.40	10.67	47.16	41.72	0.30	0.10	0.03	0.03
29	10	2	1.57	13.13	54.32	29.30	0.08	0.26	0.03	2.87
30	10	3	1.47	13.55	51.99	33.83	0.28	0.17	0.05	0.12
31	11	1	1.36	16.25	17.39	62.42	2.28	0.63	0.40	0.62
32	11	2	1.43	14.23	25.35	54.75	4.08	0.72	0.56	0.31
33	11	3	1.26	13.12	11.59	70.46	3.09	0.76	0.51	0.47
34	12	1	1.75	14.89	7.41	77.44	0.21	0.03	0.01	0.01
35	12	2	1.60	21.91	9.14	68.62	0.22	0.03	0.07	0.01
36	12	3	1.44	15.75	5.37	78.20	0.54	0.09	0.03	0.01
37	13	1	1.58	24.44	62.61	12.84	0.07	0.02	0.03	0.00
38	13	2	1.49	54.44	38.98	6.49	0.04	0.02	0.02	0.02
39	13	3	2.08	37.96	55.55	6.44	0.03	0.01	0.01	0.00

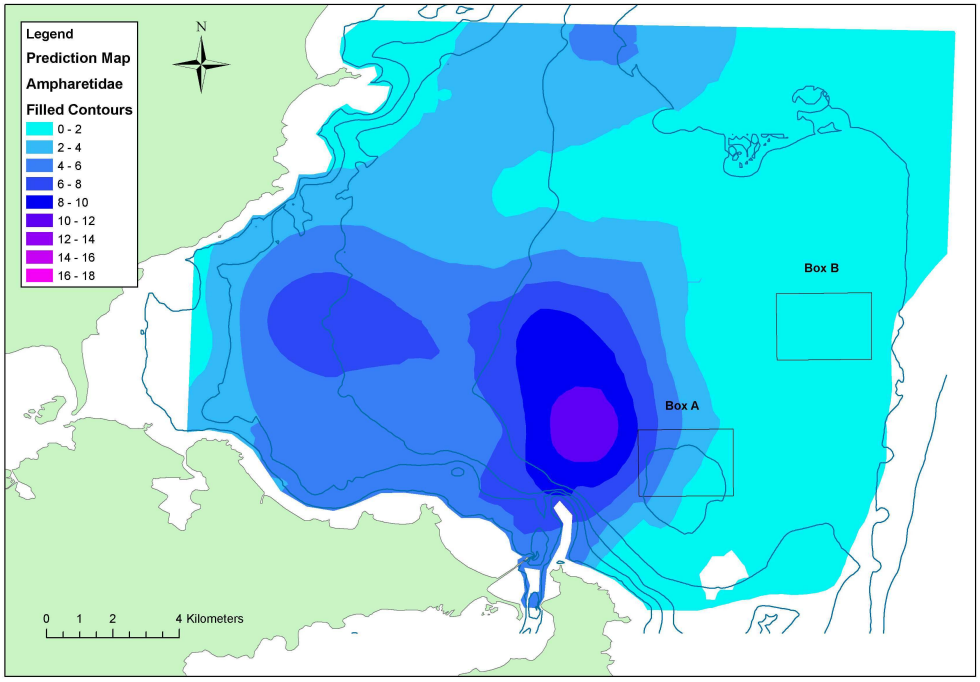
ID	Station	Repl.	LOI (%)	Silt	VFine sand	Fine sand	Med sand	Coarse sand	VCoarse sand	Gravel
40	14	1	1.13	8.17	6.08	85.46	0.22	0.02	0.05	0.01
41	14	2	0.74	5.84	8.57	85.50	0.08	0.01	0.00	0.00
42	14	3	1.09	6.48	3.21	90.14	0.11	0.02	0.03	0.00
43	15	1	1.78	35.73	13.03	50.41	0.67	0.09	0.04	0.03
44	15	2	1.21	17.70	13.08	68.11	0.93	0.12	0.06	0.01
45	15	3	1.27	10.00	2.91	86.65	0.30	0.05	0.04	0.05
46	16	1	omitted							
47	16	2	omitted							
48	16	3	omitted							
49	17	1	1.87	33.39	46.38	20.16	0.01	0.06	0.00	0.00
50	17	2	2.39	40.24	47.55	12.06	0.10	0.01	0.03	0.00
51	17	3	1.69	43.88	47.35	8.61	0.11	0.02	0.02	0.00
52	18	1	2.17	26.48	57.32	15.78	0.30	0.05	0.05	0.02
53	18	2	1.81	16.89	39.54	42.99	0.29	0.11	0.05	0.14
54	18	3	1.78	14.39	52.52	32.63	0.25	0.08	0.04	0.08
55	19	1	1.82	10.69	52.89	35.13	0.65	0.22	0.12	0.29
56	19	2	1.79	14.61	66.15	18.67	0.33	0.12	0.04	0.08
57	19	3	1.30	10.26	48.17	40.92	0.36	0.15	0.10	0.04
58	20	1	1.60	9.12	18.74	71.80	0.22	0.11	0.01	0.00
59	20	2	1.67	9.82	51.79	37.97	0.29	0.08	0.03	0.01
60	20	3	1.55	9.56	69.88	20.03	0.21	0.09	0.08	0.15
61	21	1	1.57	9.63	26.05	64.00	0.27	0.04	0.01	0.00
62	21	2	1.60	10.54	32.84	55.85	0.43	0.19	0.07	0.08
63	21	3	1.56	11.77	60.76	27.07	0.26	0.08	0.03	0.02
64	22	1	1.45	7.39	27.25	64.32	0.60	0.15	0.09	0.20
65	22	2	1.40	8.38	22.43	68.23	0.62	0.19	0.09	0.05
66	22	3	1.35	8.17	8.72	81.74	0.67	0.18	0.12	0.40
67	23	1	1.27	11.39	3.16	84.74	0.39	0.08	0.11	0.13
68	23	2	1.36	14.03	5.05	80.12	0.51	0.06	0.05	0.18
69	23	3	1.05	13.35	7.83	78.46	0.35	0.00	0.00	0.00
70	24	1	1.10	14.03	4.53	76.98	4.07	0.19	0.20	0.00
71	24	2	1.43	13.96	5.88	76.61	3.04	0.10	0.10	0.31
72	24	3	0.93	14.02	7.38	73.80	3.82	0.08	0.09	0.81
73	25	1	2.21	30.92	29.26	39.17	0.49	0.05	0.03	0.09
74	25	2	2.41	32.26	26.56	40.80	0.25	0.03	0.06	0.03
75	25	3	2.19	35.39	23.01	40.88	0.56	0.06	0.06	0.03
76	26	1	1.52	16.27	27.40	54.86	1.16	0.13	0.04	0.14
77	26	2	1.96	9.29	18.69	70.38	0.88	0.17	0.13	0.46
78	26	3	1.45	9.42	25.34	63.81	0.87	0.21	0.14	0.21
79	27	1	1.25	5.38	2.28	86.25	3.62	0.42	0.62	1.42
80	27	2	1.45	9.97	18.59	66.49	4.03	0.25	0.16	0.51
81	27	3	1.53	6.72	3.60	84.95	3.90	0.40	0.31	0.12
82	28	1	1.23	7.05	27.79	64.63	0.30	0.11	0.01	0.11
83	28	2	1.17	8.13	22.62	68.96	0.23	0.03	0.01	0.03
84	28	3	1.40	7.42	3.94	88.05	0.21	0.10	0.09	0.18
85	29	1	1.17	8.61	7.78	82.27	1.05	0.06	0.08	0.14
86	29	2	1.13	6.80	9.07	83.27	0.50	0.09	0.07	0.21

