

**BENTHIC HABITATS OF
THE DELAWARE BAY**

Benthic Habitats of Delaware Bay

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INTRODUCTION

This section describes and maps the major physical habitats of the Delaware Bay seafloor. We used information on benthic organisms, their distribution and their relationships to physical features, to delimit a distinct set of environments representing the variety of benthic habitats in the Bay. As individual species are adapted to variations in depth, sediment size, seabed topography and salinity, we examined these factors in relationship to the organism composition and classified them into basic types to illustrate the diversity of conditions existing on the seafloor. We hope that this benthic habitat map of the Delaware Bay, based on previously collected data, will provide a better understanding of the abundance and distribution of seafloor habitat types.

Benthic organisms are those that inhabit the sea floor; from the Greek word benthos, meaning “depths of the sea.” Based on a just a small sample (246 samples), the seafloor habitats of the Delaware Bay contain over 300 species in 8 phyla including:

- 106 species of arthropods (crabs, lobsters, shrimp, barnacles)
- 75 species of mollusks (clams, scallops, squid, limpets, sea slugs, snails)
- 130 species of annelids (sea worms)
- 8 species of echinoderms (sea stars, sea urchins, sea cucumbers, sand dollars)
- 5 species of cnidarians (corals, anemones, jellyfish)
- 4 species of chordates (sea squirts)
- 1 species of poriferans (sponges)
- 6 species of nemerteans (ribbon worms)

The distributions and life histories of benthic organisms are tied to their physical environment. Filter feeders tend to dominate on shallow sandy bottoms while deposit feeders, may dominate in fine-grained mud. It is these distinct physical habitats that we identified, characterized, and mapped.

This chapter represents an initial effort to define and map marine benthic habitats using information on organism distributions combined with interpolated data on bathymetry, sediment grain size, and seafloor topography. The goal was to produce a bay-wide map of broadly-defined, but distinct with respect to the organism groups found within them.

This work is builds on the methods developed in the Nature Conservancy’s Northwest Atlantic Marine assessment, (Green et al. 2010) particularly those described in chapter 3 - Benthic Habitats.

Please note that critical steps of accuracy assessment, cross-validation using independent datasets, comparisons with demersal fish habitat, and final expert peer review are ongoing

Definition of Target Habitats

The goal of this work was to identify and map the major benthic habitat types in the Delaware Bay. We defined a benthic habitat as a group of organisms repeatedly found together within a specific environmental setting. For example, silt flats in deep water typified by a specific suite of amphipods, clams, whelks and snails might be one habitat, while sand flats in shallow water might be another, providing it supports a different set of organisms. Conservation of these habitats is necessary to protect the full diversity of species that inhabit the seafloor, and to maintain the ecosystem functions of benthic communities.

METHODS

To design a conservation plan for benthic diversity in the Delaware Bay it is essential to have some understanding of the extent and location of various benthic habitats (e.g. a map). Fortunately, the challenge of mapping seafloor habitats has produced an extensive body of research (see Kostylev et al. 2001; Green et al. 2005; Auster 2006; World Wildlife Fund 2006; Todd and Greene 2008). In addition, comprehensive seafloor classification schemes have been proposed by many authors (see Dethier 1992; Brown 1993, European Environmental Agency 1999; Greene et al. 1999; Allee et al. 2000; Brown 2002; Conner et al 2004; Davies et al. 2004; Greene et al. 2005; Madden et al. 2009; Valentine et al. 2005; Kutcher 2006; and see reviews in National Estuarine Research Reserve System 2000 and Lund and Wilbur 2007). During development of the benthic map for the Nature Conservancy's Northwest Atlantic Marine Assessment (Anderson et al. 2010 in Greene et al. 2010), we reviewed the literature on seafloor classification, and examined the variety of approaches already utilized in order to develop the methodology used here.

Many of the existing schemes base their classifications on physical factors such as bathymetry, sediment grain size, sediment texture, salinity, bottom temperature, and topographic features. This is logical as there is ample evidence that benthic distribution patterns are associated with many of these variables. For example, temperature is correlated with the community composition of benthic macroinvertebrates (Theroux and Wigley 1998); substrate type is correlated with community composition and abundance of both the invertebrates and demersal fish (Auster et al. 2001; Stevenson et al. 2004); habitat complexity is correlated with species composition, diversity, and richness (Etter and Grassle 1992; Kostylev et al. 2001; Serrano and Preciado 2007, reviews in Levin et al. 2001); and depth is correlated with abundance, richness, and community composition (Stevenson et al. 2004).

The approach used here builds on existing schemes both explicitly and implicitly, and results can be readily compared to them. However, the goal of this assessment was to produce a map of broadly-defined benthic habitats in Bay using readily available information, and we are not proposing a new classification system.

Biological Factors: Benthic Organisms

The map of benthic habitats presented here is based directly on the distribution and abundance of benthic organisms in Delaware Bay, and the knowledge of these species and their distributions comes

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largely from seafloor samples described below. In the analysis of this data, groups of species with shared distribution patterns were identified, then thresholds in the physical factors were identified that correlated with those patterns. Specifically, three basic steps were followed: 1) quantitative analysis of the grab samples to identify distinct and reoccurring assemblages of benthic organisms, 2) recursive partitioning to relate the species assemblages to physical factors (bathymetry, sediment types, and seabed topographic forms), and 3) mapping the habitats based on the statistical relationships between the organism groups and the distribution of the physical factors. Although organism distributions were used to identify meaningful thresholds and cutoffs in the physical variables, the final habitat maps are composed solely of combinations of enduring physical factors and are thus closely related to the maps and classification schemes proposed by others.

This study was made possible by access to 234 samples of abundance and biomass data collected by the Delaware Estuary Benthic Inventory Partnership for the Delaware Estuary and EPA Region 2 and Region 3. Data Sampling occurred during Summer 2008 (for sampling protocol see EPA's NCA or PDE's DEBI QAPP) The DEBI effort was multidisciplinary and many federal, state and regional partners contributed with design, sampling, sample analysis and data analysis products. The Partnership for the Delaware Estuary (PDE), a National Estuary Program, was the coordinating entity and grantee, working closely with EPA Region 3 and the EPA Atlantic Ecology Division. As reports and additional data analysis products are at: http://www.delawareestuary.org/science_projects_baybottom.asp.

Twelve more samples were provided by the National Marine Fisheries Service's (NMFS) Northeast Fisheries Science Center (NEFSC). The NEFSC conducted a quantitative survey of macrobenthic invertebrate fauna from the mid 1950s to the early 1990s and a few of these samples included Delaware Bay. Organisms collected in each sample were identified to species, genus, or family. A thorough discussion of the NEFSC sampling methodology, gear types, history, and an analysis of the benthic dataset, including the distribution and ecology of the organisms, can be found in the publications of Wigley and Theroux (1981 and 1998).

Classification Methods

Classification analysis began with the entire 234 sea-floor samples obtained from the DEBIP and the 12 samples from NEFSC. These were combined into a sample-by-species table indicating the abundance (by count) of each species within each sample. Where possible the analysis was done at the species level but in some cases, when an organism was abundant in many samples but only identified to genus, the genus was treated as a species. Species that only occurred in one sample were removed from the data set before analyzing the data as was information on plants, egg masses, and organic debris.

Samples with similar species composition and abundance were grouped together using hierarchical cluster analysis (PCORD, McCune and Grace 2002). This technique starts with pairwise contrasts of every sample combination then aggregates the pairs most similar in species composition into a cluster. Next, it repeats the pairwise contrasts, treating the clusters as if they were single samples, and joins the next most similar sample to the existing clusters. The process is repeated until all samples are assigned to one of the many clusters. For our analysis, the Sorenson similarity index and the flexible beta linkage technique with Beta set at 25 was used as the basis for measuring similarity (McCune and Grace 2002).

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After grouping the samples, indicator species analysis was used to identify those species that were faithful and exclusive to each organism group (Dufrene and Legendre 1997). Lastly, Monte Carlo tests of significance were run for each species relative to the organism groups to identify diagnostic species for each group using the criterion of a p-value less than or equal to 0.10 (90% probability). The number of sets of clusters (testing 10 to 40) was determined by seeing which amount gave the lowest average p-value.

Physical Factors: Bathymetry, Substrate and Seabed Forms

To understand how the benthic invertebrate community distributions related to the distribution of physical factors, a spatially comprehensive data layer for each factor of interest was developed. Four aspects of seafloor structure were used: bathymetry, sediment grain size, topographic forms, and salinity. These factors were chosen because they are correlated with the distribution and abundance of benthic organisms. Data on each physical factor were compiled from separate sources and the techniques used to create a comprehensive map are discussed below.

Bathymetry

We based our bathymetry dataset on a publicly available digital elevation model for the Delaware Bay (estuarinebathymetry.noaa.gov). In order to use all of the biological samples in our analyses, we extended the bathymetry coverage upriver approximately 20 kilometers (Figure 1). To do this, we used depth-sounding points collected during the Delaware Bay and River Benthic Habitat Mapping Project ([project website](#)). We interpolated these data following the methods used for NOAA bathymetry, using linear interpolation to create a 30m DEM. We attributed each of the 246 organism samples with an estimate of the bathymetry at that point.

Geographic position: a proxy for salinity

In estuaries, salinity is an important driver of the composition of biological communities. This attribute is difficult to estimate over space because it is both annually and seasonally dynamic. Since we did not have access to an accurate map of the salinity gradient in the bay, we used a measure of Euclidean distance from the upper reach of our study area as a proxy for salinity to ensure that this environmental aspect was accounted for. Figure 2 shows a categorical map of salinity for the bay published by NOAA along with biological thresholds for our salinity proxy measure where we observed shifts in benthic species communities.

