Benthic Monitoring Report:
Weweantic River Estuary System 2023 Survey

Prepared for:
Watershed Planning Program
Division of Watershed Management, Bureau of Water Resources
Massachusetts Department of Environmental Protection

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Polychaete *Streblospio benedicti*. Photo by Eric A. Lazo-Wasem-Gall L (2019). Invertebrate Zoology Division, Yale Peabody Museum. Yale University Peabody Museum.

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LIST OF ACRONYMS

ATD	Average Taxonomic Distinctiveness
AU	Assessment Unit
BI	Biological Index
BBC	Buzzards Bay Coalition
BBNEP	Buzzards Bay National Estuaries Program
cm	centimeter
CMECS	Coastal and Marine Ecological Classification Standard
CMR	Code of Massachusetts Regulations
CWMP	Comprehensive Wastewater Management Plan
D_{mg}	Margalef's species richness index
DO	dissolved oxygen
EG	Ecological Grouping
ft	feet
GRTS	Generalized Random Tessellation Stratified
H'	Shannon-Wiener diversity index
HD	High Definition
J'	Pielou's evenness index
kg/ha/yr	kilogram per hectare per year
kg/yr	kilogram per year
lb/ac	pound per acre
m, m^2	meter, square meter
MA	Massachusetts
MA DMF or DMF	Massachusetts Division of Marine Fisheries
MassDEP	Massachusetts Department of Environmental Protection
MEP	Massachusetts Estuary Project
MDS	non-metric multidimensional scaling
mi, mi^2	mile, square mile
mg/L	milligrams per liter
mL	milliliter
µm	micrometer
N	abundance
NOAA	National Oceanic and Atmospheric Administration
PRIMER	Plymouth Routines in Multivariate Ecological Research
PVC	polyvinyl chloride
QAPP	Quality Assurance Project Plan
QA/QC	Quality Assurance/Quality Control
1-λ'	Simpson diversity index
S	Species richness
SOP	Standard Operating Procedure
SWQS	Surface Water Quality Standards
TMDL	Total Maximum Daily Load
TN	Total Nitrogen
TOC	Total Organic Carbon
TWMP	Target Watershed Management Plan
US EPA	United States Environmental Protection Agency
USFWS	United States Fish and Wildlife Service

US M-AMBI	Multivariate AZTI Marine Biotic Index in United States coastal waters
WPP	Watershed Planning Program
WR-2023	Weweantic River Estuary System 2023 Survey

1 Introduction

The Massachusetts Estuaries Project (MEP) was established in 2001 to monitor and protect estuarine ecosystems in southeastern Massachusetts embayments. The technical reports produced from these embayment assessments documented embayment specific baseline water quality, habitat health, and identified the actions required to restore nutrient impaired waters for approximately 70 embayments. MEP provided technical guidance in support of policies on nitrogen loading to embayments, wastewater management decisions, and establishment of nitrogen Total Maximum Daily Loads (TMDLs) for over 30 estuaries. Many communities have begun the process of integrated water resources management planning or have completed preparation of Comprehensive Wastewater Management Plans (CWMPs) or Targeted Watershed Management Plans (TWMPs).

MassDEP has generated guidance documents for the collection of post-TMDL implementation and future baseline MEP benthic monitoring data. The new guidance offers a tiered approach for previously assessed embayments and a baseline approach for unassessed embayments. The new guidance documents include a Marine Benthic Monitoring QAPP (MassDEP 2023a), which contains the Marine Benthic Monitoring Field Standard Operating Procedure (SOP) and Laboratory SOP (MassDEP 2023a Appendix A and B, respectively). These were developed for future MEP benthic monitoring efforts to describe study objectives, field and laboratory techniques, data quality requirements and assessments, and data management.

The objectives of the MEP benthic monitoring program are to:

1. Reassess the ecological health of embayments previously assessed under MEP. Embayment reassessment will confirm if ecosystem health in impaired areas has improved following the implementation of TMDLs and community measures as projected by the Linked Watershed-Embayment Model;

2. Evaluate the ecological health of southeastern Massachusetts embayments that have not been assessed. The data collected during an initial assessment will be used as a baseline to indicate current embayment health and to provide information for future management decisions; and

3. Determine if long-term changes are occurring in southeastern Massachusetts embayments that may indicate stress from eutrophication or other factors, including changes in species distribution, invasive species, and climate change.

The Weweantic River Estuary System had not previously been assessed under the MEP and was selected by MassDEP to be assessed to inform management decisions and develop TMDLs. This report provides the water quality, sediment, benthic results of the benthic monitoring conducted in the Weweantic River Estuary System, and a summary of current conditions that likely contribute to the benthic community health status.