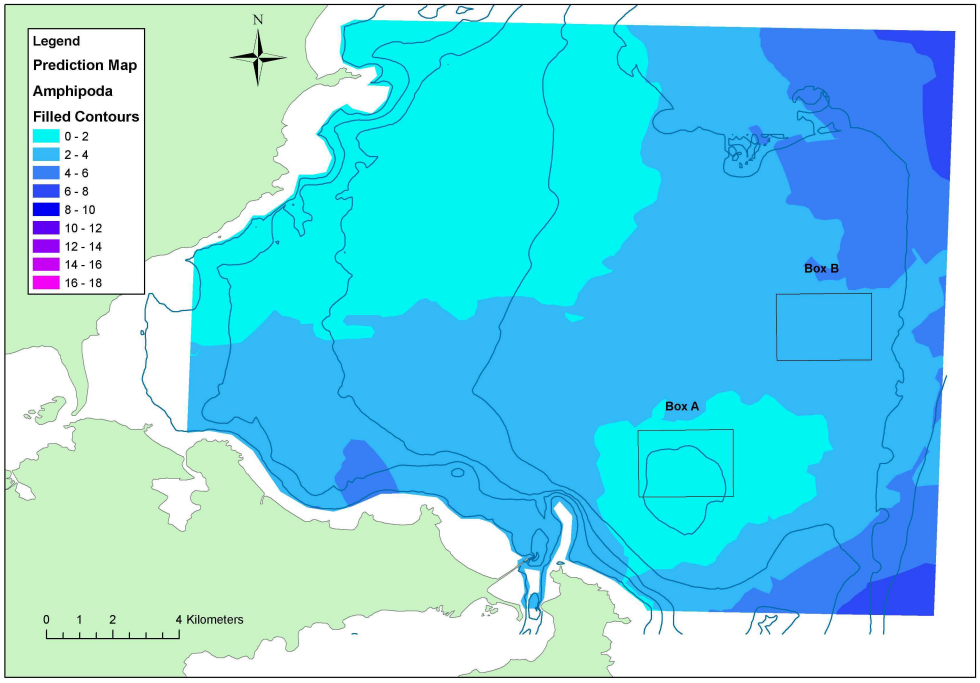
ID	Station	Repl.	LOI (%)	Silt	VFine sand	Fine sand	Med sand	Coarse sand	VCoarse sand	Gravel
87	29	3	1.07	5.29	12.96	80.75	0.56	0.06	0.08	0.31
88	30	1	0.94	3.61	3.97	91.06	1.27	0.04	0.01	0.04
89	30	2	0.82	6.30	1.76	90.12	1.71	0.03	0.06	0.01
90	30	3	0.81	4.04	2.16	92.38	1.19	0.16	0.07	0.00
91	31	1	1.41	25.07	21.26	49.00	4.30	0.11	0.07	0.20
92	31	2	1.81	21.76	17.21	57.16	3.67	0.09	0.06	0.06
93	31	3	1.27	19.32	10.32	61.85	8.35	0.05	0.05	0.05
94	32	1	0.89	3.88	6.10	87.29	2.63	0.06	0.03	0.01
95	32	2	0.90	3.26	6.11	88.57	1.94	0.04	0.05	0.03
96	32	3	1.08	4.36	6.40	85.99	3.08	0.07	0.05	0.06
97	33	1	0.59	4.18	2.62	52.29	40.10	0.56	0.11	0.13
98	33	2	0.81	3.90	2.97	48.55	44.01	0.37	0.11	0.09
99	33	3	0.58	5.56	2.52	45.25	45.15	0.48	0.10	0.92

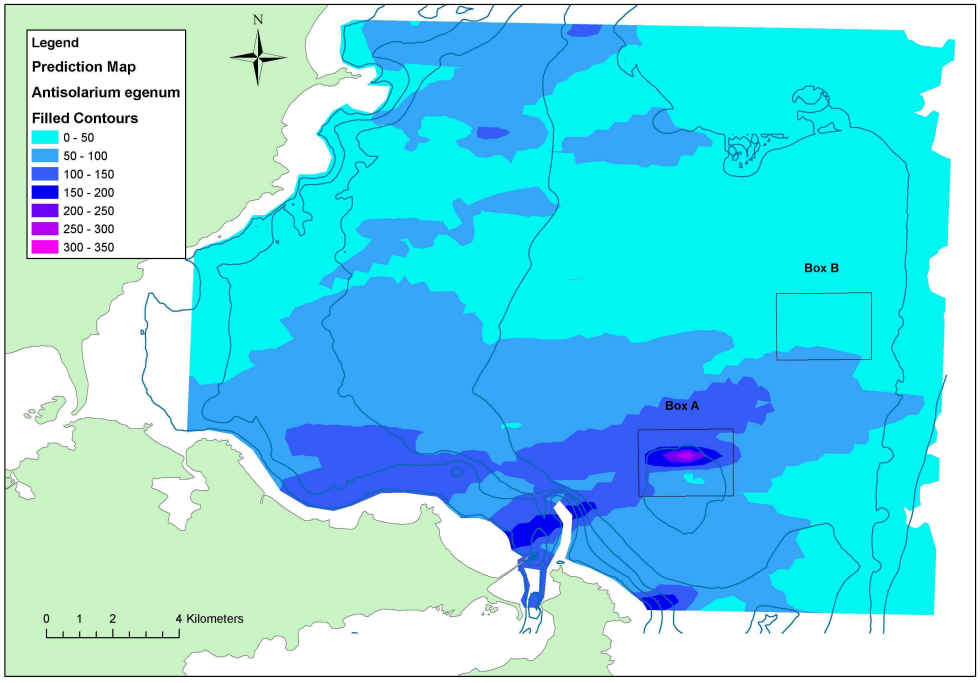
9. Appendix III – Distribution maps of key taxa

Taxa ordered alphabetically. WGS84 map projection.






