Macrobenthos Data for North Inlet Estuary LTER DATABASE

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Distribution URL for file	http://links.baruch.sc.edu/data/accessfiles/Macrobenthic_Infauna_MACRO__0_5mm_20mm_1981_1992.zip				
DATASET TITLE:	Long-Term Ecological Research (LTER) Macrobenthos Data for the North Inlet Estuary, Georgetown, South Carolina: 1981-1992				
INVESTIGATOR INFORMATION :	**Investigator 1**	**Investigator 2**	**Data Manager**		
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Country	USA	USA	USA		
OTHERS:					
Data Set Credit	**Supported by the National Science Foundation, Long-Term Ecological Research Program (LTER), grants DEB 8012165 and BSR 8514326.**				
DATA FILE INFORMATION:	The **original** metadata was created on 11/9/2004 by Ginger Ogburn-Matthews. The information in this **condensed** metadata is from the original, more extensive metadata. Links and email addresses in the **original** have not been updated as those locations and people may no longer be available. If needed, the original may be accessed at: **http://links.baruch.sc.edu/Data/MACRO/metadata/LTERMACRO.1981-1992.FGDC.METADATA.pdf** The data manager identified on this page should be contacted for any questions about the data.				
Data File Name	Macrobenthic_Infauna_MACRO__0_5mm_20mm_1981_1992.zip				
Beginning Date	20-Jan-1981				
End Date	31-Jan-1992				
Number of Data Records	1796				
RESEARCH LOCATION:	Debidue Site (DD)	Bread and Butter Site(BB)	North Inlet Estuary		
Geographic Description	The Debidue Site is located about 500 meters inside the mouth of the inlet, adjacent to the confluence of Debidue and Town Creeks (two major marsh creeks). This site has a sandy bottom and is at the south end of an extensive sand bar. It is subject to strong current and wave action. Debordieu Colony, a large development partially built on man-made canals, drains into the northern portion of Debidue Creek.	This site is located on Bread and Butter Creek, about 600 meters upstream from its juncture with Town Creek, on a muddy subtidal bank. Bread and Butter Creek is a medium sized creek lined with mud banks and oyster bars. The sediment at the sampling site is fine, silty mud and the site is sheltered from strong current and wave action. At low tide the creek is approximately 10 meters wide at the sampling location. The creek is located about 1.5 kilometers southwest of the Debidue site.	The North Inlet Estuary is located on the southeastern coast of the United States, approximately 10 kilometers east of Georgetown, South Carolina. The North Inlet Estuary is a bar-built Class C type estuary (Pritchard, 1955). It is composed of numerous winding tidal creeks dominated by Spartina alterniflora and is considered a pristine tidal estuary due to minimal anthropogenic impacts. The watershed drains a 24.8 square kilometer area of mostly pine forest and a moderately developed residential watershed to the north. Sample sites were chosen due to their proximity to an existing long-term meiofauna sampling site.		
Sampling Site Map (photographs)	View of Benthic Core Sites http://links.baruch.sc.edu/Data/MACRO/images/macrobenthos.WEB.jpg	View Benthic Core Sites http://links.baruch.sc.edu/Data/MACRO/images/macrobenthos.WEB.jpg	The ADAR 5500 infrared image was provided by the North Inlet–Winyah Bay National Estuarine Research Reserve. Locations were plotted using GPS coordinates and ArcMap software. Image date 2000		
Location Bounding Box					
West Bounding Coordinate					
East Bounding Coordinate	-79.16792	-79.18431			
North Bounding Coordinate	33.33361	33.3305			
South Bounding Coordinate					
OR if single point location					
Latitude					
Longitude					
Elevation					
TAXONOMIC COVERAGE:					
Taxonomic Protocols					
Organisms studied	Macrobenthic species; Zooplankton; Epibenthic macrozooplankton, nekton species				

KEYWORD INFORMATION

KEYWORDS: ABUNDANCE, AIR TEMPERATURE, ANIMALS, BENTHOS, COASTAL, CORE, ECOSYSTEMS, ESTUARINE, ESTUARY LONG-TERM, LONG-TERM, ECOLOGICAL RESEARCH, LTER, MACROBENTHIC, MACROBENTHOS, MARSH, MONITORING DATA
,OXIDATION, PHYSICAL DATA, REDUCTION,REDOX LAYER, SALINITY, SALT MARSH, SEDIMENT, SEDIMENT WATER INTERFACE, TAXA, TAXONOMIC, TAXONOMY, TEMPERATURE, TIDAL CREEK,TIDE LEVEL, TIDE STAGE, WATER TEMPERATURE, ATLANTIC COAST, BREAD AND BUTTER CREEK, COASTAL, DEBIDUE CREEK, DEBORDIEU COLONY, EAST COAST, GEORGETOWN COUNTY, HOBCAW BARONY, NORTH INLET, SOUTH CAROLINA, TOWN CREEK, WINYAH BAY, USA, BENTHIC, DAY, BIWEEKLY, FORTNIGHTLY, MONTH, YEAR, ANIMALS, BENTHIC ANIMALS, COLLECTION, CLASS, FMAILY, GENUS