The Weweantic watershed is the largest in the Buzzards Bay basin, encompassing both the Weweantic and Sippican Rivers. The watershed spans approximately 18,000 acres, including 588 acres of open water with a mean depth of 5.9 meters (WLT 2011). The estuarine system is 17 miles long, borders five towns, and constitutes the largest freshwater input to Buzzards Bay (approximately 20% of the total flow; BBC 2021). The river begins at the junction of Rocky Meadow and South Meadow Brooks in Carver and Middleborough, a headwater system with large wetland areas including many active cranberry bogs. The Weweantic flows through Middleborough and Rochester, a reach with two dams (Slocum-Gibbs #1 and Tremont Dams), before entering Horseshoe Pond (approximately 59 acres). Below Horseshoe Pond, the Weweantic becomes estuarine and, in Marion, widens below the confluences with the Sippican River and Beaverdam Creek, finally entering Buzzards Bay between Marion and Wareham (Figure 1).

According to the Massachusetts Surface Water Quality Standards (SWQS; 314 Code of Massachusetts Regulations [CMR] 4.00[1], MassDEP 2021), the freshwater Weweantic and Sippican River segments are designated Class B, Warm, High-Quality Waters (*see* 314 CMR 4.06(6)(b): *Table 3: Buzzards Bay Coastal Drainage Area*). The coastal and marine segments are designated Class SA, High Quality Waters and for shellfish harvesting without depuration. Beaverdam Creek is not listed in Table 3; therefore, the freshwater segment is a Class B, presumed High Quality Water, and the coastal and marine segment is Class SA and a presumed High Quality Water according to 314 CMR 4.06(5) (MassDEP 2021). Class B waters are designated as a habitat for fish, other aquatic life, and wildlife, for primary and secondary contact recreation, for irrigation and other agricultural uses, and for compatible industrial cooling and process uses. These waters shall have consistently good aesthetic value. Class SA waters are designated as an excellent habitat for fish, other aquatic life and wildlife, for primary and secondary contact recreation, for shellfish harvesting without depuration, and shall have excellent aesthetic value.

The Weweantic River winds through residential areas, undeveloped land including pine and hardwood forests and boulders, and cranberry bogs (WLT 2011). Cranberry bogs have been in operation along the Weweantic for more than 200 years and the Weweantic River watershed currently has more active cranberry bogs than any other coastal watershed in Massachusetts (WLT 2011). Cranberry bogs account for approximately 7-8% of the Weweantic River watershed area. Residential areas account for 28%, agricultural area for 26%, wetlands 13%, open land 11%, forests and water cover 2% each, and golf courses less than 1% of land use in the watershed area (MassDEP 2023b).

The total length of the estuarine reach of the Weweantic River is approximately 4 miles and the mean tidal range is 4 feet (ft; Howes et al. 2014). The health of the river is variable based on geographic location and ranges from relatively low-quality habitat in the upper estuary to improved conditions in the lower estuary, as evidenced by some sparse patches of eelgrass, (*Zostera marina*). American Eel (*Anguilla rostrata*), juvenile river herring (Alewife [*Alosa pseudoharengus*] and Blueback Herring [*Alosa aesitvalis*]), American Shad (*Alosa sapidissima*), Rainbow Smelt (*Osmerus mordax*), Sea Lamprey (*Petromyzon marinus*), White Perch (*Morone americana*), Bluefish (*Pomatomus saltatrix*), Scup (*Stenotomus chrysops*), Striped Bass (*Morone saxatilis*), Winter Flounder (*Pseudopleuronectes americanus*), and small numbers of bay scallops (*Argopecten irradians*) and Eastern oysters (*Crassostrea virginica*) can be found at the river mouth (BBC 2021). However, the upper estuary is designated for shellfish as a prohibited growing area and the lower estuary is designated conditionally restricted (MA DMF 2013) due to bacterial contamination (WLT 2011). Pollution sources include residential septic systems, fertilizer from cranberry bogs and lawns (WLT 2011), and the Bouchard 120 oil spill in Buzzards Bay (BBC 2021). The Weweantic River has significant nitrogen loading with total nitrogen (TN) concentrations greater than 0.88 mg/L in the upper estuary (MassDEP 2023b). Annual average TN concentrations from 2016 through 2020 ranged from 0.65 mg/L in 2016 to 1.04 mg/L in 2018. TN

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[1] DISCLAIMER: The descriptions of the current SWQS regulation included in this document are for informational purposes, only. The actual SWQS regulation shall control in the event of any discrepancy with the description provided. As a result, no person in any administrative or judicial proceeding shall rely upon the content of this document to create any rights, duties, obligations, or defenses, implied or otherwise, enforceable at law or in equity.

concentrations greater than 1.75 mg/L have been documented in the central area near Briarwood Beach. TN concentrations in the Weweantic River are two to three times greater than the concentrations in the Onset-Buttermilk Bays, Sippican Harbor, and Mattapoisett Harbor embayment systems (MassDEP 2023b).