Seafloor Substrates: Soft Sediments and Hard Bottoms

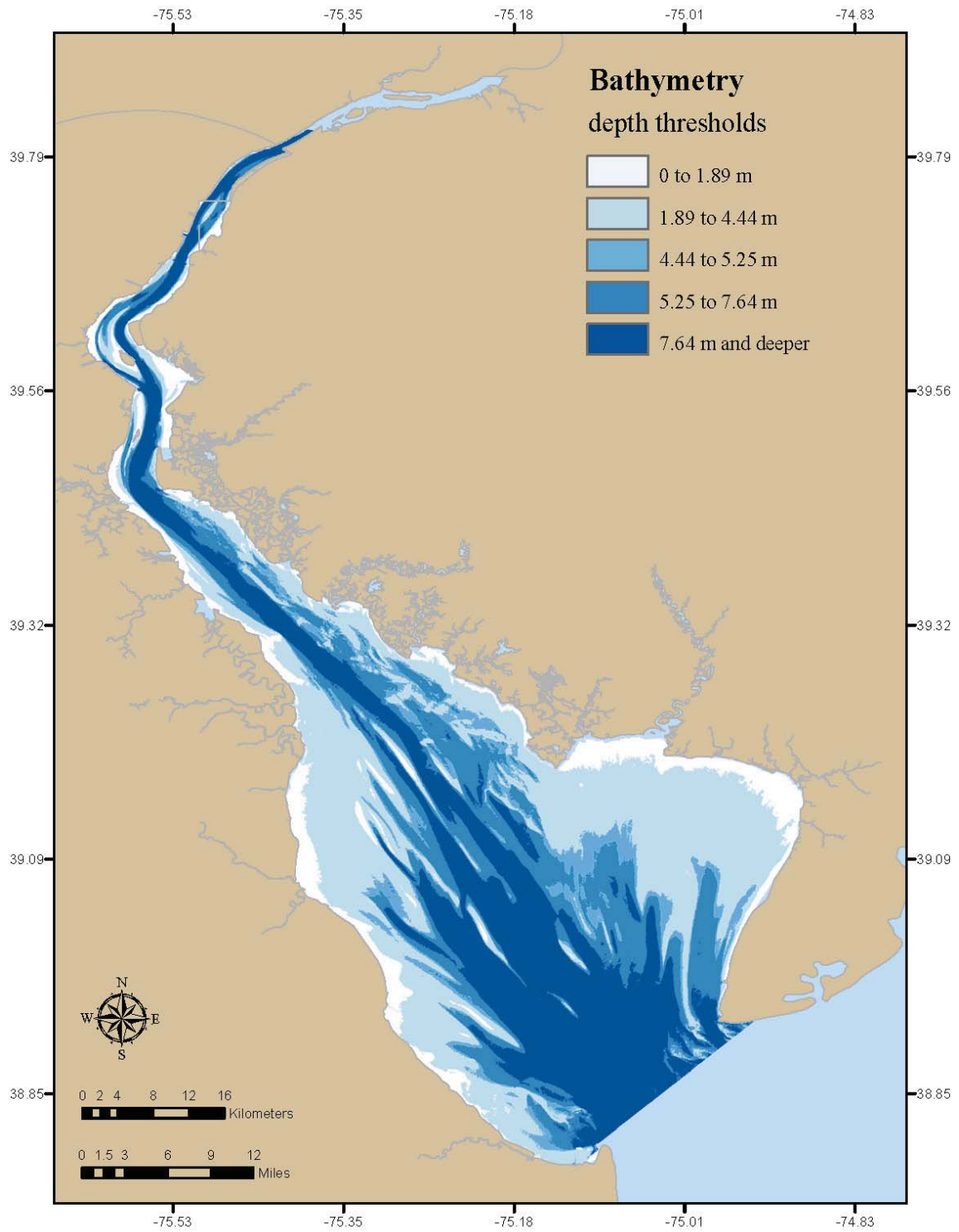
Soft Sediments and Hard Bottoms Substrate data for the entire Bay was obtained from two sources. The primary source was the Delaware Coastal Programs of Delaware Department of Natural Resources and Environmental Control (DNREC) which has initiated a benthic habitat and sub-bottom sediment mapping project using remote acoustics (i.e., Roxann Seabed Classification, Chirp Sub-Bottom Profiler, and multi-beam surface imaging system). This work will ultimately be completed on both the Delaware and New Jersey sides of the Estuary and is being supported by multiple Federal and State agencies, non-profits, and academic institutions. This highly detailed bottom substrate map is furnishing important new

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information about the geospatial character of physical conditions across the estuary. For the purposes of this study we obtained the sample points and their attributes. For interpolation purposes, we converted the information on sediment fractions to an average grain size estimate for each sample.

In addition to the DNREC samples, we obtained sediment samples from usSEABED, a regional system that brings assorted numeric and descriptive sediment data together in a unified database (Reid et al. 2005). The information includes textural, geophysical, and compositional characteristic of points collected from the seafloor, and is spatially explicit. In total we had 3,706,489 sediment samples (Figure 3).

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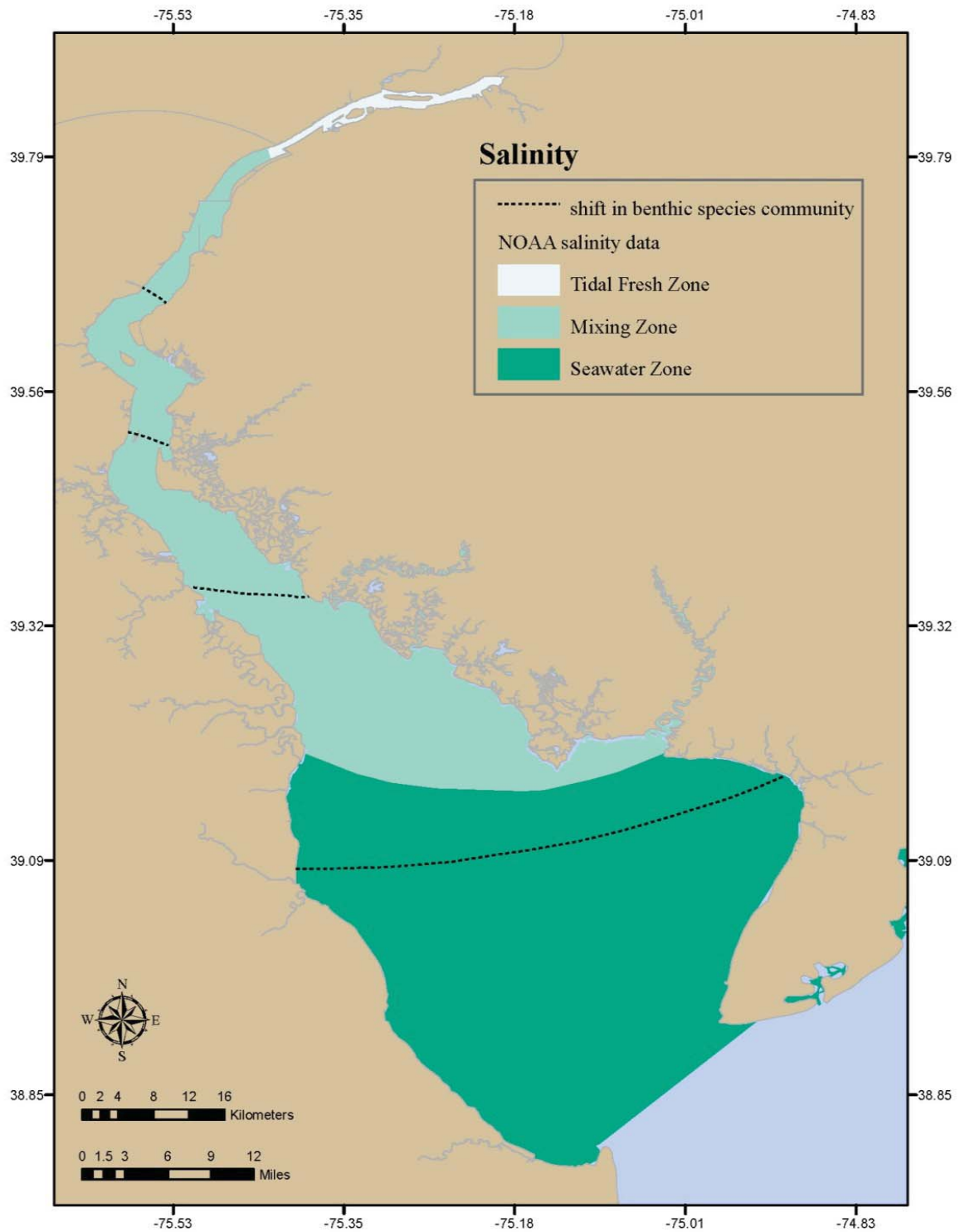


Figure 2. Salinity of the Delaware Bay: NOAA categorical delineation and ecological thresholds derived from analyses of species composition.

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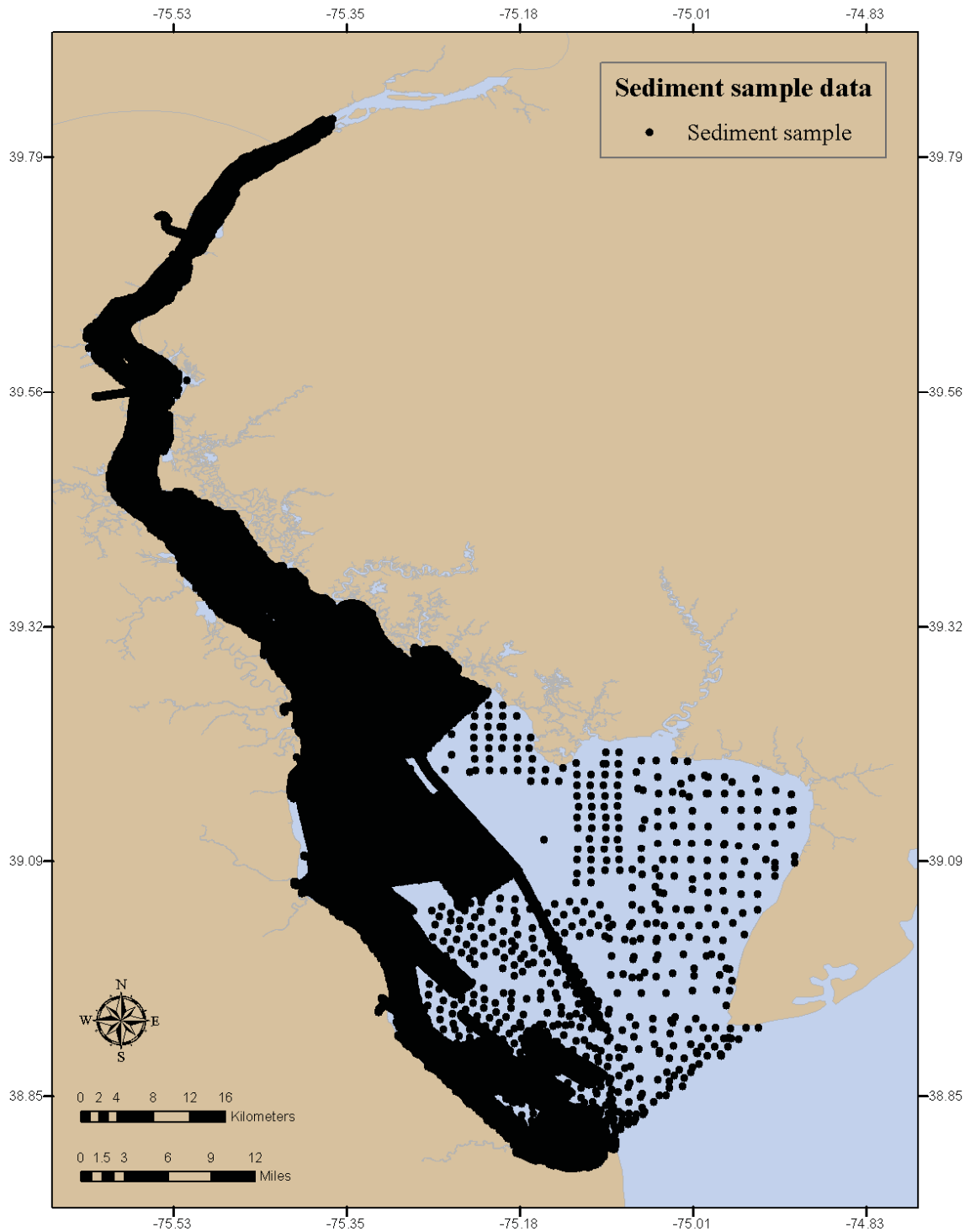