Legend
Prediction Map
Amphipoda
Filled Contours
0 - 2
2 - 4
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
14 - 16
16 - 18
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Antisolarium egenum
Filled Contours
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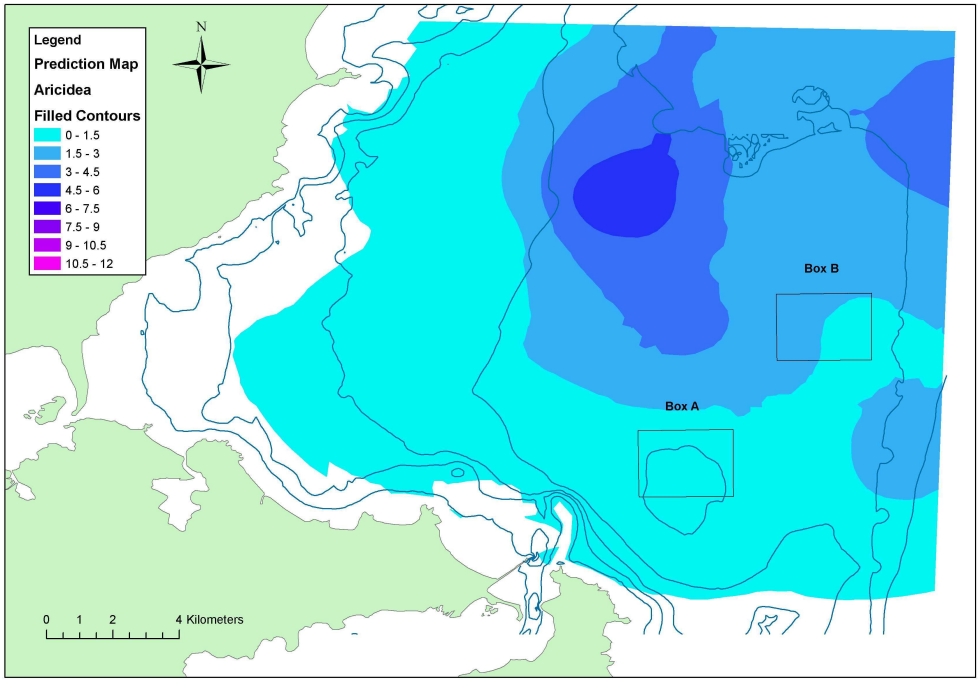
100 - 150
150 - 200
200 - 250
250 - 300
300 - 350
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Aricidea
Filled Contours
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3 - 4.5
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6 - 7.5
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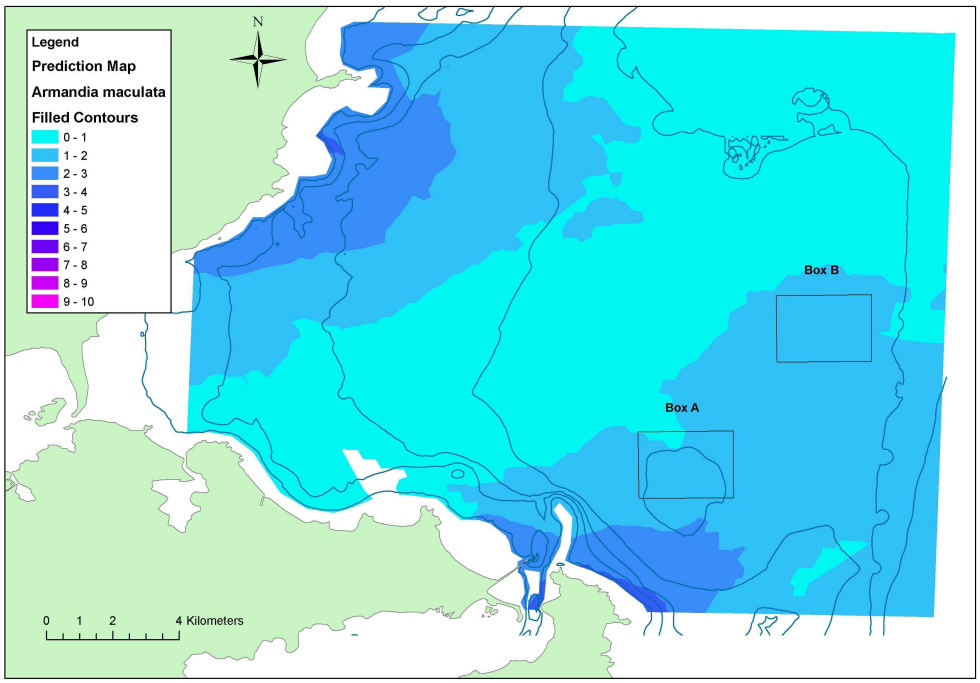
9 - 10.5
10.5 - 12
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Armandia maculata
Filled Contours
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1 - 2
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5 - 6
6 - 7