Historically, anadromous and catadromous fish migrated the length of the Weweantic River and headwaters as far as Wenham Pond near Middleborough, making it not only an important habitat for Alewives, but also the only licensed Rainbow Smelt run in Massachusetts (BBNEP 2022). In the late 1880s and early 1900s, two dams were built on the Weweantic: the Tremont Iron Works Dam in West Wareham; and the Horseshoe Dam, approximately two miles to the south. Modifications to the Tremont Iron Works Dam in the 1880's effectively blocked fish passage, leaving Horseshoe Pond as the only Alewife habitat in the Weweantic River. By 1921, the river was primarily used to power saw and grist mills and to flood cranberry bogs. The river flow was obstructed by these industries, rendering it nearly impassible for Alewives (Belding 1921). MassDEP has categorized the freshwater segment of the Weweantic River (MA95-04) as impaired due to Fish Passage Barrier to diadromous fish passage at the Tremont Mill Pond Dam (MassDEP 2023c, MassDEP 2023d). In the late 1960s Rainbow Smelt runs had declined in the region; however, they were still present in three rivers in Buzzards Bay, with the Weweantic River hosting the only viable spawning run (Enterline et al. 2012).

In 2021, the dilapidated Horseshoe Pond dam and apron was removed restoring the natural tidal exchange between the freshwater and estuarine sections of the Weweantic River (see Normandeau 2022). Recent information indicates that ecological recovery in the river and wetlands is very promising so far, with observations of migratory fish species swimming upstream as early as April 2021 (Princeton Hydro 2023).

Figure 1. The location of the Weweantic River Estuary System, Massachusetts.

2 Methods

The Weweantic River Estuary System 2023 Survey (WR-2023) followed the methods outlined in the Massachusetts Estuaries Project Marine Benthic Monitoring Quality Assurance Project Plan (QAPP; MassDEP 2023a). It was comprised of four components: water quality measurement profiles, digital images, benthic infauna, and sediment conditions (grain size and total organic carbon [TOC]). For the Weweantic River Estuary System, stations were selected using a generalized random tessellation stratified (GRTS) survey design. The target population was based on MassGIS data, the National Wetlands Inventory deep water layer for the Weweantic River, MA (MassMapper 2022). A stratified approach was utilized, based on an AU segment and/or sub-segment with equal inclusion probabilities and reverse hierarchical ordering site replacement design. The number of locations per segment was based on the area of the three main AU segments in proportion to the total area of the embayment system. The number of sampling locations per main AU segment was as follows: Weweantic River eight base sites; Sippican River one base site; and Beaverdam Creek one base site. The two replacement ("over") locations were determined for each base location. Due to the linear nature of the Weweantic River, the Weweantic River AU segment was further subdivided into eight equal-sized sub-segments (A – H) to ensure appropriate representation of the benthic communities along the entire river length and salinity gradient (Figure 2; MassDEP 2023f).

Detailed descriptions of the field and laboratory methods are contained in the MEP Benthic Monitoring QAPP, which includes the MEP Marine Benthic Monitoring Field SOP (MassDEP 2023a, App. A), and the MEP Marine Benthic Monitoring Laboratory SOP (MassDEP 2023a, App. B). A brief overview of the methods, focused on information specific to this survey, is provided below in Sections 2.1 to 2.3.

2.1 Field Methods

Sampling was conducted at ten Weweantic River stations identified in the Weweantic River Embayment-Specific Study Plan (MassDEP 2023f) on September 19 and October 26, 2023 (Table 1, Figure 2). All base stations except one were assessed as planned; base station MEP-SE-002 could not be sampled due to limited access from extremely shallow stretches in the upper reaches of the river system and was replaced with over station MEP-SE-013. A Garmin ECHOMAP UHD 64CV (accuracy +/-2 m) was used for navigation and to acquire coordinates at the location of each sample. Comparisons among sampling coordinates and target station locations confirm that sampling was conducted within the 30-m target radius at each station.

Three infaunal grabs and one sediment grab were collected at each of the ten stations with a 0.04m^2 Young-modified Van Veen grab sampler. One duplicate sediment grab was collected at Station MEP-SE-001 for quality control purposes, for a total of 30 infaunal and 22 sediment samples (11 grain size and 11 total organic carbon [TOC]). All infaunal samples were rinsed in the field with clean seawater through a 500-micrometer (µm) mesh sieve and fixed in 10% formalin in labelled jars. Samples were hand delivered to the Normandeau Falmouth, MA office, after seven days the samples were rinsed with fresh water and transferred to reagent alcohol for storage and transport to the Normandeau Bedford, NH laboratory for sorting and taxonomic identification. Samples for sediment grain size and TOC analysis were collected by scooping the surface sediment (0 to 2cm) of each grab, homogenizing, and transferring approximately 50-mL to appropriate storage bags or jars. Sediment samples were hand delivered to the Normandeau Falmouth, MA office and immediately refrigerated. The samples were then transferred to Pace Analytical Laboratories within 24 hours by a Pace Analytical courier for grain size and TOC analysis.