Figure 3. Distribution of the Sediment Samples. The dark areas are areas with high sampling density provided by the DNREC. The sparse areas were not sampled by the DNREC, but filled in with samples from usSEABED.

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Interpolation of the Sediment Dataset

We interpolated the sediment data set in GIS using Inverse Distance Weighting with a squared exponent of distance and a variable search radius based on the nearest 12 points. The resulting 30m resolution interpolated map was used to attribute each of the 246 organism sample points with an estimate of the average sediment grain size at that point. For map display we used a Kriging interpolation that creates a smoother version of the sediment variation (Figure 4). A separate dataset of hard bottom locations was created from the points coded as rock or shell in the DNREC data set or “solid” in the usSeabed dataset. We overlaid these areas on the soft sediment interpolation to create the final sediment map (Figure 5). These data are a conservative representation of hard bottom areas of the bay and, particularly for shell, do not represent their entire distribution in the bay.

Seabed Topographic Forms

The Delaware Bay is characterized by a moderately complex central trench surrounded by simple sand. With this in mind, the seabed form data layer was developed to characterize seafloor topography in a systematic and categorical way, relevant to the scale of benthic habitats. The units that emerge from this analysis, from high flats to depressions, represent depositional and erosional environments that typically differ in fluvial processes, sediments, and organism composition (Wigley and Theroux 1981).

Seabed topographic forms were created from relative seabed position and degree of slope of each seafloor cell. Seabed position (or topographic position) describes the topography of the area surrounding a particular 30 m cell. Calculations were based on the methods of Fels and Zobel (1995) that evaluate the elevation differences between any cell and the surrounding cells within a specified distance. For example, if the model cell is, on average, higher than the surrounding cells, then it is considered to be closer to the ridge top (a more positive seabed position value). Conversely, if the model cell is, on average, lower than the surrounding cells then it is considered closer to the slope bottom (a more negative seabed position value).

The relative position value is the mean of the distance-weighted elevation differences between a given point and all other model points within a specified search radius. The search radius was set at 100 cells after examining the effects of various radii. Position was grouped into six classes that were later simplified to three classes: The second element of the seabed forms, degree of slope, was used to differentiate between steep slopes and flat depressions. Slope was calculated as the difference in elevation between two neighboring raster cells, expressed in degrees. After examining the distribution of slopes across the region, slopes were grouped according to the thresholds outlined in Table 1.

Slope and relative position were combined to create 18 possible seabed forms ranging from high flat banks to low level bottoms. Initially, all 18 types were used in the analysis of organism relationships (Figure 6), but results suggested that they could be simplified while maintaining, or improving, their explanatory power. Therefore, the analysis was simplified into the following four categories: High flat low flat, high slope and low slope (Figure 7).

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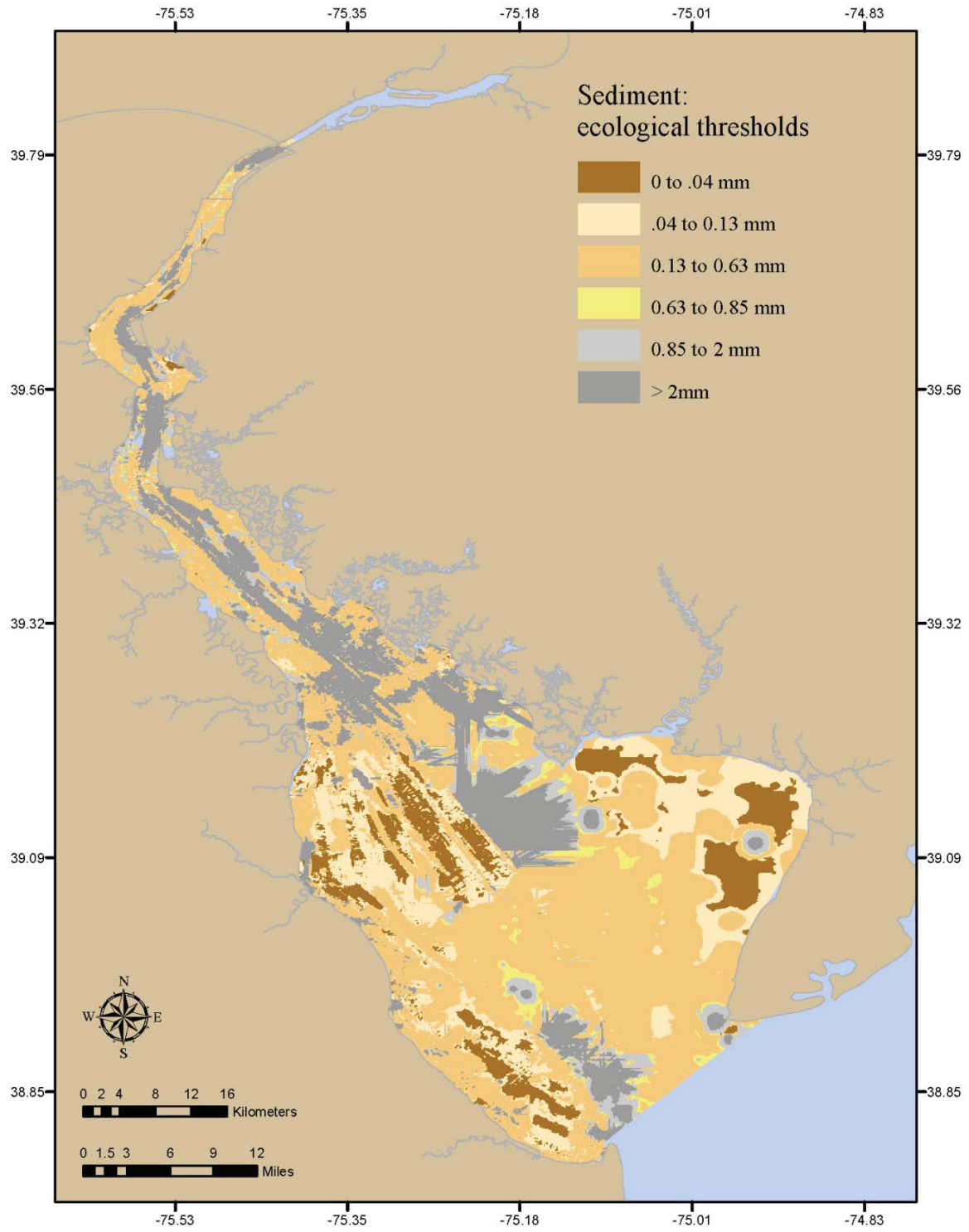


Figure 4. Interpolated map of soft sediments in Delaware Bay.

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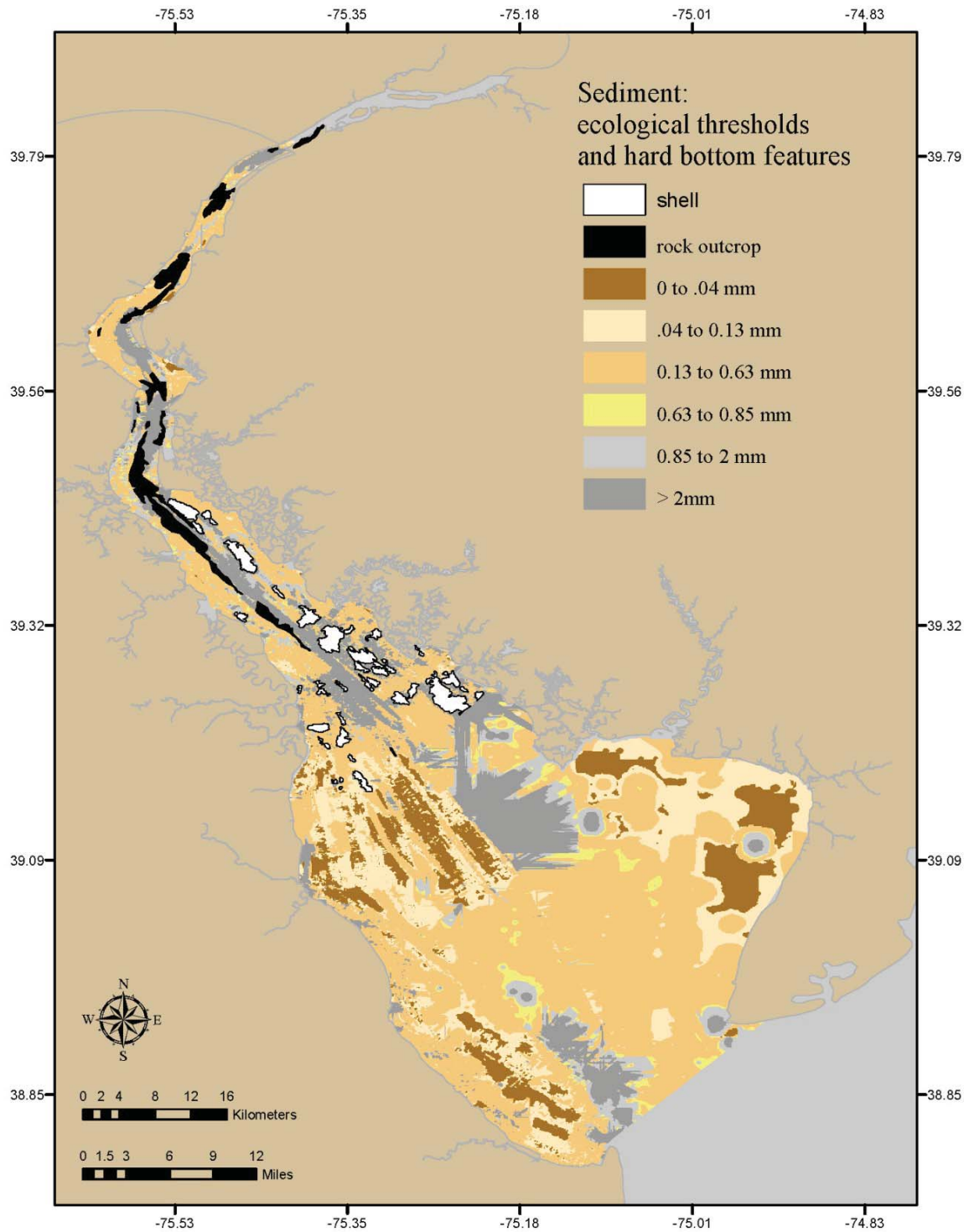