ABSTRACT:

Samples were taken from two estuarine tidal creek stations (designated BB and DD) in the North Inlet Estuary, SC. Two large cores, with a sediment surface area of 83.3 square centimeters and a depth of 15 centimeters, were collected from each of the two sites from 1981-1985. For most of this period, cores were processed in separate 5 centimeter increments for the top, middle, and bottom portions of the core. Throughout the remainder of the study (1985-1992), eight smaller cores were collected from the BB site only in an effort to increase sampling accuracy. Although the core size and number of replicates changed, the total surface area of sediment sampled remained similar. The smaller cores had a surface area of 18.1 square centimeters and a depth of 5 centimeters. Cores were collected every two weeks during the midday low tide, on the same day as almost all other LTER FAUNA samples, except when water levels were prohibitively high. Macrobenthic animals (defined here as those animals retained on a 0.5 millimeter mesh screen) were identified to the lowest practical taxa. All dominant polychaetes were identified to species. Counts per core were converted to numbers per square meter of surface sediment and standardized for core depth (to 5 centimeters) where necessary. Physical data including tide level, surface water temperature, air temperature, temperature of the sediment/water interface, surface water salinity, and the observed depth of the reduction/oxidation layer were recorded at the same time as the macrobenthic collections.

METHODS:

Field Collection Procedures and Protocols (Overall Field Collection Protocol)
Two cores, from each of the two sample sites, were collected from 1981-1985 and eight cores, from the BB site only, were collected throughout the remainder of the study (1985-1992). Cores were taken every two weeks during the midday low tide, on the same day as all other LTER FAUNA samples. Occasionally weather conditions (generally north and east winds) produced higher than usual water levels and made sample collection impossible. In these instances, cores were obtained on the next suitable low tide.
During most of the first four years of the study, a 20-centimeter long PVC pipe with 10.3 centimeter inside diameter served as the coring device and was used to collect sediment core samples with a surface area of 83.3 square centimeters. Cores were taken to a depth of 15 centimeters. On January 18, 1985 (Sample 100), sampling at the Debidue site was suspended and the core size and number of replicates changed at the Bread and Butter site, but the total surface area of sediment sampled remained similar to previous years. The coring device used from this date, and throughout the rest of the database, was a 30 centimeter length of plexiglass pipe with an inside diameter of 4.8 centimeters. The resulting sediment core samples had a sediment surface area of 18.1 square centimeters. Eight cores were collected, as opposed to 2, in an effort to increase sampling accuracy. In addition, cores were only taken to a depth of 5 centimeters.
Cores were collected in approximately 20 centimeters of water and care was taken to ensure that all replicates were collected in the same area, but that they never overlapped and were all collected from undisturbed sediment. The coring device was marked in centimeter increments with a waterproof pen. For each sediment sample, the technician would core deeper into the sediment than the desired depth. After inserting the coring device into the sediment, a rubber stopper was placed securely into the upper end to facilitate core removal. The technician would then pull up the coring device and allow the sediment to flow out the bottom, until the core sample was at the correct level, so that the desired core depth remained in the coring device (e.g. 5 cm depth). This technique was at least accurate to the nearest 0.5 centimeters. The discarded bottom section of the core was tossed out on the other side of the boat to ensure that it would not interfere with any other replicates to be collected. The excess water in the top portion of the coring device was retained to ensure that no animals were lost from the top layer. Core samples were immediately placed into 1-Liter jars, and from the mid-1980's to early 1990's, they were preserved in 10 percent buffered formalin-seawater preservative mixture stained with Rose Bengal.
For the period of January 20, 1981 through December 19, 1983 (samples 1-73), cores were taken to a depth of 15 centimeters and, where feasible, split into 5-centimeter deep increments in order to determine the depth at which animals occurred in the substrate. Occasionally the substrate was too watery to be sectioned successfully and the core was processed as either one 15 centimeter section, or as a 10 and a 5 centimeter section. For the period of January 3, 1984 through January 8, 1985 (samples 74-99), cores were taken to a depth of 15 centimeters and were not sectioned, but processed as a whole. For the remainder of the database (01/18/1985 – 01/31/1992) cores were taken to a depth of 5 centimeters and were processed as a whole.