Water quality measurement profiles were taken using an In-Situ Aqua TROLL 600 multi-parameter water quality sonde with data recorder and temperature, dissolved oxygen (DO), pH, and salinity/conductivity probes. The 0.1 m below the surface measurements were not recorded at the ten stations, all other profile measurements were collected following the depths and protocol specified in the Marine Benthic Monitoring QAPP and Field SOP (MassDEP 2023a).

Digital video images for each sampling location were recorded using a Delta Vision Splashcam HD camera in a waterproof housing attached to a PVC frame designed to match the MassDEP eelgrass camera frame. The camera is set in a fixed position 1 m above the bottom. A GoPro Hero 3+ was also attached to the camera frame to provide digital still images and camera redundancy. Due to elevated and prolonged turbidity of fine sands and silt as well as consistent shallow depths (<3 ft) at many of the stations, images used to visualize bottom sediments may vary in clarity and the scaling frame may not be visible.

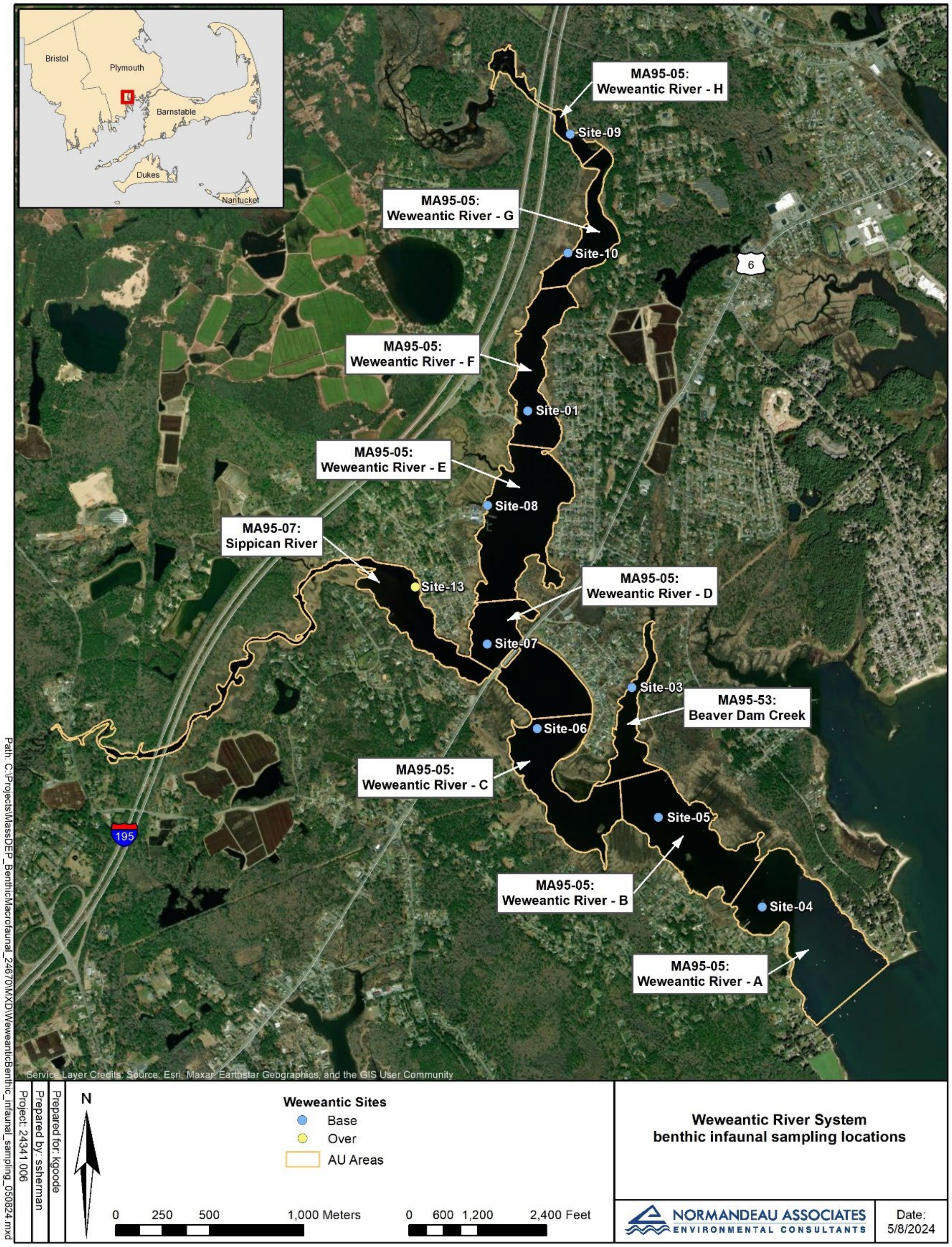

Figure 2. Benthic infaunal sampling locations in the Weweantic River Estuary System, delineated by the MassDEP Assessment Units (AUs).