Figure 5. Soft sediment interpolation overlaid with hard bottom and shell areas. Hard bottom areas are cretaceous outcrops composed of highly compacted sand and silt. These data are a conservative representation of hard bottom areas of the bay and, particularly for shell, do not represent their entire distribution in the bay.

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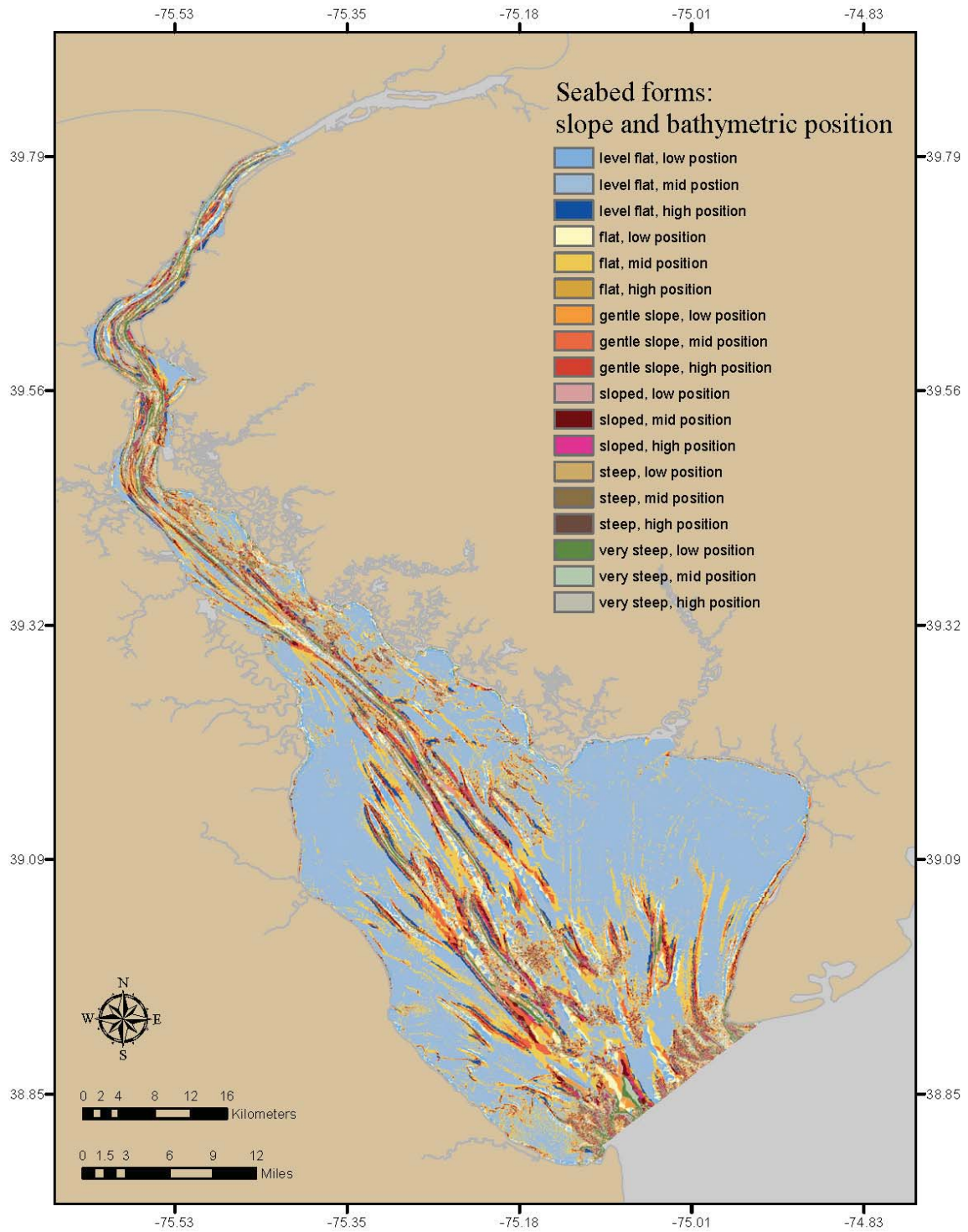


Figure 6. The eighteen-part seabed form model based on slope and position.

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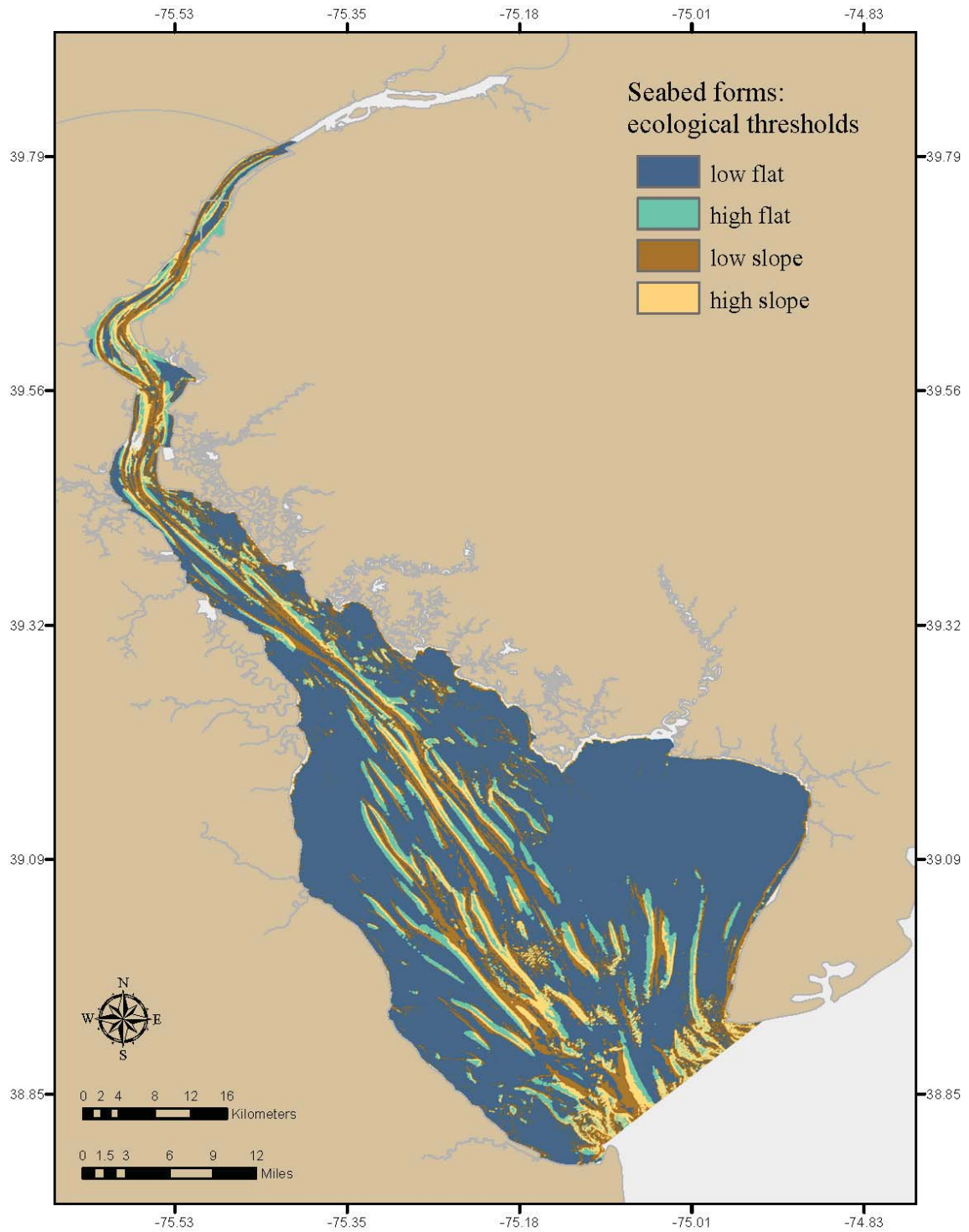


Figure 7. The simplified four-part seabed form model.

Table 1. Thresholds and simplification used in the seabed form model.

	Relative Position		
Slope	High (positive)	Mid (0)	Low (negative)
0 – 0.30 level flat	High flat	High flat	Low flat
0.30 – 1.15 flat	High flat	High flat	Low flat
1.15 – 2.30 gentle slope	High slope	High slope	Low slope
2.30 – 4.20 slope	High slope	High slope	Low slope
4.20 – 8.0 moderate slope	High slope	High slope	Low slope
8.0 + steep slope	High slope	High slope	Low slope

Linking the Organisms to Physical Factors

Recursive partitioning (JMP software package) was used to uncover relationships between benthic communities and the physical environment. Recursive partitioning is a statistical method that creates decision trees to classify members of a common population (the classification types) based on a set of dependent variables (the physical variables).