Field Collection Procedures and Protocols (Physical Field Data Collection)
After securing the boat at each station and prior to core collection, the LTER MACRO technician(s) recorded physical data and field observations in waterproof Field Notebooks. The Eastern Standard Time and the tide stage were recorded first. The tide stage value is an experienced/trained field technician's estimate of the departure from the average low tide. The estimate is dependent on the field technician's ability to gauge (using oyster reefs and other physical cues) the water level in the tidal creek relevant to the water level at mean low tide. Positive values were used to indicate the water level's departure above (higher than) an average low tide, and negative values indicate the departure below (lower than) the average low tide mark. Using a hand-held thermometer, the air temperature was then measured in the shade, followed by the sediment/water interface temperature. Measurements were taken in this order to ensure that a wet thermometer would not influence the air temperature values. Next, a conductivity meter was used to determine the surface water temperature and surface water salinity values. Finally, the depth of the reduction/oxidation layer was estimated and recorded by the field technician. The redox layer depth was generally observed when the meiobenthic samples were collected (immediately prior to the MACRO core collection).

Laboratory Procedures and Protocol (Benthic Core Sample Processing, Sorting)
During the first years of the study, core samples were soaked for 48 hours in a 10 percent buffered formalin-seawater preservative mixture stained with Rose Bengal, immediately after returning to the lab. After soaking, each sample was gently rotated in the jar to suspend the sample in the formalin mixture. Beginning in 1987, the samples were preserved in the field immediately after collection in the same manner. The jars were then stored on shelves in the field laboratory and shaken lightly every few days until they were processed. When the technicians were ready to begin processing, the samples were poured onto/through a 0.5 millimeter mesh sieve. All remaining sample debris was rinsed from the inside of the jar and lid onto the sieve. The sieve, with the sample on it, was then placed into a water bath and gently raised and lowered in the water (not rotated) until no more sediment or small particulate matter were lost with this method. The sample remaining on the screen was then rinsed from underneath to remove lingering sediment and concentrate the animals in one location on the screen. This prevented the animals from being damaged or forced through the screen. All sample material was then gently washed into a beaker. From the beaker, small amounts of sample were rinsed into a small, homemade PVC sieve with 0.5 millimeter mesh and a 3.5 centimeter interior diameter. The sample was carefully rinsed again in this smaller sieve until only the macrobenthic organisms (larger than 0.5 mm) remained. These small subsamples were then rinsed into gridded petri dishes and the animals were removed, grid by grid, from any remaining sediment with forceps and the aid of a dissecting microscope at 12x power. The petri dish was then reexamined for animals using 6x power to ensure that no animals were overlooked. If any additional animals were found, the petri dish was reexamined once again, until no animals were found on the last examination. This process was repeated until the entire sample core was sorted. Animals from each sorting dish were placed in a small jar or vial of 70 percent pure ethanol (not denatured) with glycerin (alcohol:water:glycerin = 15:15:1 by volume) and labeled inside and out with the date, sample, sample station, and replicate number.

Laboratory Procedures and Protocols (Benthic Core Sample Processing, Animal Identifications)
The sample replicate to be identified was rinsed with alcohol (same concentration as above) into a watch glass. For samples 1-111, all animals were identified to the lowest possible taxa. Beginning with sample 112 (07/15/1985), and for the remainder of the database, only dominant polychaetes were identified to species. Other organisms were identified to family, class, or phylum. For more information on the transformation of the count data from this earlier identification protocol to the later (to be included in the final, published database), see the Process Section of this document. Animals of the same species or category were counted and placed together into labeled shell vials containing the alcohol:water:glycerin preservative described above. The MACRO technician used a Counting Sheet (hardcopy) to record the identification and count results for each sample replicate, as well as any other relevant comments, measurements, or notes. Jar (shell vial) numbers were also recorded on the Counting Sheets.

Laboratory Procedures and Protocols (Archival of Samples)
The processed animals (separated, identified, and counted) were placed in shell vials containing a 70 percent Ethanol solution (stock = 95% ETOH + tap water + glycerin, 15:5:1 by

volume). Each shell vial contains a label detailing the sample date, station, replicate, jar (vial) number, and identity of the animals. The jar (vial) numbers correspond to those listed on the Counting Sheets, and therefore, the Counting Sheets can be used to trace specimens for recounting or identification purposes. The shell vials are then placed in sealed quart-size storage jars and maintained in the archive sample room at the Baruch Marine Field Laboratory, Georgetown, SC. For
more information on the archival of raw data sheets, see the Process section.