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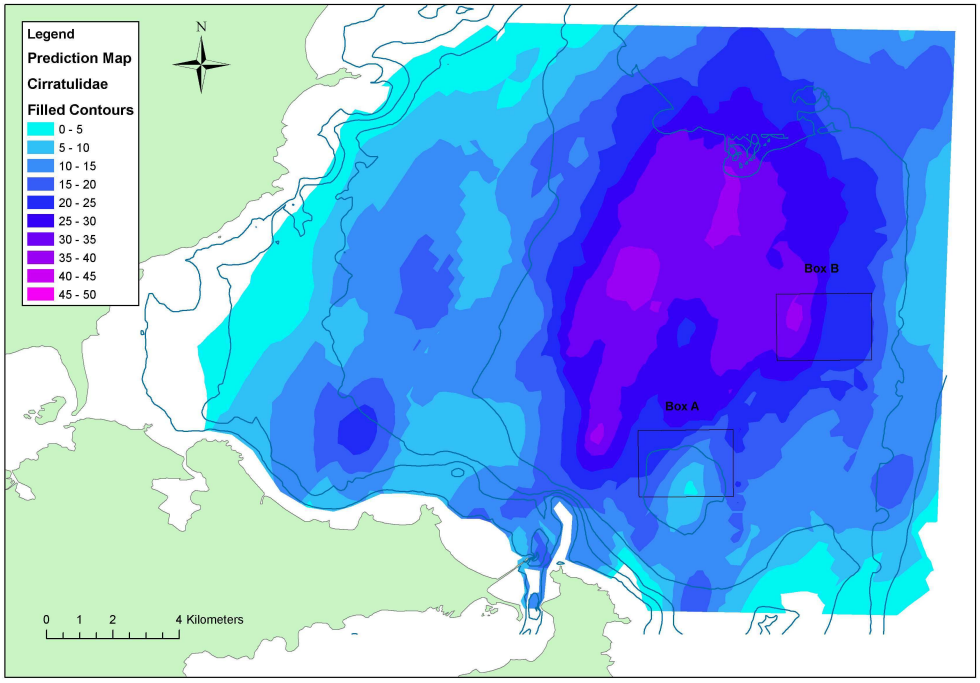
8 - 9
9 - 10
N
Box B
Box A
0 1 2 4 Kilometers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Prediction Map
Cirratulidae
Filled Contours
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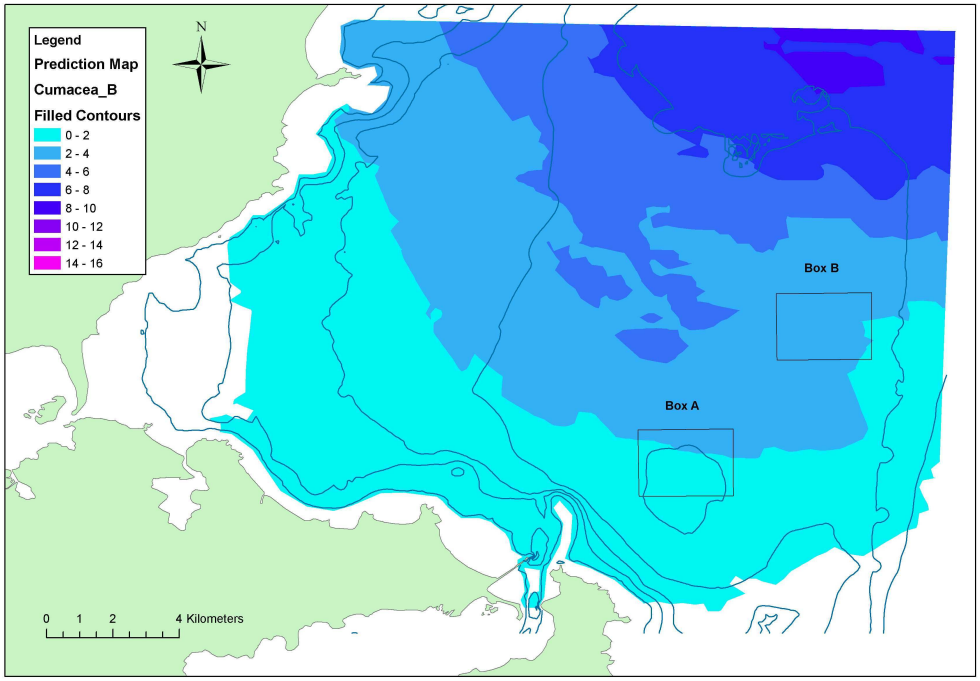
5 - 10
10 - 15
15 - 20
20 - 25
25 - 30
30 - 35
35 - 40
40 - 45
45 - 50
N
Box B
Box A
0 1 2 4 Kilometers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Prediction Map
Cumacea_B
Filled Contours
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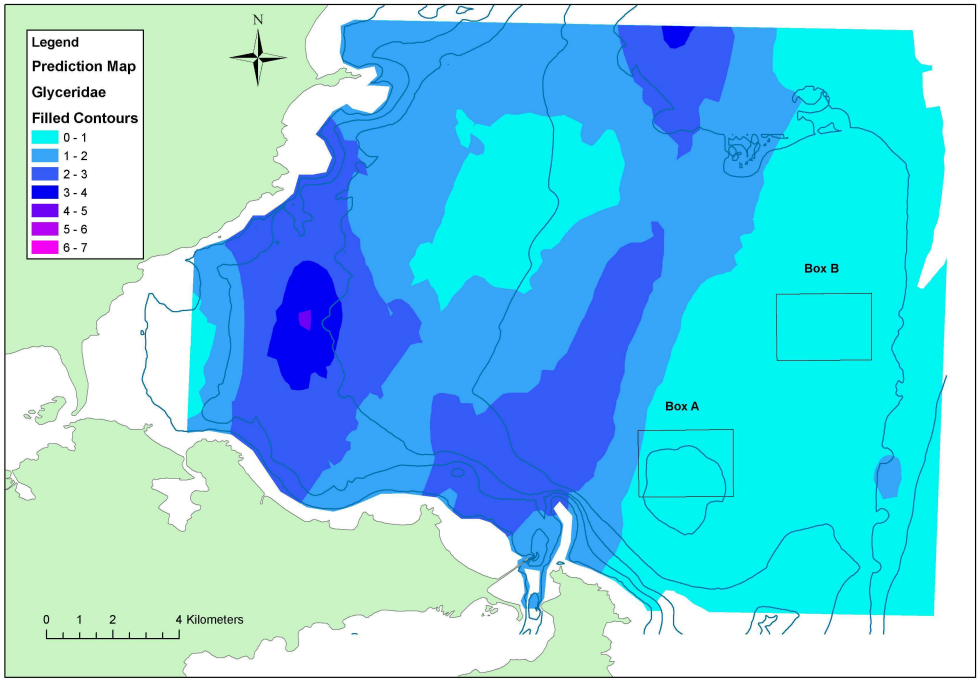
2 - 4
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
14 - 16
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Glyceridae
Filled Contours
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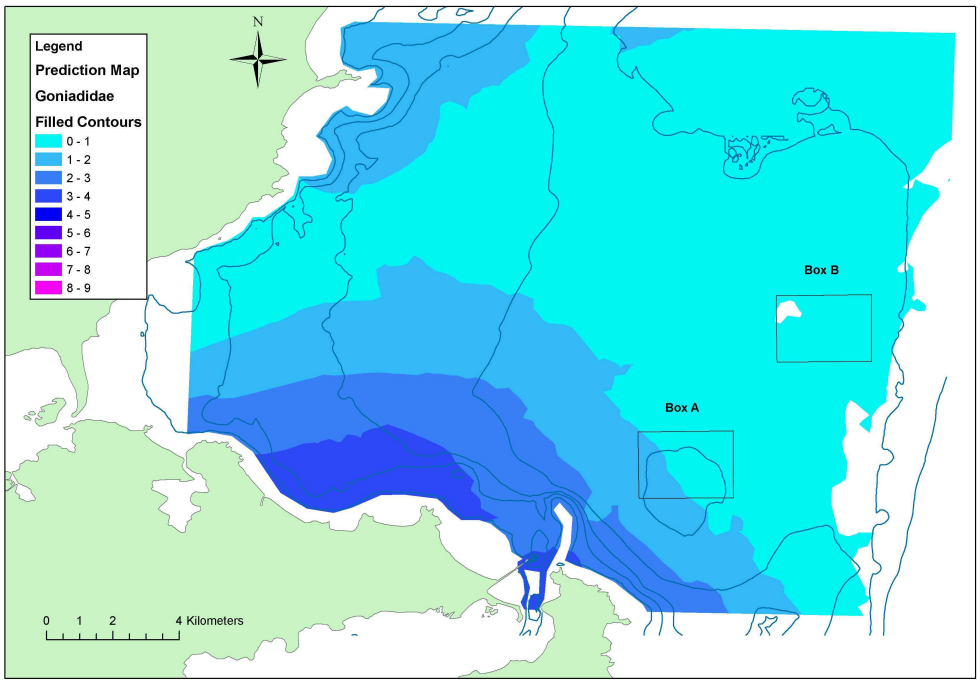
1 - 2
2 - 3
3 - 4
4 - 5
5 - 6
6 - 7