The analysis required each benthic grab sample to be attributed with the benthic community type that it belonged to, overlaid on the standardized base maps, and attributed with the information on depth, sediment grain size and seabed form appropriate to the point. Additionally, we attributed each point with the distance of the sample from the upper freshwater reach of the Bay as a proxy for salinity, as we had no direct measure of salinity. Regression trees were first built using all variables collectively to identify the variables driving organism differences. After examining the variable contributions collectively, individual regression trees were built for depth, grain size, and seabed forms to identify critical thresholds that separated sets of organism groups from each other. In recursive partitioning, these cuts are identified by exhaustively searching all possible cuts and choosing the one that best separates the dataset into non-overlapping subsets. For example, the first run of the organism groups on the bathymetry data separated the deep water samples from the shallow water samples while identifying the exact depth that most cleanly separated the two sets.

RESULTS

Based on the bathymetry dataset, the region varied in depth from 0 m at the coast to 47 m along the central trench. Critical depth thresholds (Figure 1) for benthic organisms are discussed under the organism classification. The sediment maps show a seafloor dominated by fine sand, along with large regions of finer silt. Hard bottom areas are concentrated in the upper estuary shell areas predominate in the mid and lower estuary (Figures 4 and 5).

Organism Classification

We classified the 246 data samples into 20 organism groups based species composition and abundance. A summary of the characteristic species and their indicator values for each is given in Appendix 1. This

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appendix includes a species-by-group table that gives diagnostic species for each organism group and shows its distribution across all the organisms groups. The mean indicator value and the probability of this distribution being random chance were calculated for each species in the group that it is most closely associated with. Most species don't have a common name, so only scientific names are listed. Local names can be found in Gosner (1979), Weiss (1995) and Pollock (1998) but they are often only for the family or genus, not the species.

Relationship of the organism groups to the physical factors

Salinity, or at least a proxy of distance from the upper reach, appeared to be the driving explanatory variable. This was most apparent in the initial clustering of the samples into four broad organism groups. These groups corresponded spatially to several published maps of salinity thresholds in the Bay (Figure 8 and 9, Table 2 a and b)

Table 2a. Organisms associated with group 1 (upper bay) and group 22 (mid bay). These patterns correspond spatially with fresh/brackish and brackish areas in the bay, although we did not test salinity.

Group 1			Group 22		
Fresh/Brackish (0-23,001 m)	Importance value	P*	Brackish (23,001 -52,240 m)	Importance value	P*
Annelida : Oligochaeta			Annelida : Oligochaeta		
Limnodrilus hoffmeisteri	44.9	0.0002	Tubificoides spp.	32.6	0.0002
Limnodrilus maumeensis	10	0.0026	Annelida : Polychaeta		
Limnodrilus udekemianus	13	0.0004	Boccardiella ligERICA	26.9	0.0002
Tubificidae imm.	51.7	0.0002	Neanthes succinea	21.9	0.0002
Annelida : Polychaeta			Arthropoda : Amphipoda		
Marenzelleria viridis	31	0.0002	Leptocheirus plumulosus	7	0.0952
Arthropoda : Amphipoda			Arthropoda : Isopoda		
Apocorophium lacustre	26.8	0.0002	Cyathura polita	45.7	0.0002
Gammarus daiberi	55.5	0.0002	Mollusca : Bivalvia		
Arthropoda : Chironomidae			Macoma balthica	19.9	0.0002
Cryptochironomus sp.	7.8	0.0168	Macoma mitchelli	7.2	0.0336
Polypedilum halterale-grp.	28	0.0002	Mulinia lateralis	14.4	0.0126
Procladius sp.	6.5	0.0158	Rangia cuneata	19.7	0.0002
Arthropoda : Isopoda			Nemertina		
Cassidinidea ovalis	7.8	0.0092	Carinoma tremaphoros	22.1	0.0002
Chiridotea almyra	43.2	0.0002			
Mollusca : Bivalvia					
Corbicula fluminea	37.7	0.0002			
Sphaeriidae	5.2	0.0356			

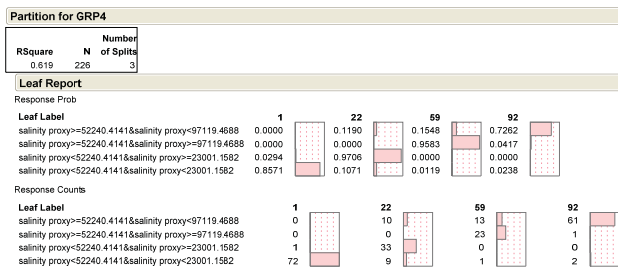
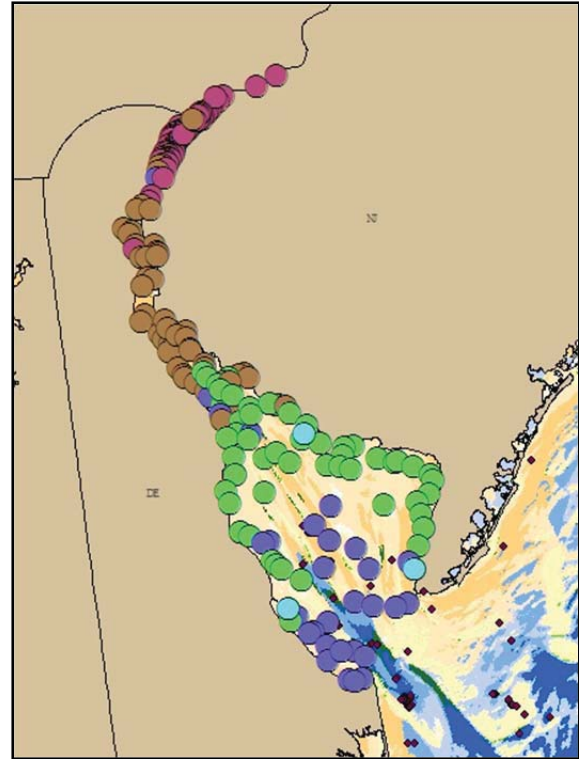
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Table 2b. Organisms associated with group 92 (lower bay) and group 59 (lowest). These patterns correspond spatially with saline and marine areas in the bay, although we did not test salinity.

Group 92			Group 59		
Saline 1 (52,240 -97,119 m)	Importance value	p*	Saline 2 (>97,119 m)	Importance value	p*
Annelida : Polychaeta			Annelida : Oligochaeta		
Ampharetidae	19	0.0002	Oligochaeta	36.8	0.0002
Diopatra cuprea	6.2	0.0222	Annelida : Polychaeta		
Eteone heteropoda	25.3	0.0002	Amastigos caperatus	35.1	0.0002
Exogone dispar	7.8	0.0052	Aricidea catherinae	24.3	0.0002
Glycera dibranchiata	6.7	0.0414	Asabellides oculata	19	0.0004
Glycinde solitaria	58.7	0.0002	Brania wellfleetensis	6.9	0.0208
Heteromastus filiformis	19.4	0.0036	Caulieriella venefica	8.1	0.0028
Leitoscoloplos robustus	18.5	0.0002	Dipolydora socialis	4.2	0.0820
Mediomastus ambiseta	54.5	0.0002	Drilonereis longa	12.1	0.0002
Onuphidae	4.7	0.0340	Glycera americana	10.8	0.0004
Paraprionospio pinnata	25.1	0.0002	Glyceridae	4.2	0.0780
Pectinaria gouldii	38.4	0.0002	Leitoscoloplos spp.	20.8	0.0004
Podarkeopsis levifuscina	4.7	0.0384	Nephtyidae	21.6	0.0002
Polycirrus eximius	4.4	0.0648	Nephtys bucera	10.8	0.0016
Polydora cornuta	15.2	0.0014	Nephtys picta	24.3	0.0002
Sabellaria vulgaris	20.8	0.0002	Nereididae	8.1	0.0026
Spiochaetopterus costarum	36.1	0.0002	Paraois fulgens	6.6	0.0180
Streblospio benedicti	32.4	0.0002	Parapionosyllis longicirrata	18.9	0.0002
Arthropoda : Amphipoda			Phyllodoce arenae		
Ampelisca abdita	48.2	0.0002	Polynoidae	5.4	0.0246
Ampelisca spp.	5.7	0.0660	Scoloplos spp. Or Scolelepis spp	12.1	0.0002
Ampelisca vadorum	17.4	0.0002	Sphaerosyllis erinaceus	5.4	0.0222
Batea catharinensis	5.8	0.0176	Spiophanes bombyx	16.2	0.0002
Cerapus tubularis	17.2	0.0008	Tharyx sp. A	38.8	0.0002
Elasmopus laevis	4.7	0.0328	Arthropoda : Amphipoda		
Gammarus palustris	10.9	0.0012	Acanthohaustorius intermedius	5.4	0.0264
Incisocalloipe aestuarius	4.4	0.0674	Acanthohaustorius millsi	5.4	0.0228
Paracaprella tenuis	11.3	0.0042	Americhelidium americanum	9.4	0.0030
Arthropoda : Cumacea			Ampelisca verrilli	23.4	0.0002
Cyclaspis varians	28	0.0002	Erichthonius brasiliensis	10.9	0.0026
Leucon americanus	35.1	0.0002	Haustorius canadensis	8.1	0.0042
Arthropoda : Decapoda			Listriella barnardi	5.4	0.0268
Eurypanopeus depressus	7.8	0.0056	Microtopopus raneyi	15.9	0.0006
Arthropoda : Isopoda			Monocorophium tuberculatum	22.6	0.0002
Edotea triloba	37.9	0.0002	Parametopella cypris	5.4	0.0274
Synidotea laticauda	14	0.0012	Protohaustorius cf. deichmannae	18.9	0.0002
Chordata : Ascidiacea			Rhepoxynius hudsoni	20.2	0.0002
Molgula manhattensis	18.7	0.0002	Unciola serrata	17.5	0.0004
Cnidaria : Anthozoa			Arthropoda : Cumacea		
Diadumene leucolena	8	0.0174	Oxyurostylis smithi	23.3	0.0002
Edwardsia elegans	6.2	0.0210	Arthropoda : Decapoda		
Mollusca : Gastropoda			Brachyura	6.8	0.0130
Acteocina canaliculata	57.4	0.0002	Pagurus spp.	14.2	0.0002
Astyris lunata	10.6	0.0058	Pinnixa retinens	5.4	0.0266
Boonea seminuda	6.3	0.0152	Pinnixa spp.	5.9	0.0320
Crepidula fornicata	6.2	0.0222	Arthropoda : Isopoda		
Eupleura caudata	6.2	0.0186	Chiridotaea caeca	8.1	0.0058
Ilyanassa obsoleta	14.1	0.0002	Arthropoda : Tanaidacea		
Odostomia engonia	32.3	0.0002	Tanaissus psammophilus	8.1	0.0042
Rictaxis punctostriatus	68.3	0.0002	Chordata : Ascidiacea		
Nemertina			Ascidiacea	9.1	0.0046
Amphiporus bioculatus	21.9	0.0002	Chordata : Cephalochordata		
Carinomella lactea	13	0.0022	Branchiostoma caribaeum	5.4	0.0280
Micrura leidyi	17.9	0.0004	Mollusca : Bivalvia		
Platyhelminthes : Turbellaria			Cylocardia borealis	5.4	0.0244
Stylochus ellipticus	25	0.0002	Ensis directus	32.3	0.0002
			Gemma gemma	9.4	0.0926
			Nucula proxima	18.8	0.0002
			Spisula solidissima	13.5	0.0002
			Tellina agilis	65.3	0.0002
			Yoldia limatula	8.1	0.0040
			Mollusca : Gastropoda		
			Crepidula plana	7.5	0.0118
			Crepidula spp.	26.9	0.0002
			Kurtziella astrostyla	5.9	0.0322
			Nassarius trivittatus	14.4	0.0006
			Nudibranchia	6.3	0.0370
			Polinices duplicatus	5.9	0.0282
			Nemertina		
			Cerebratulus lacteus	5.1	0.0638
			Nemertina	12.3	0.0090