Example jar label: 04/18/1981 D1 Top #4 *Spiophanes bombyx* contains all *Spiophanes bombyx* found at the Debidue station, on 04/18/1981, replicate 1, in the top 5 centimeters of sediment, and was the fourth jar in that replicate.

Beginning in May of 1986 and for an entire year, researchers collected three additional (replicate) cores from the BB site during each sampling event and determined the biomass of these macrobenthic samples. These cores were processed in the same manner as described above, however the preserved animals sieved out of the samples were rinsed thoroughly in fresh water and then placed in pre-weighed and oven-dried aluminum pans. These pans were oven-dried at 60 degrees Celsius for 24 hours, cooled for 15 minutes in the desiccator, and weighed. They were then placed back into the oven for an additional 3 hours, cooled, and weighed again. This process was repeated until a constant weight (in milligrams) was attained. These data were used to track monthly changes in the total biomass of an 18.1 square centimeter area.
Species level biomass data were also obtained seasonally for abundant taxa and over the entire year for less abundant taxa. Qualitative samples were collected periodically and preserved animals were identified and placed into species-specific size classes based on measurements of a specific body dimension (in ocular micrometer units from the dissecting scope). Several specimens of each size class, for each species, were placed in pre-weighed aluminum pans. These pans were also oven-dried at 60 degrees Celsius for 24 hours, cooled for 15 minutes in the desiccator, and weighed. As described above, the technician continued to dry, cool, and weigh until a constant weight (expressed in micrograms) was attained. Each size class/species pan was replicated at least 3 times and an average weight was calculated for each size class. These biomass values were then converted to non-preserved values following the procedures of Frithsen et al. (1986). Finally, a width (or length)/weight regression was then calculated for each species using natural log(ln)-transformed data. With these regressions, average species biomass could be estimated from the biweekly samples simply by measuring the appropriate dimension under the microscope.
Size classes were determined by making the following body dimension measurements:
Polychaetes: measured by the width of the first setigerous segment in micrometer units at 12x magnification (some of the larger polychaetes were measured at lower magnification).
Oligochaetes: measured by the width of the first setigerous segment in micrometer units at 12x magnification.
Amphipods: measured by carapace length in micrometer units at 25x magnification.
Cumaceans: measured by carapace length in micrometer units at 12x magnification.
Isopods: measured by _____ at 12x magnification.*
Shrimp: measured by carapace length at 12x magnification.
Bivalves: measured by the longest anterior-posterior dimension in micrometer units at 12x magnification.
*This information is unavailable.

TAXON	REGRESSION EQUATION	R**2
Streblospio benedicti	ln(weight) =3.485[ln(size)]-8.07	0.968
Mediomastus ambiseta	ln(weight) =2.766[ln(size)]-6.35	0.957
Cirratulidae	ln(weight) =1.96[ln(size)]-5.736	0.852
Oligochaetes	ln(weight) =2.08[ln(size)]-6.255	0.953
Juvenile Bivalves (Shelled)	ln(weight) =3.048[ln(size)]-11.398	0.932

VARIABLE DESCRIPTIONS:

Variable Name	Variable Description	Units	Measurement Scale	Code Information	Number Type
STATION	two letter code designation for the tidal marsh creek, within North Inlet Estuary, where the macrobenthic sample was collected. (BB = Bread and Butter site, DD = Debidue site)	BB, DD	nominal		
DATE	date that the sample was collected (not necessarily processed or analyzed) in mm/dd/yyyy format.	1-12, 1-31, 1981-1992	datetime		integer
SAMPLE	the sample number, assigned in sequential order (in increments of 1), to the macrobenthic collection based on date. SAMTIME = the Eastern Standard Time that the macrobenthic sample was collected in hhmm format	1 – 274	ordinal		integer
REPLICAT	the replicate number, assigned in sequential order (in increments of 1), to each replicate sample for each sample/date.	1 – 8	ordinal		integer
TSTAGE	the estimated tide level or stage (in meters). The value reported is the estimated departure from an average low tide at the time of sampling. A positive value indicates the estimated amount above (higher than) an average low tide water level and a negative value indicates the estimated amount below (lower than) the average low tide mark.	meters	nominal		real
STEMP	surface water temperature measured in degrees Celsius.	degrees Celsius	nominal		real