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Goniadidae
Filled Contours
0 - 1
1 - 2
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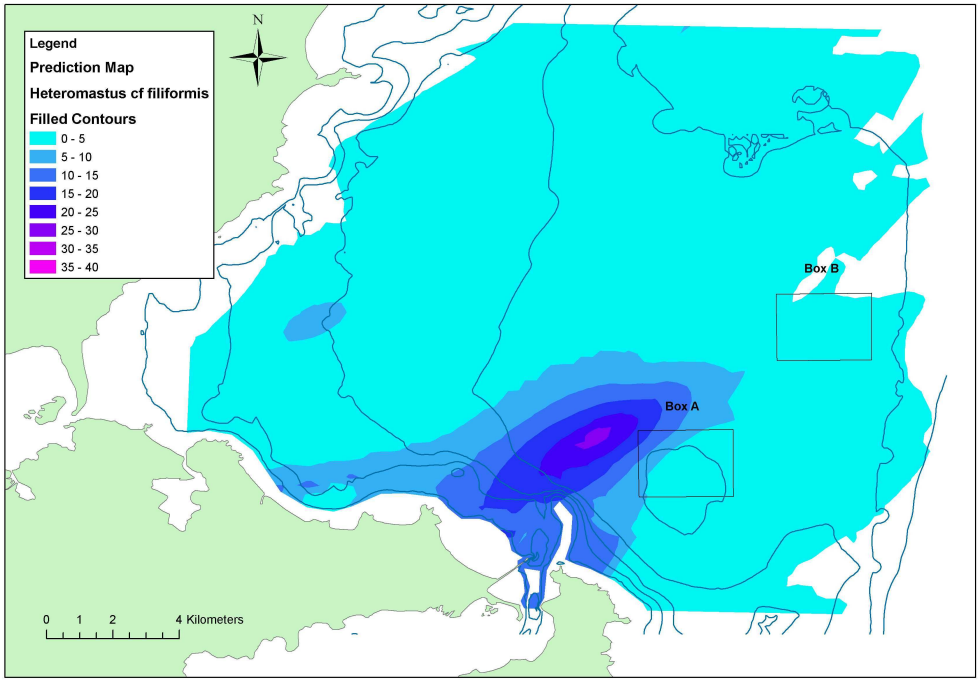
3 - 4
4 - 5
5 - 6
6 - 7
7 - 8
8 - 9
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Heteromastus cf filiformis
Filled Contours
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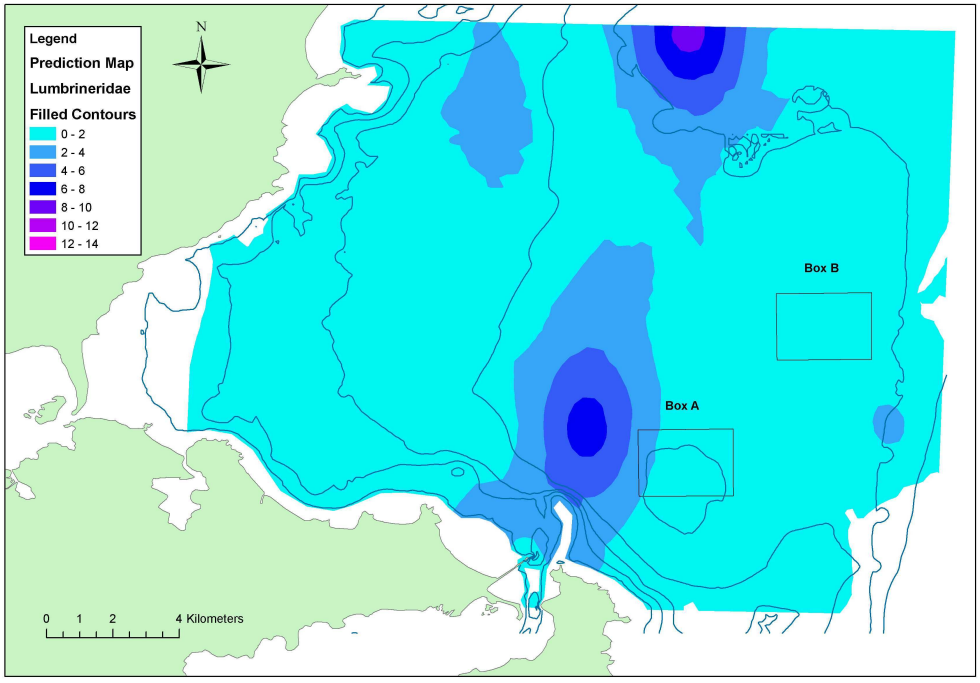
10 - 15
15 - 20
20 - 25
25 - 30
30 - 35
35 - 40
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Lumbrineridae
Filled Contours
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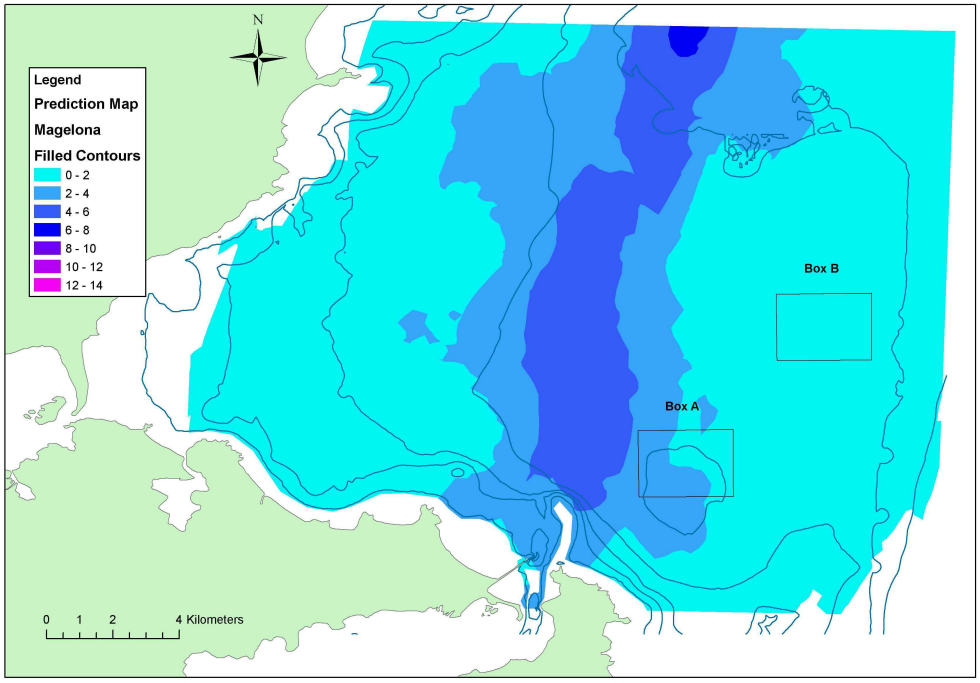
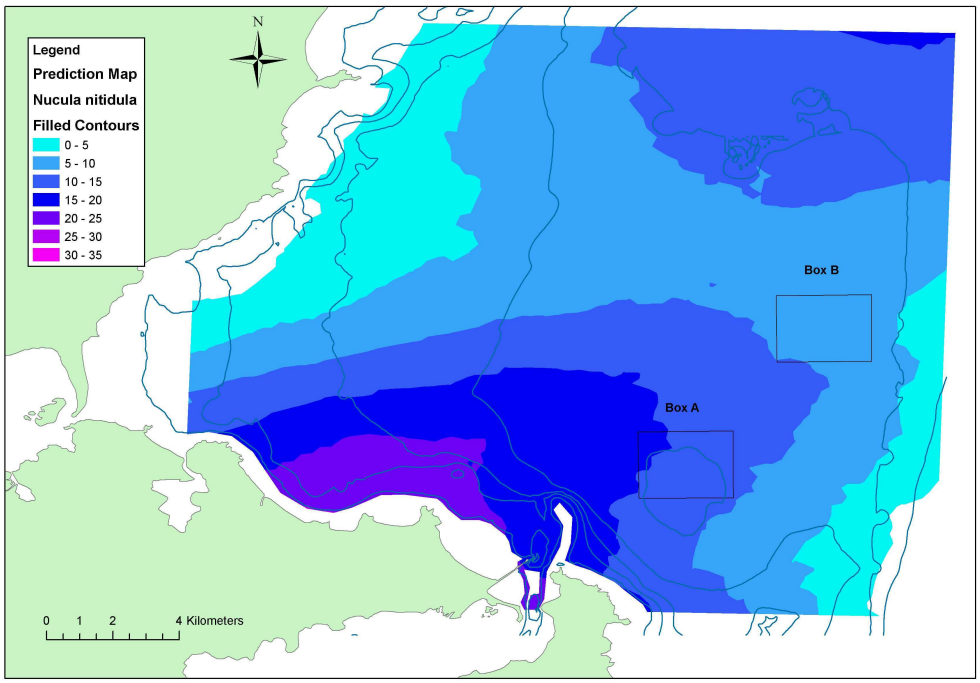
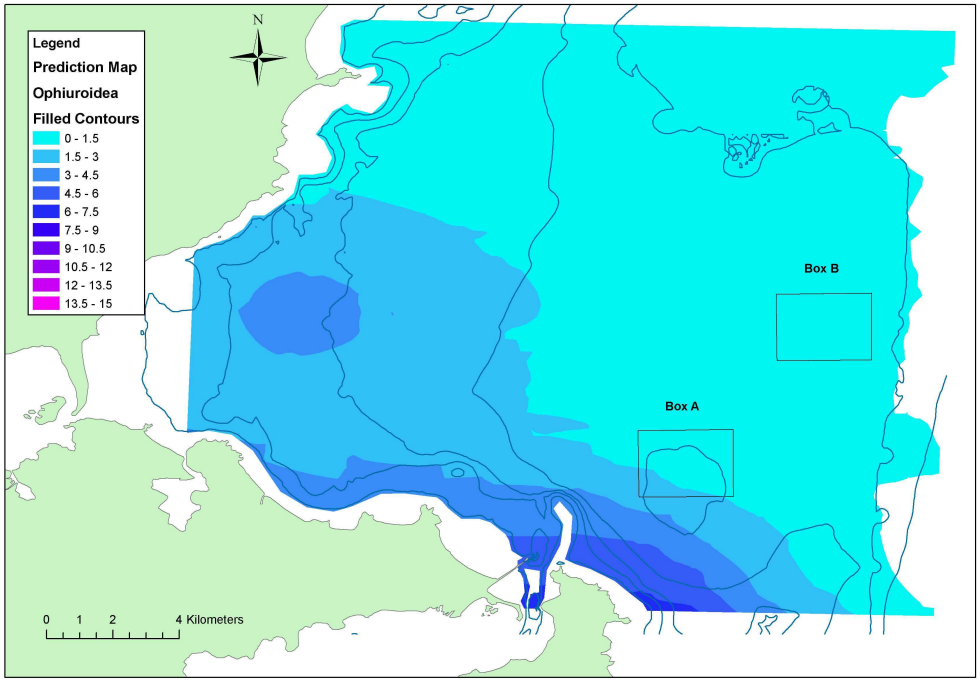
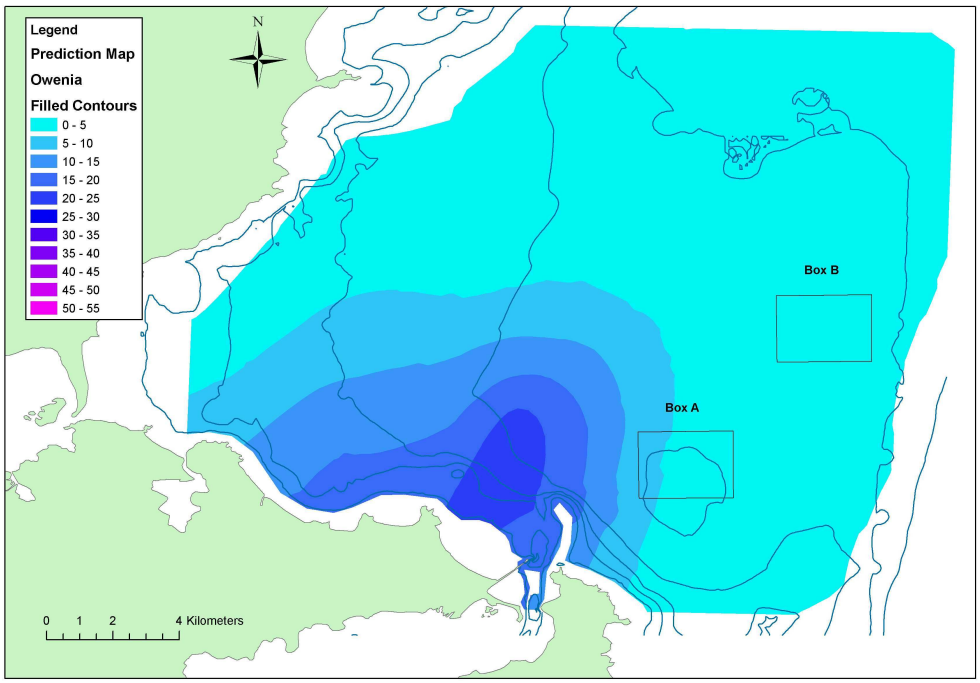
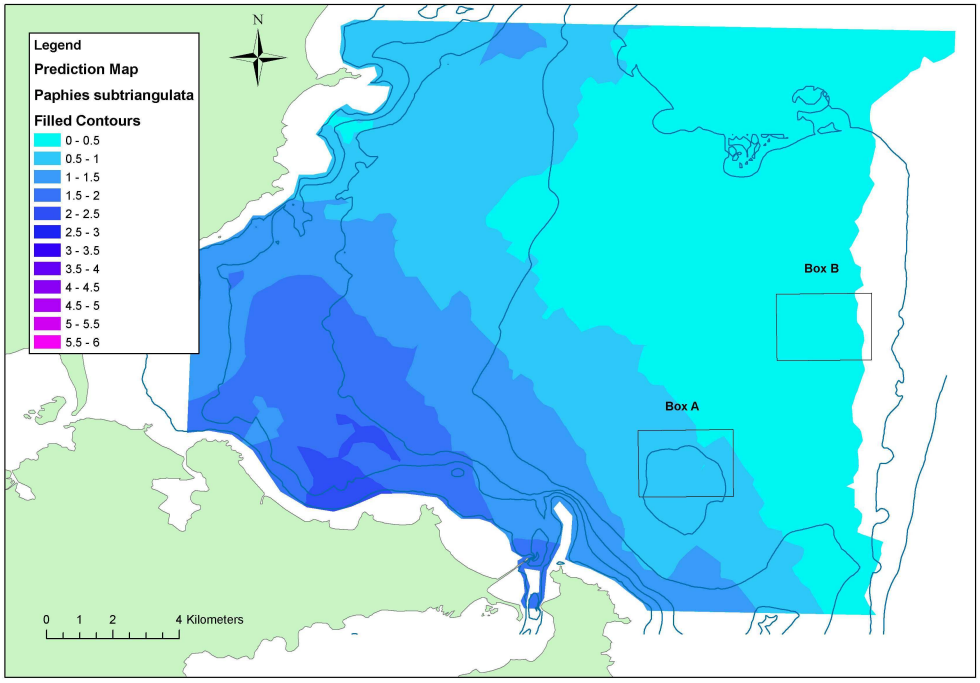
2 - 4
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
N
Box B
Box A
0 1 2 4 Kilometers