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Figure 8. The distribution of the four broad organism groups across the bay. Data samples are color coded to groups where purple corresponds to group 1 (distance 0-23,001 m, “fresh/brackish”); brown corresponds to group 22 (distance 23,001 to 54,000, “brackish”); green corresponds to group 91 (distance 54,000 to 97,119 m, “saline”), and blue corresponds to group 59 (distance > 97,119 m “saline”). A list of the organisms found in each group is given in table 2. These groups are strongly separated by position in the bay which likely corresponds with salinity (R^2 0.619). Details shown in chart below where the bars show the proportion of samples that fall within the each criterion.



Distance from the freshwater upper bay was the single best explanatory variable ($R^2 = 0.61$), followed by bathymetry, grain size and seabed form. To determine what thresholds were important for each variable we ran the recursive partitioning analysis separately for each variable alone to see what cutoffs best separated the 19 organism groups from each other. We also ran tested these individually within the samples from the four position groups shown in figure 7. From this we extracted thresholds that were consistent both for the whole data set and within the four groups (Table 3)

Table 3. Thresholds for distance, depth, grain size and seabed forms derived from the organism data.

Distance from Fresh (m)	Depth Zones (m)	Ave Grain Size (mm)	Seabed Forms
0	0	0	Low flat (slope 1-2, position 1)
23,001	-1.89*	0.04	High flat (slope 1-2, position 2)
52,240	-4.44	0.13	Low slope (slope 3-6, position 1)
97,119	-5.25***	0.63***	High slope (slope 3-6, position 2)
	-7.64	0.85	
		2	

Benthic Habitat Types and Ecological Marine Units

The benthic habitat types we identified are presented in the following section of this document. Because the final results are a product of several steps, e.g. the macrofauna classification; the identification of relationships between the organism groups and the factors of depth, grain size and topography; and the mapping of benthic environments, the results and details on each step are provided separately in the appendices.

Two separate, but closely related final maps were created. The Ecological Marine Units (EMU) represent all four-way combinations of depth, sediment grain size, salinity, and seabed forms based on the ecological thresholds revealed by the benthic-organism relationships (Table 3). Benthic Habitats are EMUs clustered into groups that contain the same species assemblage. The two terms are not synonymous, but they are based on the same information, and thus, represent two perspectives on the seafloor. Essentially, the EMU maps show the full diversity of physical factor combinations, regardless of whether a specific habitat type was identified for the combination. The benthic habitat map shows only the combinations of factors, or groups of combinations, for which a benthic organism group was identified. It should be noted that the numbers of the EMUs and benthic habitats were derived from the statistical relationships and is completely arbitrary.

The Ecological Marine Unit map is based on a slightly simpler version of a Table 3, to emphasize the thresholds that were the most consistent across the whole bay and across the individual groups (Table 4, Figure 8).

Table 4. Thresholds used to create the Ecological Marine Units (Figure 8).

Distance from Fresh (m)	Depth Zones (m)	Ave Grain Size (mm)	Seabed Forms
0	0	0	Low flat (slope 1-2, position 1)
23,001	-1.89	0.04	High flat (slope 1-2, position 2)
52,240	-5.25	0.63	Low slope (slope 3-6, position 1)
97,119	< -5.25	2	High slope (slope 3-6, position 2)

The threshold and models used to map the benthic habitats were simpler and the maps should be considered schematic (Figure 9). To create the habitat map a separate model was developed within in “salinity” group (e.g. groups shown in figure 7 based on distance from the upper bay) because the analysis suggested that there were relatively different ecological correlates driving the patterns within each area (Table 5). Creating a more naturalistic map will require better information on salinity.

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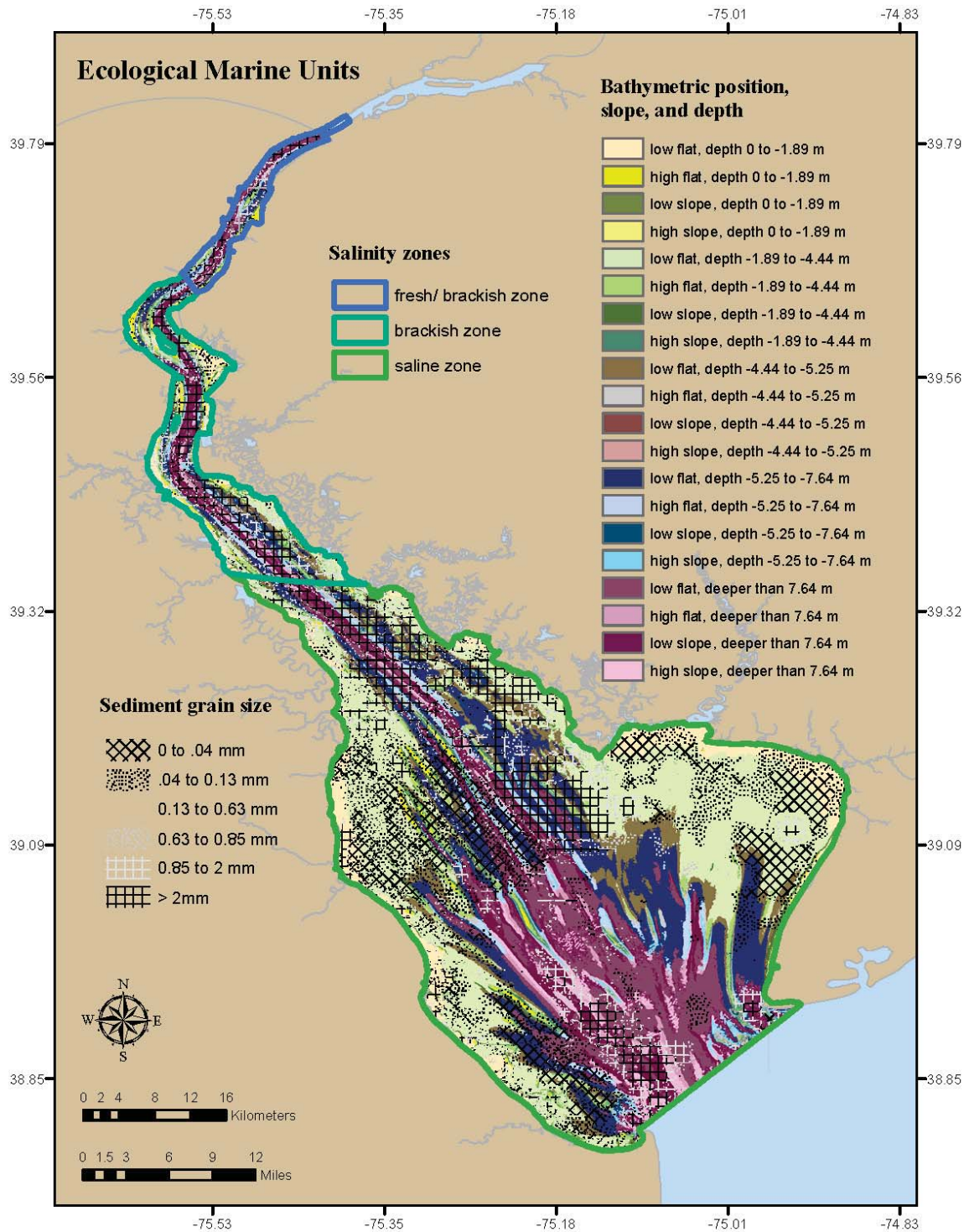