Table 1. Listing of Preliminary Field Data from the Weweantic River Estuary System 2023 Survey (WR-2023).

Weweantic River Estuary System								
Station[1]	**Site Use**	**AU ID**	**Sub-embayment**	**Arrival Date (time)**	**Bottom Depth (m)**	**Latitude[2]**	**Longitude**	**Comments**
MEP-SE-009	base	MA 95-05	Weweantic River	10/26/2023 (1418)	0.5	41.76307	-70.74259	soft silty packed mud, sand
MEP-SE-010	base	MA 95-05	Weweantic River	10/26/2023 (1050)	0.6	41.75737	-70.74282	black silt
MEP-SE-001	base	MA 95-05	Weweantic River	10/26/2023 (0956)	1.1	41.74979	-70.74549	soft silty packed mud
MEP-SE-008	base	MA 95-05	Weweantic River	10/26/2023 (1654)	0.5	41.74528	-70.74812	soft, silty
MEP-SE-013	over	MA 95-07	Sippican River	10/26/2023 (1614)	0.5	41.74139	-70.75279	silty mud
MEP-SE-007	base	MA 95-05	Weweantic River	10/26/2023 (1534)	0.5	41.73863	-70.74821	silty mud
MEP-SE-006	base	MA 95-05	Weweantic River	09/19/2023 (1318)	2.8	41.73455	-70.74505	sandy soft bottom
MEP-SE-003	base	MA 95-53	Beaverdam Creek	09/19/2023 (1225)	1.0	41.73647	-70.73897	smooth mud
MEP-SE-005	base	MA 95-05	Weweantic River	09/19/2023 (1426)	1.9	41.73023	-70.73734	strong wind & current
MEP-SE-004	base	MA 95-05	Weweantic River	09/19/2023 (1508)	1.7	41.72588	-70.73073	station behind rock pile

[1] Sites are organized from innermost to outermost locations within the Weweantic River Estuary System; see Figure 2.
[2] Latitude and longitude coordinates are in decimal degrees

2.2 Laboratory Methods

Laboratory methods were consistent with the MEP Marine Benthic Monitoring Laboratory SOP (MassDEP 2023a Appendix B). Two infauna samples from each station were randomly selected for processing, while the third was archived. A total of 20 benthic samples from the Weweantic River Estuary System were sorted, and ten samples were archived. Organisms were sorted and identified to the lowest possible taxonomic level using a dissecting microscope. Each new distinct taxon to the MEP was saved separately in a labeled vial with reagent alcohol and archived in a reference collection as directed under Section B4.1 of the MEP Benthic Monitoring QAPP.

Grain size samples were analyzed by Pace Analytical Laboratories following Section III of the MEP Marine Benthic Monitoring Laboratory SOP, using the ASTM Method D6913/D7928. One sediment sample (50 mL total volume) from each station, plus one additional sample from MEP-SE-001 for quality control (QC) purposes, for a total of 11 samples were analyzed in the laboratory.

The analytical laboratory reported grain size in the Unified Soil Classification System. Grain size results were converted to the Coastal and Marine Ecological Classification Standard (CMECS) mineral grain size descriptors adopted from Wentworth (1922; FGDC 2012) using stated sieve size and the Folk (1974) conversion table. Grain size results were reported as a percentage by weight in five categories as follows:

- gravel = 2 mm to < 4,096 mm
- coarse sand = 500 µ to < 2 mm (includes the very coarse sand fraction)
- medium sand = 250 µ to < 500 µ
- very fine sand = 63 µ to < 250 µ (includes the fine sand fraction)
- silt = <63 µ

Marine and estuarine sediments generally consist of a mixture of grain sizes. For example, silty sand is defined as the combination of the three smallest sediment size classifications: fine sand, very fine sand, and silt.

Sediment samples for TOC followed the MEP Benthic Monitoring QAPP (MassDEP 2023a Appendix A) for preservation and hold times. Analytical methods for TOC followed the US EPA Method 9060 (US EPA 2021).

2.3 Data Analysis

Benthic infauna data were analyzed for the following community parameters: abundance, Shannon-Wiener diversity index (H'), Pielou's evenness (J'), Margalef's species richness index (D_{mg}), Simpson (1-λ'), and Average Taxonomic Distinctiveness (ATD), using the PRIMER v7 (Plymouth Routines in Multivariate Ecological Research) software program (Warwick and Clarke 1991, Clarke and Gorley 2001). Calculations for all the above parameters were on untransformed data and Shannon-Weiner (H') was calculated using log base e data.