AIRTEMP	air temperature taken in the shade with a hand-held thermometer, measured in degrees Celsius.	degrees Celsius	ratio		real
SEDWATER	temperature of the sediment / water interface measured with a hand-held thermometer in degrees Celsius.	degrees Celsius	ratio		real
SSAL	salinity of the surface waters over the sample location, reported in parts per thousand.	micromolePerLiter	ratio		real
REDOX	depth, in centimeters, at which the reduction/oxidation layer was observed below the surface sediments. Measurements are reported from 0 to 10 centimeters. All values of 10 centimeters or greater are reported in the database as 10, and are considered anomalous because they are not true values.	centimeter	ratio		integer
COREAREA	surface sediment area, in square centimeters, sampled by the coring device. Calculated from the inside diameter of the coring device (COREDIAM).	gramPerLiter	ratio		integer
COREDIAM	the inside diameter, in centimeters, of the coring device.	partPerThousand	ratio		integer
SEDVOL	the volume, in cubic centimeters, of the sediment core sample used for count data in the final database, not necessarily the volume of the total core collected. Calculated from the core area (COREAREA) and core depth (COREDEP).	9 – 1700 cubic centimeters	ratio		integer
COREDEP	the depth, in centimeters, of the sediment core sample used to calculate the number of individuals per square meter for the final database, not necessarily the depth of the total core collected. Earlier protocols called for sample cores to be collected to a depth of 15 centimeters and either processed whole or sectioned into 5 centimeter top, middle, and bottom portions. Sectioning was sometimes impossible. Later protocol (beginning 01/18/1985 through the end of the database) called for only a 5 centimeter deep core. Results from cores that were processed in sections greater than 5 centimeters deep had to be converted for easy comparison to the later data in the final database. If the depth listed in the final database is greater than 5 centimeters (10 or 15 centimeters), the counts were converted estimates for the 5 centimeter top section of the sample core (see Method and Process sections for more information).	5 – 15 centimeters	ratio		integer
COLLECT	the initials of the technician who collected (not necessarily processed) the benthic samples.	PM,CR,LB,SKS,DMA,GO,SS,GOM,RW	nominal		
UNIDCAPIT	(UNIDCAPI) = Unidentified Capitellidae: number of individuals in the family Capitellidae that were not identified as Heteromastus filiformis, Mediomastus ambiseta, or Capitella capitata.	0.0 – 4419.9 number per square meter	ratio		real
TOTCAPIT	Total Capitellidae = UNIDCAPIT + MEDIAMBI + HETEFILI + CAPITCAPI, total number of individuals in the family Capitellidae.	0.0 – 43093.9 number per square meter	ratio		real
MEDIAMBI	Mediomastus ambiseta: number of individuals identified as Mediomastus ambiseta. Includes animals that were originally identified incorrectly as Capitella capitata in samples 1-146.	0.0 – 42541.4 number per square meter	ratio		real
HETEFILI	Heteromastus filiformis: number of individuals identified as Heteromastus filiformis.	0.0 – 4096.4 number per square meter	ratio		real
CAPITCAPI	Capitella capitata: number of individuals identified as Capitella capitata. Does not include Mediomastus ambiseta individuals that were originally identified incorrectly as Capitella capitata in samples 1-146.	0.0 – 1105.0 number per square meter	ratio		real
UNIDCIRRA	(UNIDCIRR) = Unidentified Cirratulidae: number of individuals in the family Cirratulidae that were not identified as species in the Caulleriella or Tharyx genus.	0.0 – 28588.2 number per square meter	ratio		real
TOTCIRRA	Total Cirratulidae: UNIDCIRR + CAULLESP + THARYXSP, total number of individuals in the family Cirratulidae	0.0 – 35911.6 number per square meter	ratio		real
CAULLESP	Caulleriella species: number of individuals identified as a species (most likely the juvenile Caulleriella killariensis) in the Caulleriella genus.	0.0 – 35359.1 number per square meter	ratio		real
THARYXSP	Tharyx species: number of individuals identified as a species in the Tharyx genus.	0.0 – 6077.4 number per square meter	ratio		real