Figure 9. Ecological Marine Units of Delaware Bay

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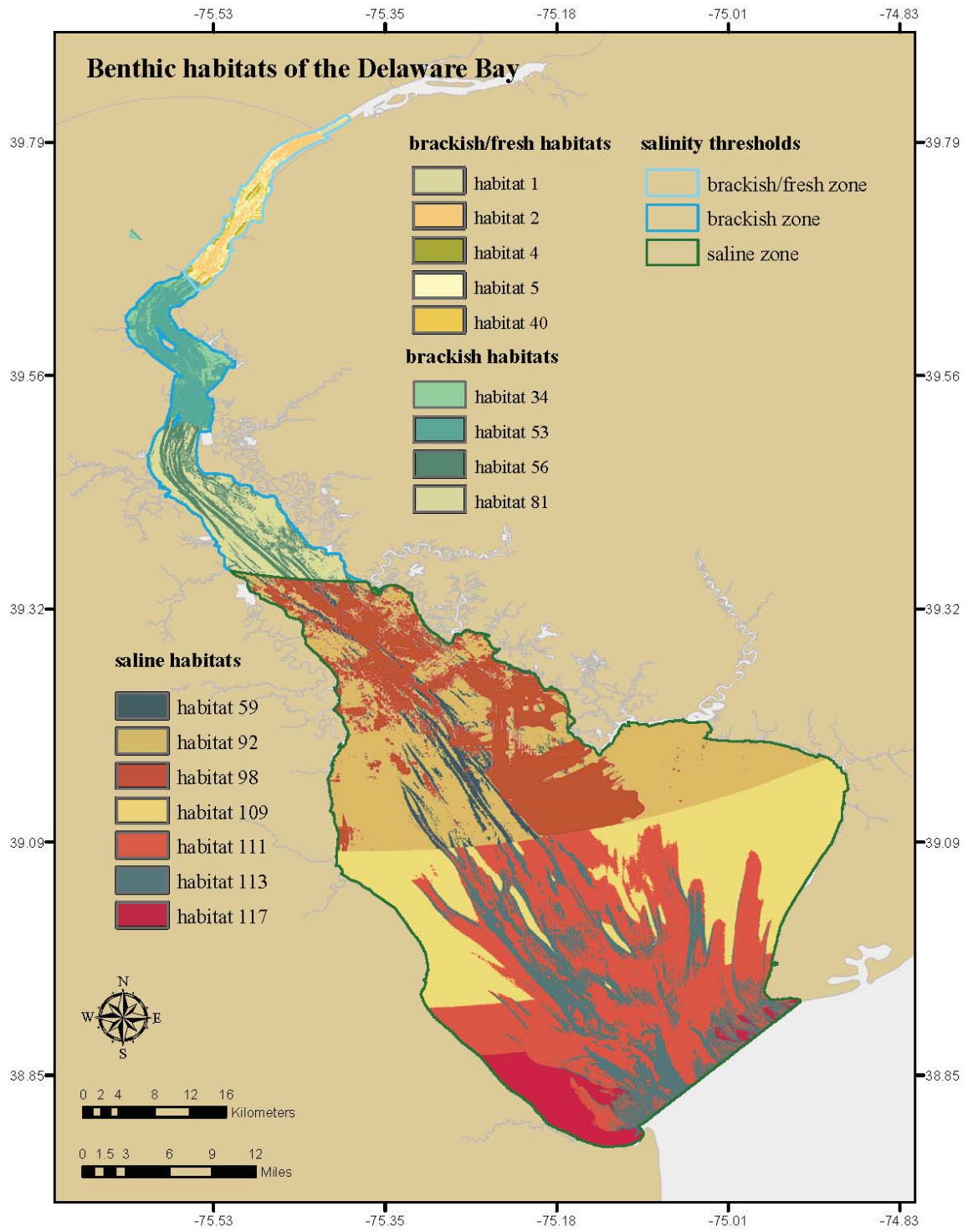


Figure 10. Benthic habitats of the Delaware Bay.

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Figure 1. Bathymetry map of Delaware Bay.

Figure 3. Distribution of the Sediment Samples. The dark areas are areas with high sampling density provided by the DNREC. The sparse areas were not sampled by the DNREC, but filled in with samples from usSEABED.

Figure 2. Salinity of the Delaware Bay: NOAA categorical delineation and ecological thresholds derived from analyses of species composition.

Figure 4. Soft sediment interpolation.

Figure 5. Soft sediment interpolation overlaid with hard bottom and shell areas.

Figure 6. The eighteen-part seabed form model based on slope and position

Figure 7. The simplified four-part seabed from model.

Figure 8. The distribution of the four broad organisms groups across the bay.

Figure 9 Ecological Marine Units of Delaware Bay.

Figure 10. Benthic habitats of the Delaware Bay.

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APPENDIX: Descriptions of the Benthic Habitats.

Table 1a. Organisms associated with groups (clusters) 1 through 53. The last two columns give the P-value for a Monte Carlo test of significance as an indicator of the group, and the average importance value in the group (average abundance times average frequency).

Cluster	Taxa Group	Species Name	Average of p*	Average of IV
1	Annelida : Oligochaeta	Isochaetides freyi	0.2979	8.3
		Tubificidae imm. with capilliform chaetae	0.0002	21.9
	Arthropoda : Amphipoda	Leptocheirus plumulosus	0.0836	12.1
	Arthropoda : Chironomidae	Chironomidae pupae	0.8596	4.2
		Chironomus sp.	0.8610	4.2
		Cryptochironomus sp.	0.0706	13.0
		Procladius sp.	0.0182	20.8
	Arthropoda : Diptera	Ceratopogonidae	0.3005	8.3
	Arthropoda : Isopoda	Cyathura polita	0.0006	12.6
	Arthropoda: Chironomidae	Stenochironomus spp.	0.8646	4.2
	Mollusca : Bivalvia	Musculium spp.	0.8616	4.2
		Pisidium spp.	0.1630	12.5
	1 Total			0.3651
2	Annelida : Polychaeta	Marenzelleria viridis	0.0018	16.7
	Arthropoda : Isopoda	Chiridotea almyra	0.0002	33.1
2 Total			0.0010	24.9
4	Annelida : Oligochaeta	Branchiura sowerbyi	0.6549	5.0
	Arthropoda : Amphipoda	Apocorophium lacustre	0.0012	18.8
	Arthropoda : Chironomidae	Axarus sp.	0.4127	7.1
		Rheotanytarsus sp.	0.6549	5.0
	Mollusca : Gastropoda	Littoridinops tenuipes	0.2084	10.0
4 Total			0.3864	9.2
5	Arthropoda : Amphipoda	Gammarus daiberi	0.0124	18.0
		Polypedilum halterale-grp.	0.0014	27.2
		Tanytus neopunctipennis	0.2719	10.0
	Arthropoda : Cirripedia	Balanus improvisus	0.0108	25.5
	Arthropoda : Decapoda	Rhithropanopeus harrisi	0.0010	32.6
	Arthropoda : Isopoda	Cassidinidea ovalis	0.0018	45.5
	Arthropoda : Mysidacea	Mysidae	0.2707	10.0
	Mollusca : Bivalvia	Corbicula fluminea	0.0004	35.5
		Sphaeriidae	0.7660	3.7
	Mollusca : Gastropoda	Laevapex fuscus	0.2769	10.0
5 Total			0.1613	21.8
16	Annelida : Oligochaeta	Limnodrilus hoffmeisteri	0.0002	40.3
		Limnodrilus maumeensis	0.0656	13.2
		Limnodrilus spp.	0.1880	11.1
		Limnodrilus udekemianus	0.3023	7.3
		Quistidrilus multisetosus	0.1880	11.1
		Tubificidae imm. with capilliform chaetae	0.3035	8.1
16 Total			0.1746	15.2
22	Arthropoda : Amphipoda	Ameroculodes species complex	0.1698	9.8
22 Total			0.1698	9.8
34	Arthropoda : Chironomidae	Coelotanytus sp.	0.3785	8.3
	Mollusca : Bivalvia	Rangia cuneata	0.0018	30.9
34 Total			0.1902	19.6
53	Annelida : Polychaeta	Boccardiella ligerica	0.0002	54.1
	Platyhelminthes : Turbellaria	Euplana gracilis	0.1452	12.5
53 Total			0.0727	33.3

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Table 1b. Organisms associated with groups (clusters) 56 through 91. The last two columns give the P-value for a Monte Carlo test of significance as an indicator of the group, and the average importance value in the group (average abundance times average frequency).

Cluster	Taxa Group	Species Name	Average of p*	Average of IV	
56	Arthropoda : Amphipoda	Caprellidae	0.0736	20.0	
	Arthropoda : Chironomidae	Harnischia sp.	0.0964	16.6	
	Cnidaria : Anthozoa	Anthozoa	0.1976	10.9	
		Diadumene leucolena	0.0078	29.7	
	Mollusca : Bivalvia	Macoma balthica	0.0178	19.0	
	Mollusca : Gastropoda	Pyramidellidae	0.5263	6.0	
		Turbonilla interrupta	0.2160	10.7	
56 Total			0.1622	16.1	
81	Annelida : Polychaeta	Heteromastus filiformis	0.0036	18.9	
	Arthropoda : Chironomidae	Parakiefferiella sp.	0.7506	4.3	
	Arthropoda : Cumacea	Leucon americanus	0.0002	26.1	
	Mollusca : Bivalvia	Mulinia lateralis	0.0070	23.5	
		Mya arenaria	0.4021	6.4	
	Nemertina	Carinoma tremaphoros	0.1938	9.5	
		81 Total		0.2262	14.8
91	Annelida : Polychaeta	Eteone foliosa	0.0768	20.0	
		Leitoscoloplos spp.	0.0054	21.4	
		Paraonis fulgens	0.0004	55.9	
		Scoloplos spp.	0.0232	18.9	
	Arthropoda : Amphipoda	Haustorius canadensis	0.0040	29.5	
		Pseudohaustorius caroliniensis	0.0760	20.0	
		Rhepoxynius hudsoni	0.1158	12.0	
	Arthropoda : Decapoda	Ovalipes ocellatus	0.0760	20.0	
	Arthropoda : Isopoda	Chiridotea caeca	0.0040	32.0	
		Mollusca : Bivalvia	Gemma gemma	0.0056	22.3
	Mytilidae		0.0768	20.0	
	Tellinidae		0.1272	15.2	
	Nemertina	Micrura leidyi	0.0066	19.5	
	91 Total			0.0460	23.6
	92	Annelida : Oligochaeta	Tubificoides spp.	0.0002	16.6
Annelida : Polychaeta		Leitoscoloplos fragilis	1.0000	3.1	
		Onuphidae	0.2681	9.4	
		Polygordius spp.	0.2655	9.4	
Arthropoda : Decapoda		Pagurus longicarpus	1.0000	3.1	
Mollusca : Gastropoda		Ilyanassa obsoleta	0.0178	20.0	
Platyhelminthes : Turbellaria		Turbellaria	0.9646	2.3	
92 Total			0.5023	9.1	

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Table 1c. Organisms associated with groups (clusters)92 through 98. The last two columns give the P-value for a Monte Carlo test of significance as an indicator of the group, and the average importance value in the group (average abundance times average frequency).