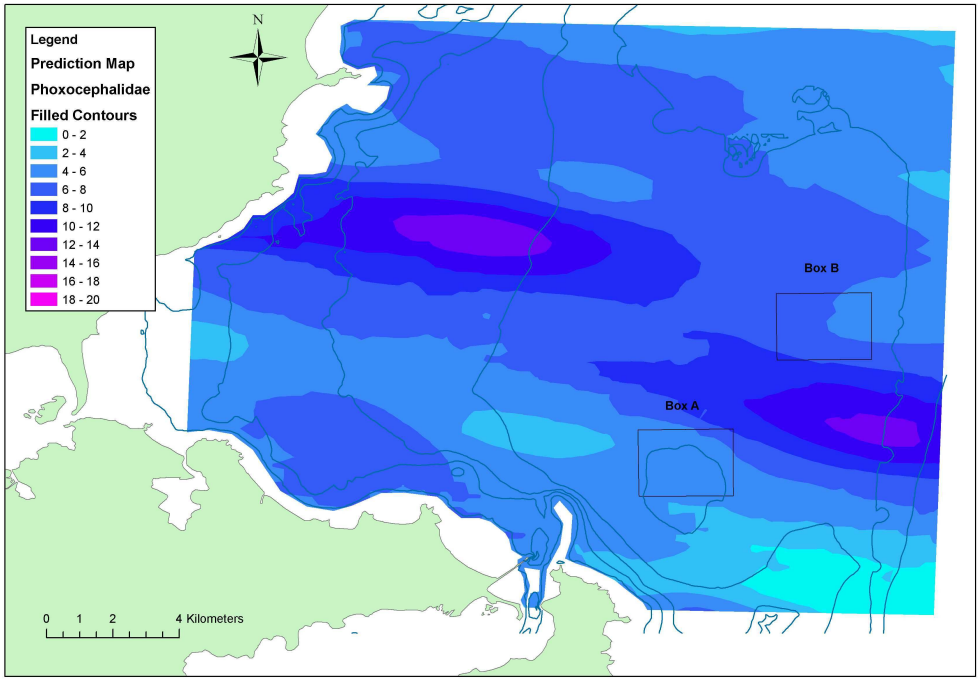

N
Legend
Prediction Map
Magelona
Filled Contours
0 - 2
2 - 4
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
Box B
Box A
0 1 2 4 Kilometers

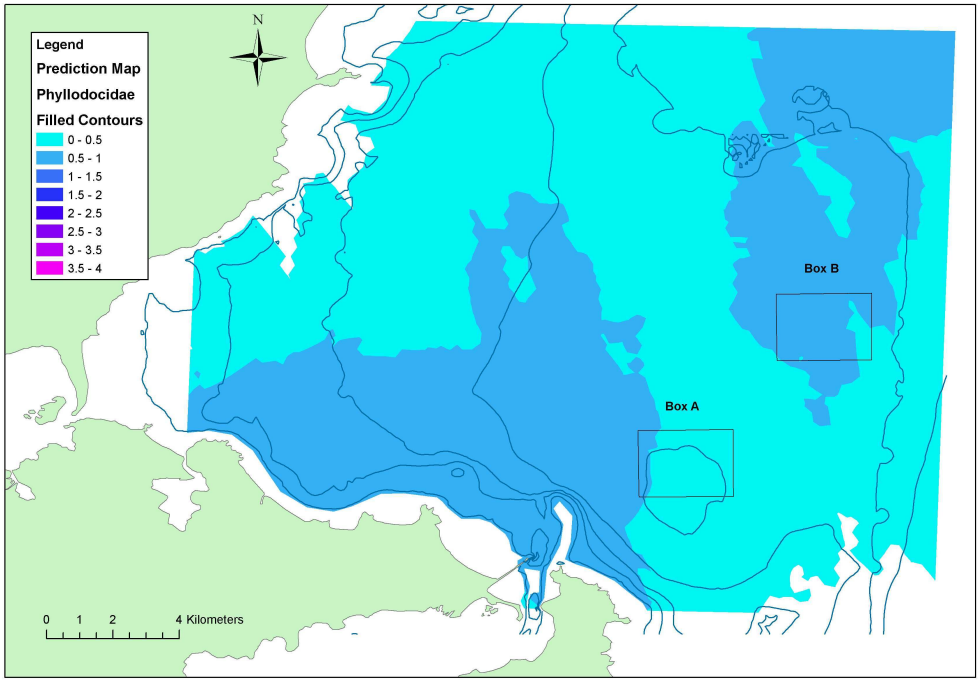

N
Legend
Prediction Map
Nucula nitidula
Filled Contours
0 - 5
5 - 10
10 - 15
15 - 20
20 - 25
25 - 30
30 - 35
Box B
Box A
0 1 2 4 Kilometers