UNIDGLYCE	(UNIDGLYC) = Unidentified Glycera: number of individuals in the genus Glycera, none of which were identified to the species level. Unidentified Glycera were the only members of the Glyceridae family collected. As a result, the Total Glyceridae values are equal to the Unidentified Glycera (UNIDGLYC) values.	0.0 – 2762.4 number per square meter	ratio		real
TOTGLYCE	Total Glyceridae: Total number of individuals in the family Glyceridae, all of these individuals were members of the Glycera genus and were not identified to the species level. As a result, the Unidentified Glycera (UNIDGLYC) values are equal to the Total Glyceridae values.	0.0 – 2762.4 number per square meter	ratio		real
TOTGONIA	Total Goniadidae: Total number of individuals in the family Goniadidae, none of these were identified to the genus or species level. The 2004 Data Manager removed the Unidentified Goniadidae (UNIDGONI) parameter because it was identical to the Total Goniadidae parameter.	0.0 – 1657.5 number per square meter	ratio		real
UNIDLUMBR	(UNIDLUMB) = Unidentified Lumbrineridae: number of individuals in the family Lumbrineridae that were not identified as Lumbrineris tenuis or the other Lumbrineris species.	0.0 – 2530.1 number per square meter	ratio		real
TOTLUMBR	Total Lumbrineridae: UNIDLUMBR + LUMBRTENU + LUMBRSP01, total number of individuals in the family Lumbrineridae.	0.0 – 4972.4 number per square meter	ratio		real
LUMBRTENU	Lumbrineris tenuis: number of individuals identified as Lumbrineris tenuis.	0.0 – 4972.4 number per square meter	ratio		real
LUMBRSP01	Lumbrineris species number 1: number of individuals identified as a species (other than Lumbrineris tenuis) in the Lumbrineris genus.	0.0 – 3867.4 number per square meter	ratio		real
UNIDMAGEL	(UNIDMAGE) = Unidentified Magelonidae: number of individuals in the family Magelonidae that were not identified as Magelona phyllisae or the other Magelonidae species.	0.0 – 552.5 number per square meter	ratio		real
TOTMAGEL	Total Magelonidae: UNIDMAGEL + MAGELPHYL + MAGELSP01, total number of individuals in the family Magelonidae.	0.0 – 1105.0 number per square meter	ratio		real
MAGELPHYL	(MAGEPHYL) = Magelona phyllisae: number of individuals identified as Magelona phyllisae.	0.0 – 1105.0 number per square meter	ratio		real
MAGELSP01	(MAGESP01) = Magelonidae species number 1: number of individuals identified as a species (other than Magelona phyllisae) in the Magelonidae family.	0.0 – 552.5 number per square meter	ratio		real
UNIDNEREI	(UNIDNERE) = Unidentified Nereididae: number of individuals in the family Nereididae that were not identified as Nereis succinea or the other Nereididae species (after sample #111).	0.0 – 2306.0 number per square meter	ratio		real
TOTNEREI	Total Nereididae: UNIDNEREI + NEREISUCC + NEREISP01, total number of individuals in the family Nereididae.	0.0 – 6077.4 number per square meter	ratio		real
NEREISUCC	(NERESUCC) = Nereis succinea: number of individuals identified as Nereis succinea. According to the Integrated Taxonomic Information System on-line database (http://www.itis.usda.gov), as retrieved on 07/16/04, this species name is no longer valid. The correct name is: Neanthes succinea (it is classified as a member of the Neanthes genus).	0.0 – 6077.4 number per square meter	ratio		real
NEREISP01	(NERESP01) = Nereididae species number 1: number of individuals identified as a species (other than Nereis succinea) in the Nereididae family. In samples 112-274 this is most likely a member of the Nereis genus, this category was not used before sample 112 and these individuals would have been lumped in with the UNIDNEREI.	0.0 – 552.5 number per square meter	ratio		real
UNIDORBIN	(UNIDORBI) = Unidentified Orbiniidae: number of individuals in the family Orbiniidae that were not identified as Haploscoloplos robustus or the other Orbiniidae species (after sample #111).	0.0 – 6629.8 number per square meter	ratio		real
TOTORBIN	Total Orbiniidae: UNIDORBIN + HAPLROBU + ORBINSP01, total number of individuals in the family Orbiniidae.	0.0 – 13812.2 number per square meter	ratio		real
HAPLROBU	Haploscoloplos robustus: number of individuals identified as Haploscoloplos robustus.	0.0 – 7734.8 number per square meter	ratio		real