Cluster	Taxa Group	Species Name	Average of p*	Average of IV	
92	Annelida : Oligochaeta	Tubificoides spp.	0.0002	16.6	
	Annelida : Polychaeta	Leitoscoloplos fragilis	1.0000	3.1	
		Onuphidae	0.2681	9.4	
		Polygordius spp.	0.2655	9.4	
	Arthropoda : Decapoda	Pagurus longicarpus	1.0000	3.1	
	Mollusca : Gastropoda	Ilyanassa obsoleta	0.0178	20.0	
	Platyhelminthes : Turbellaria	Turbellaria	0.9646	2.3	
92 Total			0.5023	9.1	
98	Annelida : Polychaeta	Exogone dispar	0.0044	31.2	
		Glycera dibranchiata	0.1090	10.9	
		Glycinde solitaria	0.0002	18.3	
		Hydroides dianthus	0.3247	7.2	
		Maldanidae	0.5447	4.9	
		Mediomastus ambiseta	0.0002	15.6	
		Neanthes succinea	0.0002	30.4	
		Paranaitis speciosa	0.1600	12.5	
		Pectinaria gouldii	0.0030	26.4	
		Podarkeopsis levifusca	0.2480	10.0	
		Polycirrus eximius	0.0476	17.9	
		Polydora cornuta	0.0008	35.8	
		Sabellaria vulgaris	0.0002	37.3	
		Sabellidae	0.5695	6.2	
		Scoloplos rubra	0.1154	12.4	
		Streblospio benedicti	0.0002	16.9	
	Arthropoda : Amphipoda	Batea catharinensis	0.0664	15.5	
		Elasmopus laevis	0.0508	18.8	
		Gammarus palustris	0.0016	43.8	
		Incisocallope aestuarius	0.0420	18.3	
		Melita nitida	0.0196	19.4	
		Mucrogammarus mucronatus	0.7636	4.2	
		Paracaprella tenuis	0.0160	21.6	
		Unciola serrata	0.0128	20.1	
	Arthropoda : Cumacea	Cyclaspis varians	0.0030	24.4	
	Arthropoda : Decapoda	Dyspanopeus sayi	0.5695	6.2	
		Euceramus praelongus	0.5695	6.2	
		Eurypanopeus depressus	0.0026	31.2	
	Arthropoda : Isopoda	Edotea triloba	0.0004	19.3	
		Synidotea laticauda	0.0158	21.7	
	Chordata : Ascidiacea	Molgula manhattensis	0.0004	49.1	
	Mollusca : Bivalvia	Anadara ovalis	0.5695	6.2	
		Anomia simplex	0.5715	6.2	
		Crassostrea virginica	0.5673	6.2	
		Geukensia demissa	0.8230	3.7	
		Ischadium recurvum	0.5673	6.2	
		Lyonsia hyalina	0.1370	12.6	
		Mercenaria mercenaria	0.4147	6.3	
		Mollusca : Gastropoda	Astyris lunata	0.0438	14.1
			Boonea seminuda	0.1264	12.0
			Busycon carica	0.5719	6.2
			Crepidula fornicata	0.0078	25.0
Epitonium rupicola			0.1746	12.5	
Epitonium spp.	0.9636		2.3		
Eupleura caudata	0.1078		14.1		
Nudibranchia	0.0574		13.9		
	Odostomia engonia	0.0044	23.7		
	Urosalpinx cinerea	0.8608	3.1		
98 Total			0.2256	16.4	

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Table 1d. Organisms associated with groups (clusters) 109 through 111. The last two columns give the P-value for a Monte Carlo test of significance as an indicator of the group, and the average importance value in the group (average abundance times average frequency).

Cluster	Taxa Group	Species Name	Average of p*	Average of IV	
109	Annelida : Polychaeta	Diopatra cuprea	0.0758	16.1	
		Dispio uncinata	0.5697	6.2	
		Eteone longa	0.5661	6.2	
		Loimia medusa	0.5625	6.2	
		Lumbrineres hebes	0.5541	6.2	
		Paraprionospio pinnata	0.0010	34.3	
		Scolelepis texana	0.5697	6.2	
		Spiochaetopterus costarum	0.0002	24.8	
		Spionidae	0.5625	6.2	
		Arthropoda : Amphipoda	Ampelisca abdita	0.0002	23.0
			Ampelisca vadorum	0.0300	18.3
			Cerapus tubularis	0.0020	28.7
		Arthropoda : Decapoda	Caridea	0.5541	6.2
	Arthropoda : Merostomata	Limulus polyphemus	0.1264	11.8	
	Arthropoda : Mysidacea	Americamysis spp.	0.5697	6.2	
	Cnidaria : Anthozoa	Edwardsia elegans	0.3709	7.1	
	Echinodermata : Holothuroidea	Leptosynapta tenuis	0.5625	6.2	
	Mollusca : Gastropoda	Acteocina canaliculata	0.0002	22.4	
		Rictaxis punctostriatus	0.0002	32.9	
	Nemertina	Amphiporus bioculatus	0.0158	17.1	
	Platyhelminthes : Turbellaria	Stylochus ellipticus	0.0344	14.5	
	109 Total			0.2728	14.6
	111	Annelida : Oligochaeta	Haplotaxis sp.	0.3219	9.1
Annelida : Polychaeta		Arabellidae	0.3163	9.1	
		Aricidea catherinae	0.0044	35.2	
		Asabellides oculata	0.0002	35.9	
		Eteone heteropoda	0.0322	14.5	
		Glycera americana	0.0432	20.0	
		Lumbrineridae	0.6337	5.4	
		Microphthalmus szcelkowi	0.4331	6.8	
		Microphthalmus spp.	0.0648	14.8	
		Nereididae	0.1892	11.7	
		Orbiniidae	0.3231	9.1	
		Paranaitis speciosa	0.6327	5.4	
		Phyllodoce arenae	0.0002	42.5	
		Polynoidae	0.0594	18.2	
		Terebellidae	0.3163	9.1	
		Arthropoda : Amphipoda	Americhelidium americanum	0.0946	13.9
			Ampelisca spp.	0.6269	4.9
			Ampelisca verrilli	0.0006	39.3
Caprella penantis			0.3245	9.1	
Caprella spp.			0.2999	9.1	
Ericthonius brasiliensis			0.0514	14.4	
Microprotopus raneyi			0.0208	18.8	
Monocorophium tuberculatum			0.0192	20.5	
Arthropoda : Cumacea			Oxyurostylis smithi	0.0002	36.7
Arthropoda : Decapoda			Crangon septemspinosa	0.2999	9.1
			Pinnixa spp.	0.3587	7.9
Arthropoda : Mysidacea			Neomysis americana	0.3289	8.0
Echinodermata : Asteroidea			Asteroidea	0.3163	9.1
Echinodermata : Echinoidea			Echinoidea	0.3193	9.1
Echinodermata : Holothuroidea			Pentamera pulcherrima	0.6341	5.4
Mollusca : Bivalvia			Nucula proxima	0.0004	38.8
		Pandora gouldiana	0.3177	9.1	
		Tellina agilis	0.0090	21.0	
		Mollusca : Gastropoda	Busycon canaliculatum	0.3187	9.1
		Crepidula convexa	0.2999	9.1	
		Crepidula plana	0.5549	5.4	
		Crepidula spp.	0.0086	24.5	
		Kurtziella atrostyla	0.0354	18.7	
		Polinices duplicatus	0.3421	8.1	
Nemertina		Carinomella lactea	0.0150	20.7	
		Cerebratulus lacteus	0.0644	16.2	
111 Total				0.2203	15.7

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Table 1e. Organisms associated with groups (clusters) 113 through 133. The last two columns give the P-value for a Monte Carlo test of significance as an indicator of the group, and the average importance value in the group (average abundance times average frequency).

Cluster	Taxa Group	Species Name	Average of p*	Average of IV	
113	Annelida : Polychaeta	Amastigos caperatus	0.0012	35.0	
		Apoprionospio pygmaea	0.2621	10.0	
		Capitella capitata complex	0.2663	10.0	
		Caulerella venefica	0.1328	13.7	
		Cirriformia grandis	0.2721	10.0	
		Clymenella torquata	0.5055	6.2	
		Dipolydora commensalis	0.2681	10.0	
		Dipolydora socialis	0.7694	3.9	
		Drilonereis longa	0.0066	26.4	
		Glyceridae	0.6769	4.5	
		Harmothoe extenuata	0.2681	10.0	
		Nephtys picta	0.0022	38.9	
		Polydora websteri	0.2663	10.0	
		Polygordius spp.	0.3841	8.1	
		Scoloplos spp.	0.2667	10.0	
		Sigambra tentaculata	0.2667	10.0	
		Spio setosa	0.2621	10.0	
		Spiophanes bombyx	0.0344	15.8	
		Arthropoda : Amphipoda	Listriella barnardi	0.0556	20.0
			Listriella smithi	0.2603	10.0
		Arthropoda : Decapoda	Pinnixa chaetoptera	0.2603	10.0
			Pinnixa retinens	0.0530	20.0
		Chordata : Cephalochordata	Branchiostoma caribaeum	0.0582	20.0
Echinodermata : Echinoidea	Echinoidea	0.2667	10.0		
Mollusca : Bivalvia	Ensis directus	0.0012	33.1		
	Tellina tenella	0.2721	10.0		
Mollusca : Gastropoda	Nassarius trivittatus	0.0790	12.4		
	Vitrinella spp.	0.2721	10.0		
113 Total			0.2370	14.0	
117	Annelida : Polychaeta	Ampharetidae	0.0130	18.1	
		Glycera spp.	0.4813	5.7	
		Leitoscoloplos robustus	0.1520	9.6	
		Nephtyidae	0.0590	14.7	
		Nephtys incisa	0.1122	14.3	
		Tharyx sp. A	0.0030	24.4	
		Arthropoda : Amphipoda	Parametopella cypris	0.2410	8.7
			Pagurus pollicaris	0.0998	14.3
		Arthropoda : Decapoda	Pagurus spp.	0.0228	17.2
			Americamysis bigelowi	0.1058	14.3
Mollusca : Bivalvia	Yoldia limatula	0.4287	6.1		
117 Total			0.1562	13.4	
133	Annelida : Oligochaeta	Oligochaeta	0.0034	28.2	
	Annelida : Polychaeta	Brania wellfleetensis	0.0002	74.6	
		Euclymene zonalis	0.0124	33.3	
		Nephtys bucera	0.0004	41.7	
		Parapionosyllis longicirrata	0.0002	71.4	
		Sphaerosyllis erinaceus	0.0260	25.6	
		Travisia sp. A	0.0124	33.3	
		Arthropoda : Amphipoda	Acanthohaustorius intermedius	0.0002	66.7
	Acanthohaustorius millsii		0.0002	66.7	
	Bathyporeia parkeri		0.0134	33.3	
	Protohaustorius cf. deichmannae		0.0012	34.4	
	Protohaustorius wigleyi		0.0134	33.3	
	Arthropoda : Decapoda	Brachyura	0.0438	19.2	
	Arthropoda : Tanaidacea	Tanaissus psammophilus	0.0002	100.0	
	Chordata : Ascidiacea	Ascidiacea	0.0040	31.4	
		Mollusca : Bivalvia	Cyclocardia borealis	0.0002	66.7
	Macoma mitchelli		0.0996	11.5	
	Spisula solidissima		0.1080	13.3	
	Nemertina	Nemertina	0.0184	19.9	
	133 Total			0.0188	42.3