Multivariate analyses were performed using PRIMER v7 software to examine spatial patterns in the overall similarity of benthic assemblages in the Weweantic River Estuary System (Clarke 1993, Clarke and Warwick 2001). These analyses included classification (cluster analysis) by hierarchical agglomerative clustering with group average linking and ordination by non-metric multidimensional scaling (MDS). Bray-Curtis similarity was used as the basis for both classification and ordination. Similarity measures compare counts within each taxon between all possible pairs of samples. Values range from 0, when two samples have no taxa in common, to 100 when two samples are identical in taxa and counts within taxa. MDS outputs a two-dimensional plot where spatial proximity illustrates relative similarity between samples and is interpreted by the closeness of the samples. Clarke (1993) suggested that a stress level less than 0.20 (shown in the upper right corner of the plot) indicates that a potentially useful two-dimensional representation has been achieved. The results are also presented with a hierarchical clustering tree diagram (a dendrogram), with the x-axis representing the full set of samples, and the y-axis defining a similarity level at which two samples or groups are considered to have fused (Clarke and Warwick 2001). To reduce the influence of high-density outliers, densities were square-root transformed before calculating similarity. The square-root transformation decreases the influence of the most abundant species so that rare species factor in more heavily when calculating similarity.

US M-AMBI (multivariate AZTI Marine Biotic Index in United States coastal waters) was calculated following Pelletier et al. (2018) to determine Weweantic River sub-embayment and embayment soft bottom habitat health. Modifications to the existing M-AMBI taxonomic classification (Ecological Grouping [EG]) were made prior to using the program utilizing the taxonomic list and corresponding EGs established by Pelletier et al. (2018) to be specific for the northeast US region. Each taxon identified is classified as EG I, II, III, IV, or V, with I taxa being considered those found in healthy benthic habitats, and V taxa inhabiting low quality habitat. The available published EG taxonomic list is for European studies, and some classifications are not the same as those for other regions. The revised taxonomic EG list specific to the northeast US region was provided by M. Pelletier (personal communication 2024). In this updated EG list oligochaetes are assigned an EG code of V, which is different from previous US M-AMBI calculations in which oligochaetes were not included in the calculation. This change was recommended by M. Pelletier based on updated information (personal communication 2024).

The data were prepared for US M-AMBI by first coding each station in the Weweantic River Estuary System by salinity categories as defined by Pelletier et al. (2010): tidal fresh (< 0.5 ppt), low mesohaline (≥ 5 – 12 ppt), high mesohaline (≥ 12 – 18 ppt), and polyhaline (≥ 18 ppt) and then assigning each taxon with the Northeast United States EG codes (categories I-V). Some taxa in the Weweantic River Estuary System samples were not included in the data set because no EG code was available for this region at this time (i.e., polychaete *Kirkegaardia hampsoni*, shrimp *Penaeus aztecus*, Nemertea, and a few others), or the specimens were not able to be identified to a low enough taxonomic level (i.e., Gastropoda and Bivalvia). The Biological Index (BI) was then calculated for each sample using the following formula:

$BI = 0*\%EG(I) + 1.5*\%EG(II) + 3*\%EG(III) + 4.5*\%EG(IV) + 6*\%EG(V)$

Species richness (S) and Shannon-Weiner diversity index (H’) were calculated for all species (including those that were not assigned an EG code; e.g., *K. hampsoni*, Nemertea, etc.) using PRIMER. These four parameters (salinity code, BI, S, and H’) were then run through the R script for the Northeast United States provided by M. Pelletier (personal communication 2024). The output number corresponding to benthic health condition falls within the following categories (Table 2): Bad (<0.20), Poor (0.20 to 0.39), Moderate (0.39 to 0.53), Good (0.53 to 0.77), and High (>0.77).

Table 2. US M-AMBI Benthic Health Conditions Categories and Scores

US M-AMBI Category	US M-AMBI Score
High	>0.77
Good	0.53-0.77
Moderate	0.39-0.53
Poor	0.20-0.39
Bad	<0.20

In addition to the US M-AMBI scores, AMBI scores and corresponding categories[2] (M. Pelletier personal communication 2024) were reported. AMBI is an abundance-weighted, tolerance value index that assesses habitat condition based upon the relative abundance of taxa in different tolerance value groups (i.e., EG codes) but does not account for salinity. While M-AMBI, in addition to factoring in the AMBI metric, also includes diversity, species richness, percentage of oligochaetes (for both freshwater and all marine/estuarine salinity categories), and salinity. The reporting of the two indices can be helpful to explain habitats for which the US M-AMBI scores do not appear to correlate with other information (e.g., community parameters, BBC Health Scores, high percentage of silt and/or TOC, etc.). US M-AMBI is reported in the National Coastal Condition Assessment as a condition indicator. AMBI is a metric used to calculate M-AMBI, and thus is not used solely as an indicator. However, both US M-AMBI scores/categories and the categories associated with AMBI can be considered together when trying to understand nuances of complex estuaries, such as the Weweantic River Estuary System.