ORBINSP01	(ORBISP01) = Orbiniidae species number 1: number of individuals identified as a species (other than Haploscoloplos robustus) in the Orbiniidae family. In samples 112-274, this is a member of the Haploscoloplos genus, this category was not used before sample 112 and these individuals would have been lumped in with the UNIDORBIN.	0.0 – 13812.2 number per square meter	ratio		real
UNIDPHYLL	(UNIDPHYL) = Unidentified Phyllodocidae: number of individuals in the family Phyllodocidae that were not identified as Eteone heteropoda or the other Phyllodocidae species.	0.0 – 1657.5 number per square meter	ratio		real
TOTPHYLL	Total Phyllodocidae: UNIDPHYLL + ETEOHETE + PHYLLSP01, total number of individuals in the family Phyllodocidae.	0.0 – 9392.3 number per square meter	ratio		real
ETEOHETE	Eteone heteropoda: number of individuals identified as Eteone heteropoda.	0.0 – 9392.3 number per square meter	ratio		real
PHYLLSP01	(PHYLSP01) = Phyllodocidae species number 1: number of individuals identified as a species (other than Eteone heteropoda) in the Phyllodocidae family. In samples 190-274 this is a member of the Phyllodoce genus, prior to these samples it is uncertain.	0.0 – 1105.0 number per square met	ratio		real
UNIDSPION	(UNIDSPIO) = Unidentified Spionidae: number of individuals in the family Spionidae that were not identified as Paraprionospio pinnata, Prionospio cirrifera, Prionospio cirrobranchiata, Spiophanes bombyx, Streblospio benedicti, either of the Polydora species, or the other Spionidae species.	0.0 – 3314.9 number per square meter	ratio		real
TOTSPION	Total Spionidae: UNIDSPION + SPIONSP01 + PARAPINN + POLYDSP01 + POLYDSP02 + PRICIRRI + PRICIRRO + SPIOBOMB + STREBENE, total number of individuals in the family Spionidae.	0.0 – 26519.3 number per square meter	ratio		real
SPIONSP01	(SPIONSPA) ((SPIONIDAE SP. A)) = Spionidae species number 1: number of individuals identified as a species (other than those listed below) in the Spionidae family.	0.0 – 602.4 number per square meter	ratio		real
PARAPINN	Paraprionospio pinnata: number of individuals identified as Paraprionospio pinnata.	0.0 – 2209.9 number per square meter	ratio		real
POLYDSP01	(POLYDSPI) = Polydora species number 1: number of individuals identified as a species in the Polydora genus. Possibly a different growth stage of the same species as POLYDSP02 (unidentified polydorid).	0.0 – 552.5 number per square meter	ratio		real
PRICIRRI	Prionospio cirrifera: number of individuals identified as Prionospio cirrifera. According to the Integrated Taxonomic Information System on-line database (http://www.itis.usda.gov), as retrieved on 06/18/04, this species name is no longer valid. The correct name is: Minuspio cirrifera	0.0 – 9944.8 number per square meter	ratio		real
PRICIRRO	Prionospio cirrobranchiata: number of individuals identified as Prionospio cirrobranchiata. According to the Integrated Taxonomic Information System on-line database (http://www.itis.usda.gov), as retrieved on 06/18/04, this species name is no longer valid. The correct name is: Minuspio cirrobranchiata	0.0 – 4972.4 number per square meter	ratio		real
SPIOBOMB	Spiophanes bombyx: number of individuals identified as Spiophanes bombyx.	0.0 – 4216.9 number per square meter	ratio		real
STREBENE	Streblospio benedicti: number of individuals identified as Streblospio benedicti.	0.0 – 26519.3 number per square meter	ratio		real
UNIDSYLLI	Unidentified Syllidae: number of individuals in the family Syllidae that were not identified as Syllidae species number 1.	0.0 – 8839.8 number per square meter	ratio		real
TOTSYLLI	Total Syllidae: UNIDSYLLI + SYLLISP01, total number of individuals in the family Syllidae.	0.0 – 8839.8 number per square meter	ratio		real
SYLLISP01	(SYLLSP01) = Syllidae species number 1: number of individuals identified as a species in the Syllidae family.	0.0 – 552.5 number per square meter	ratio		real