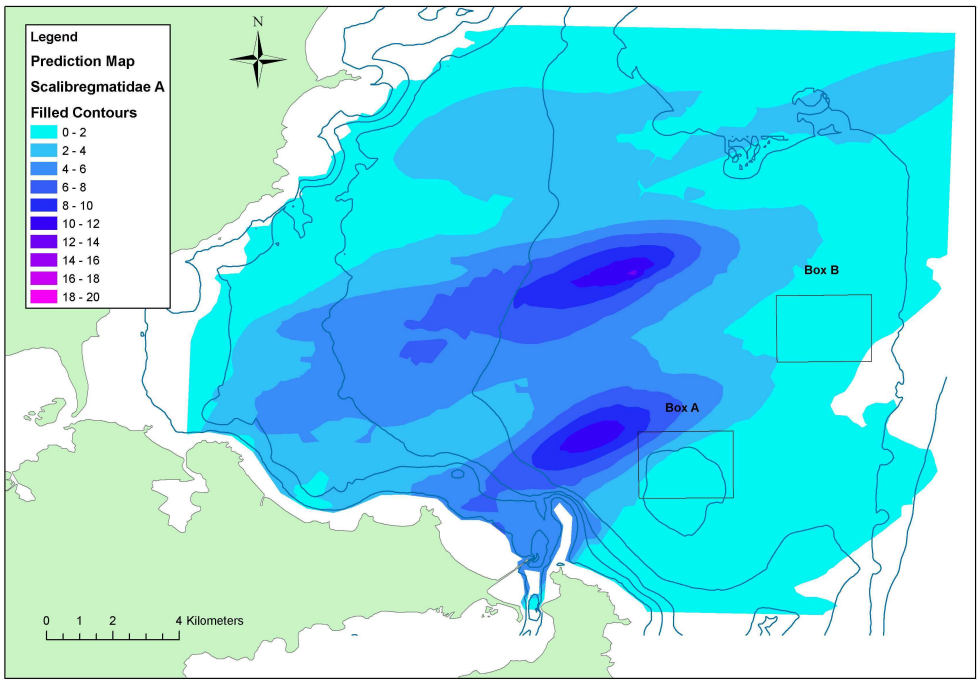

Legend
Prediction Map
Ophiuroidea
Filled Contours
0 - 1.5
1.5 - 3
3 - 4.5
4.5 - 6
6 - 7.5
7.5 - 9
9 - 10.5
10.5 - 12
12 - 13.5
13.5 - 15
N
Box B
Box A
0 1 2 4 Kilometers

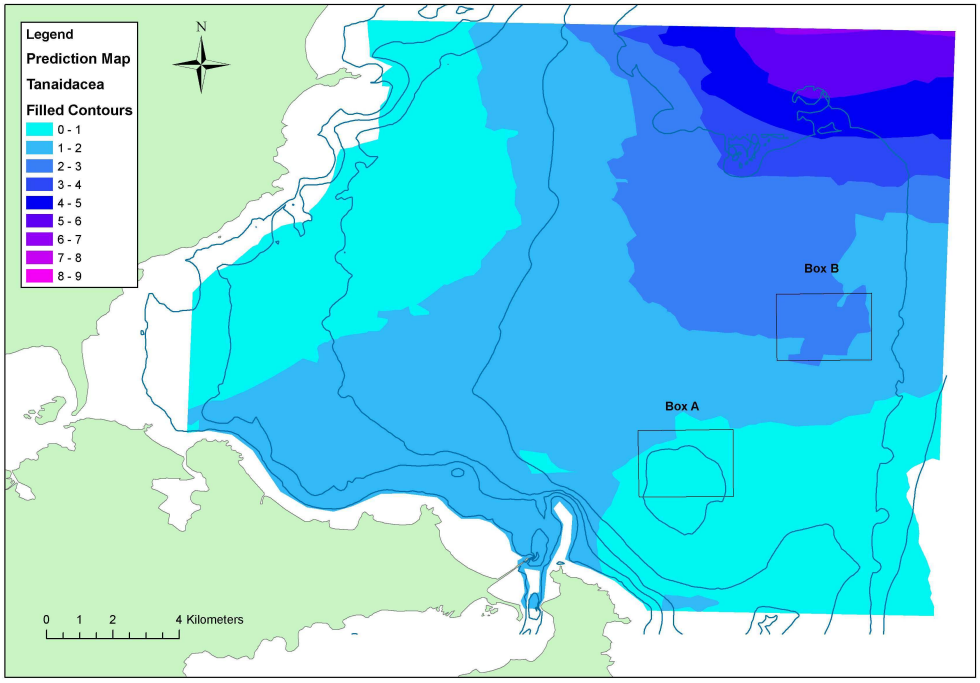

Legend
Prediction Map
Owenia
Filled Contours
0 - 5
5 - 10
10 - 15
15 - 20
20 - 25
25 - 30
30 - 35
35 - 40
40 - 45
45 - 50
50 - 55
N
Box B
Box A
0 1 2 4 Kilometers

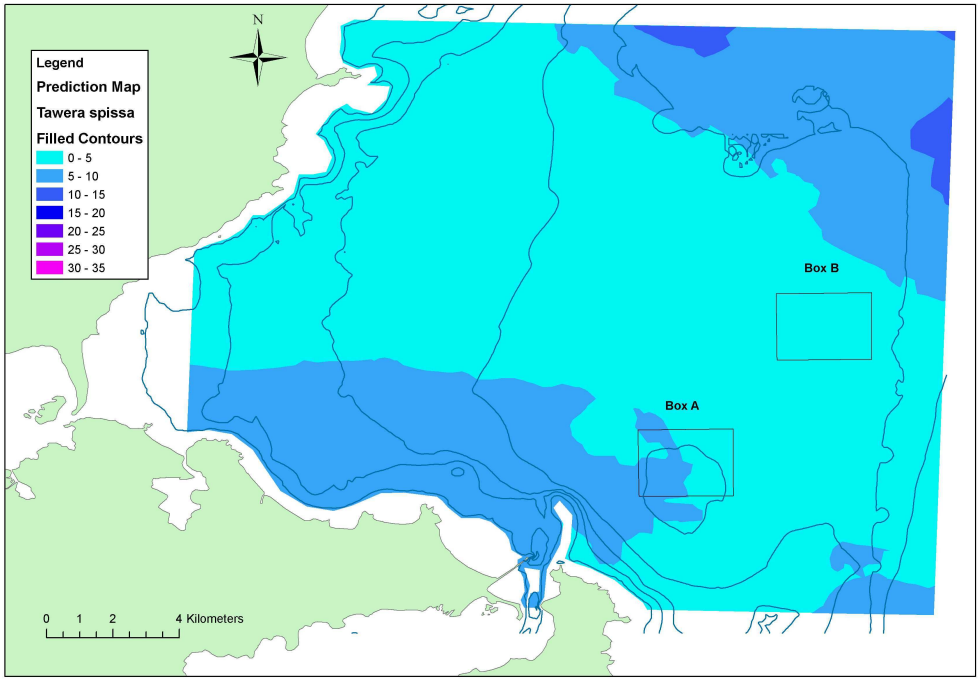

Legend
Prediction Map
Paphies subtriangulata
Filled Contours
0 - 0.5
0.5 - 1
1 - 1.5
1.5 - 2
2 - 2.5
2.5 - 3
3 - 3.5
3.5 - 4
4 - 4.5
4.5 - 5
5 - 5.5
5.5 - 6
N
Box B
Box A
0 1 2 4 Kilometers