3 Results and Discussion

3.1 Water Quality

Water quality in the Weweantic River Estuary System was characterized in 2023 by measuring four parameters at each of the 10 sampling locations: water temperature, DO, pH, and salinity (Appendix A). As mentioned above, the Weweantic River is designated as a Class SA water. The criteria for SA waters are that DO shall not be less than 6.0 mg/L, temperature shall not exceed 29.4°C (85°F) nor a maximum daily mean of 80°F (26.7° C), and pH shall be between 6.5 and 8.5 standard units and not more than 0.2 standard units outside of the natural background range (MassDEP 2021) The majority of the water quality readings recorded during this survey met the SA water quality criteria. Four DO readings at two stations in the middle reaches of the Weweantic River Estuary System fell below 6.0 mg/L (two at Station MEP-SE-005 and two at Station MEP-SE-006 with a minimum DO of 5.7 mg/L [Appendix A]).

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[2] Benthic health categories associated with AMBI are as follows: <1.2 = undisturbed; 1.3-3.2 = slightly disturbed; 3.3-4.9 = moderately disturbed; 5.0-6.9 = heavily disturbed; 7= azoic.

3.2 Sediment Composition

Sediment conditions in the Weweantic River Estuary System were characterized in 2023 by measuring two parameters at each sampling location where grab samples could be collected: (1) grain size and (2) total organic carbon (Table 3). In addition, the following field observations of the bottom conditions were recorded.

Sediments in the Weweantic River Estuary System ranged from sand at stations MEP-SE-004, 005, and 006 in the lower Weweantic River to silt, silty sand, and mud at the remaining stations in the Weweantic River and station MEP-SE-013 in the Sippican River (Figure 3). The sediment at the only station sampled in Beaverdam Creek (MEP-SE-003) was mud.

Notes on sediment and benthic infaunal recorded in the field at the following stations included:

- MEP-SE-004: *Crepidula sp.* shell hash, sponge in the grab jaws
- MEP-SE-005: Shells, rocks, and polychaete worms were observed
- MEP-SE-006: Sandy with rocks, difficult to obtain full grab; quahog in jaws of the grab
- MEP-SE-010: Sticks and leaves were observed

No eelgrass was observed in the field at any of the stations.

3.2.1 Grain Size Analysis

Surface sediments collected at 10 sampling locations in 2023 contained a range of sand and silt sediments summarized in Table 3 and Figure 3 below. Percentage of sediment types in the Weweantic River samples varied within and among basins; overall sediments were less silty at the stations in the lower River, with the most direct access to tidal flushing (Stations MEP-SE-006, 005, and 004, the three outermost stations; Table 3, Figure 3). The exception was Station MEP-SE-009 in the upper reaches just downstream from the former Horseshoe Pond Dam which also had a relatively low percentage of silt, but with little access to tidal flushing. This is consistent with the sediments observed both up- and downstream from the Horseshoe Pond Dam area prior to dam removal, where fine-grained sediments up to 6 feet deep were observed behind the dam, with rock and cobble riffle observed immediately downstream (NOAA 2017). Percent silt ranged from 0.5% at Beaverdam Creek Station MEP-SE-003 to 51.6% at Station MEP-SE-010 located in the upper reaches of the Weweantic River.

In general, higher percentages of organic matter deposition (e.g. silt) to the sediments result in relatively lower benthic habitat quality (Howes et al. 2014). Silty sediments are generally inhabited by low-diversity, shallow-dwelling organisms compared to high-diversity deep-burrowing organisms found in more sandy sediments (Howes et al. 2014). However, the lower percent silt level in the Beaverdam Creek (MEP-SE-003) compared to those in the lower Weweantic River is highly unusual, unexpected, and may indicate an error. Pace Analytical Laboratories was contacted to determine whether an error may have occurred in sample processing or data entry. The laboratory indicated that an error was very unlikely to have occurred and unfortunately no bench notes on the sample were available. The grain size results at Station MEP-SE-003 are also suspicious as the field notes recorded when the samples were collected described the sediment to be “soft mud” with Van Veen grab penetration depth measurements of 10 cm for all four replicates. Grain size results for soft mud have higher percentages of finer sand and silt, which was not the case with sediment sample MEP-SE-003. The TOC for Station MEP-

SE-003 (7.3%) is relatively high (see Figure 4) and indicative of silty sediment, which was expected based on the field notes, but not reflected in the grain size results. In future surveys, it is recommended to include photographic images of the benthic grab contents upon retrieval and at least two sample locations per separate body of water if budget allows to prevent such data anomalies.