POLYCSP01	(POLYSP01) = Polychaete species number 1: number of individuals identified as a species in the class Polychaeta. In samples 141-274 this species is Armandia maculata from the family Ophellidae, prior to these samples it is uncertain.	0.0 – 15469.6 number per square meter	ratio		real
UNIDPOLYC	(UNIDPOLY) = Unidentified Polychaetes: number of individuals in the class Polychaeta that were not identified by subclass, order, family, species, OR otherwise categorized (POLYCSP01, POLYDSP01, and POLYDSO02, etc.) Note: any families (and their associated species) identified on old data sheets (old format) from samples 1-111 that were not identified in the new format were lumped under this category. Species of polychaetes no longer identified in the new format, but whose families are (Cirratulidae, Glyceridae, Goniadidae, Lumbrineridae, Nereidae, Orbinidae, Spionidae, Magelonidae, Phyllodocidae, Syllidae, and Capitellidae), were lumped into the “unidentified” category of their respective families.	0.0 – 3867.4 number per square meter	ratio		real
TOTPOLYC	Total Polychaetes: TOTCAPIT + TOTCIRRA + TOTGLYCE + TOTGONIA + TOTLUMBR + TOTMAGEL + TOTNEREI + TOTORBIN + TOTPHYLL + TOTSPION + TOTSYLLI + POLYCSP01 + UNIDPOLYC, total number of individuals in the class Polychaeta.	0.0 – 75138.1 number per square meter	ratio		real
TOTSPECI	Total number of polychaete species identified in the sample. It appears that, from 01/20/1981 through 12/19/1983, only species that were identified to the species level were included in this count. For the remainder of the database, this value is a count of all unique species in the sample, whether they were identified to species level or not. As a result, data for this parameter are not consistent and should not be used to compare between these time frames. Users should consult the raw data sheets (RAW.ARCHIVE CDs) for detailed information on sample composition.	0 – 16 number per sample	ratio		integer
TOTFAMIL	Total number of polychaete families identified in the sample.	0 – 14 number per sample	ratio		integer
AMPHIPOD	Amphipods: Number of individuals in the order Amphipoda.	0.0 – 8839.8 number per square meter	ratio		real
TOTSHRIMPS	(TSHRIMPS) = Total Shrimps: number of individuals identified as shrimps.	0.0 – 2209.9 number per square meter	ratio		real
CUMACEAN	Cumaceans: Number of individuals in the order Cumacea.	0.0 – 1657.5 number per square meter	ratio		real
ISOPODS	Isopods: number of individuals in the order Isopoda.	0.0 – 2762.4 number per square meter	ratio		real
UNIDCRUS	Unidentified Crustaceans: number of individuals in the subphylum Crustacea that were not identified as Amphipods, Shrimps, Cumaceans, or Isopods.	0.0 – 2762.4 number per square meter	ratio		real
TOTCRUST	Total Crustaceans: AMPHIPOD + TOTSHRIMPS + CUMACEAN + ISOPODS + UNIDCRUS, total number of individuals in the subphylum Crustacea.	0.0 – 8839.8 number per square meter	ratio		real
TOTBIVAL	Total Bivalves: number of individuals in the class Bivalvia.	0.0 – 29281.8 number per square meter	ratio		real
UNIDNEME	Unidentified Nemerteans: number of individuals in the phylum Nemertea.	0.0 – 43093.9 number per square meter	ratio		real
OLIGOCHA	Oligochaetes: number of individuals in the subclass Oligochaeta.	0.0 – 43093.9 number per square meter	ratio		real
SIPUNCUL	Sipunculids: number of individuals in the family Sipunculidae.	0.0 – 2209.9 number per square meter	ratio		real
SHELGAST	Shelled Gastropods: number of individuals identified as shelled gastropods.	0.0 – 5524.9 number per square meter	ratio		real
UNIDMISC	Unidentified Miscellaneous: number of unidentified animals that don’t fit under any other category.	0.0 – 31491.7 number per square meter	ratio		real
TOTMISCE	Total Miscellaneous: SHELGAST + UNIDMISC, total number of shelled gastropods and unidentified miscellaneous animals	0.0 – 31491.7 number per square meter	ratio		real

TOTUNIDORG	(TOTUNORG) = Total Unidentified Organisms: number of organisms not identified to the species level. Includes all non-Polychaete organisms, Polychaetes that were not identified by family or genus (UNIDPOLYC), and Polychaetes that were identified by family or genus, but classified as unidentified within that group (e.g. UNIDSPION). This count can be found on the raw Data Entry Sheets (.JPG images archived on the MACRO RAW.ARCHIVE CDs and hardcopies on site at the Baruch Marine Field Lab). Data for this parameter are not consistent due to changes in identification methodology. In the early years of the study (01/20/1981 – 06/28/1985) all organisms were identified to species level if at all possible. In the later years (07/15/1985 – 01/31/1992), only dominant species were identified to species. As a result, these data vary greatly and should not be used to compare between these time frames.	0.0 – 58011.1 number per square meter	ratio		real
TOTALLORG	(TALLORGA) = Total All Organisms: TOTPOLYC + TOTCRUST + TOTBIVAL + UNIDNEME + OLIGOCHA + SIPUNCUL + TOTMISCE, number of organisms counted and recorded for the sample core.	91.7 – 98342.5 number per square meter	ratio		real
POLYDSP02	(POLYSPII) = Polydora species number 2: number of individuals identified as a second species in the Polydora genus. Possibly a different growth stage of the same species as POLYDSP01 (unidentified polydorid).	0.0 – 552.5 number per square meter	ratio		real