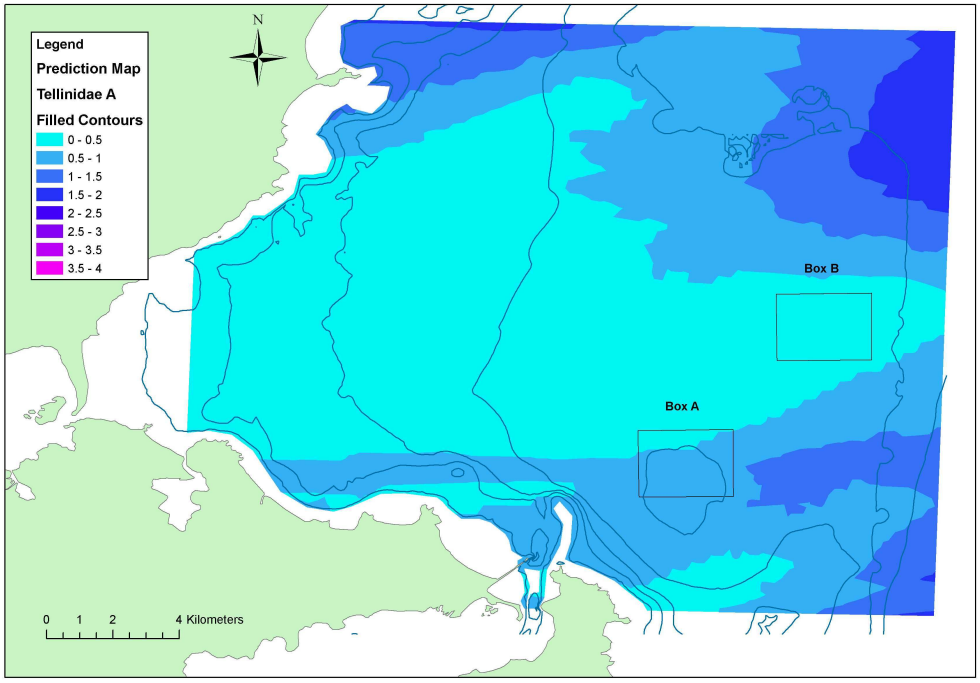

Legend
Prediction Map
Phoxocephalidae
Filled Contours
0 - 2
2 - 4
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
14 - 16
16 - 18
18 - 20
N
Box B
Box A
0 1 2 4 Kilometers

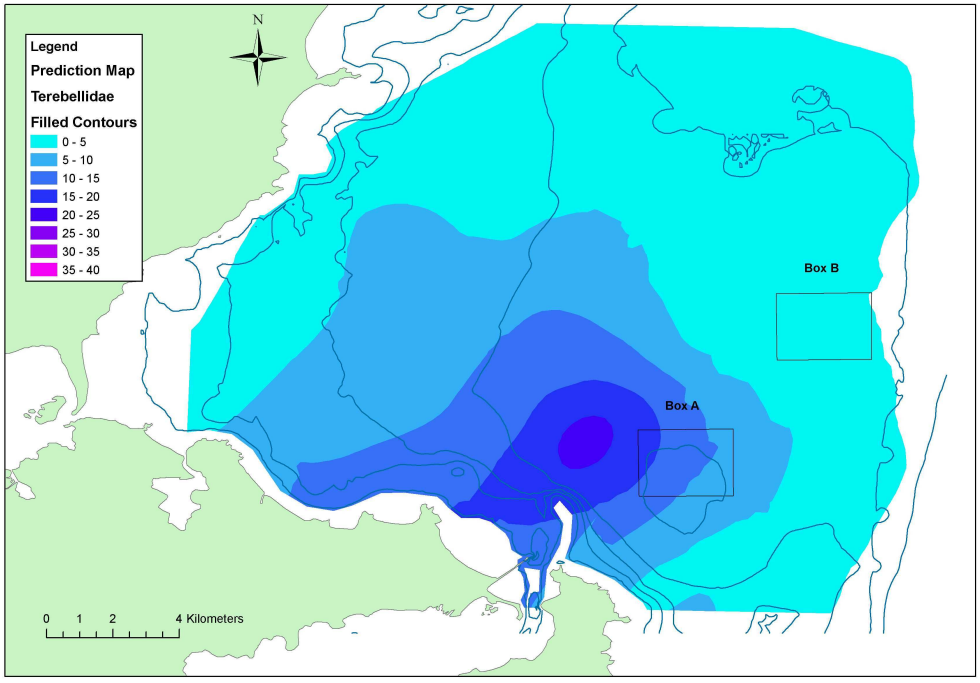

Legend
Prediction Map
Phyllodocidae
Filled Contours
0 - 0.5
0.5 - 1
1 - 1.5
1.5 - 2
2 - 2.5
2.5 - 3
3 - 3.5
3.5 - 4
N
Box B
Box A
0 1 2 4 Kilometers

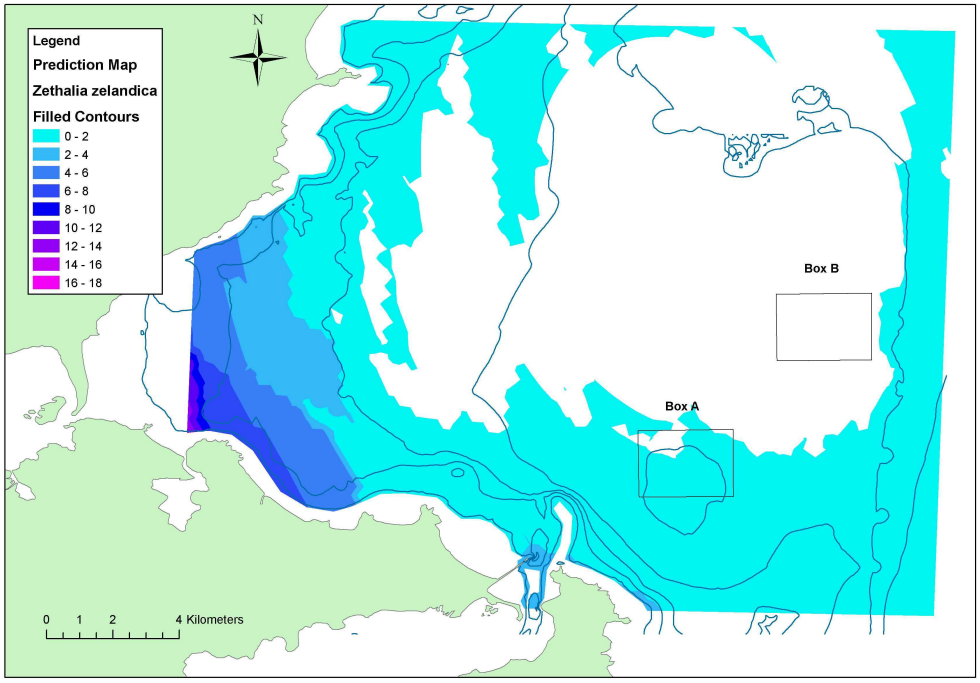

Legend
Prediction Map
Scalibregmatidae A
Filled Contours
0 - 2
2 - 4
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
14 - 16
16 - 18
18 - 20
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Tanaidacea
Filled Contours
0 - 1
1 - 2
2 - 3
3 - 4
4 - 5
5 - 6
6 - 7
7 - 8
8 - 9
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Tawera spissa
Filled Contours
0 - 5
5 - 10
10 - 15
15 - 20
20 - 25
25 - 30
30 - 35
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Tellinidae A
Filled Contours
0 - 0.5
0.5 - 1
1 - 1.5
1.5 - 2
2 - 2.5
2.5 - 3
3 - 3.5
3.5 - 4
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Terebellidae
Filled Contours
0 - 5
5 - 10
10 - 15
15 - 20
20 - 25
25 - 30
30 - 35
35 - 40
N
Box B
Box A
0 1 2 4 Kilometers


Legend
Prediction Map
Zethalia zelandica
Filled Contours
0 - 2
2 - 4
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
14 - 16
16 - 18
N
Box B
Box A
0 1 2 4 Kilometers

10. Appendix IV – Comparison of Box A and Box B

N = 6 grabs per box. Numbers are summed from all replicates in sites 26 and 27 (Box A) and 20 and 21 (Box B).

Taxon	Box A	Box B
Antisolarium egenum	883	64
Cirratulidae sp.	61	177
Aglaophamus sp. A	64	84
Nucula nitidula	70	43
Terebellidae	72	1
Phoxocephalidae sp.	30	35
Spiophanes cf bombyx	23	38
Tawera spissa	39	17
Haustoriidae	3	44
Amphipoda	1	35
Owenia sp.	20	8
Tanaidacea	2	19
Spionidae unident.	6	14
Lysianassidae sp.	8	9
Armandia maculata	8	9
Cumacea B	4	12
Ampharetidae	14	2
Magelona sp.	11	4
Prionospio spp.	9	5
Other taxa	62	66
Total	**1390**	**686**