3.2.2 Total Organic Carbon

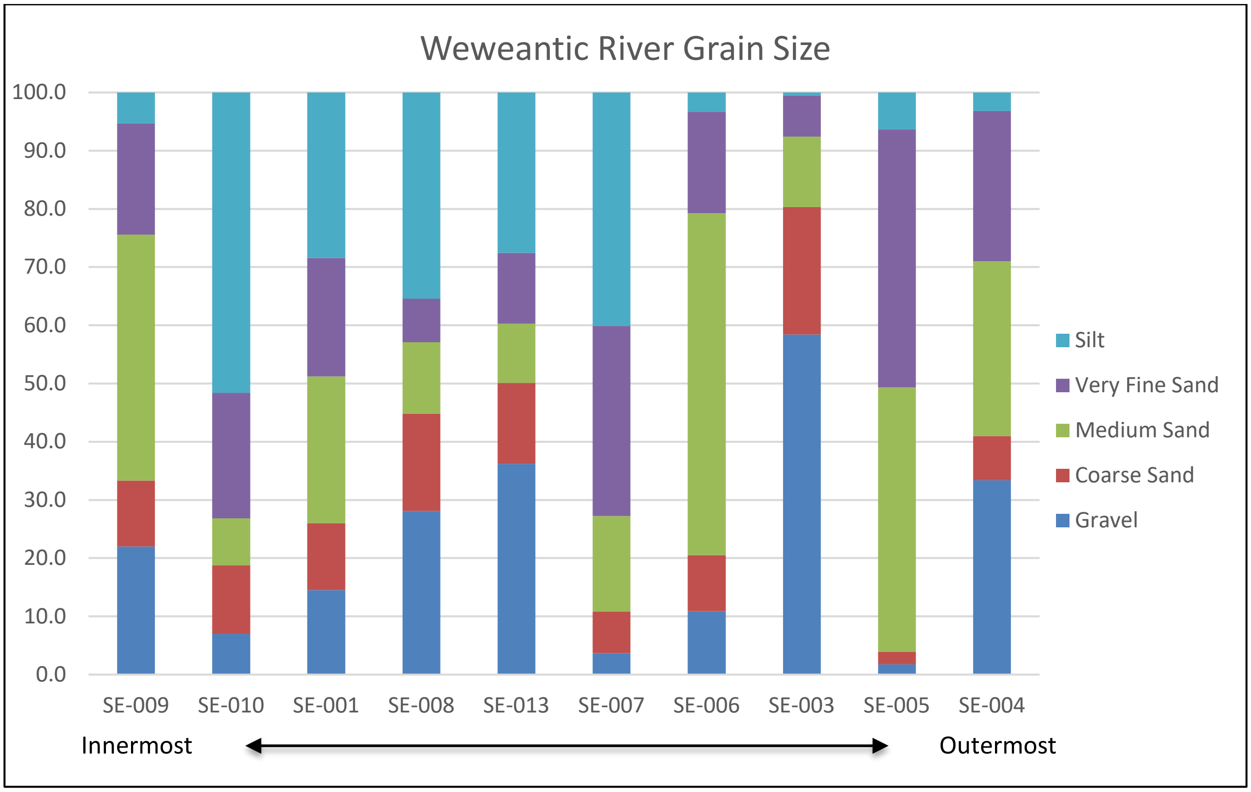
Organic matter in sediments can form water-soluble and water-insoluble complexes with metal ions and hydrous oxides, interact with clay minerals binding particles together, adsorb and desorb both natural and man-made organic compounds, and absorb and release nutrients (Schumacher 2002). Therefore, total organic carbon (TOC) can be an important parameter in characterizing the health status of a site because the level of TOC can markedly influence how chemicals will react in the sediment (Schumacher 2002). Three basic forms of carbon may be present in sediments: elemental carbon (from charcoal, soot, graphite, and coal), inorganic carbon (from geologic or soil parent material sources), and organic carbon (derived from the decomposition of plants and animals). In addition to the naturally occurring organic carbon sources, anthropogenic activities can also increase the total carbon content to sediment. For example, spills or releases of contaminants into the environment increase the total carbon content in the sediment. In general, though, the total carbon contribution from contaminants to the TOC content in sediment is relatively small to negligible unless a fresh spill has occurred (Schumacher 2002). The level of TOC can be used as a general indicator for sediment quality and impairment from organic waste and other anthropogenic pollutants (Hyland et al. 2005 and Pelletier et al. 2011). For example, sediments with percentages of TOC <1% are generally considered to be minimally impaired, between 1% and 3.5% moderately impaired, and >3.5% degraded (Hyland et al. 2005).

TOC in the stations sampled in the Weweantic River Estuary System were variable ranging from 0.4% in two lower River stations (Station MEP-SE-004 and 006) to 7.3% in Beaverdam Creek (Station MEP-SE-003; Table 3, Figure 4). In general, TOC was higher in the upstream locations (e.g., Stations MEP-SE-010 [6.8%] and MEP-SE-008 [6.9%]) located above Route 6, as well as the sub-embayment Stations MEP-SE-013 in the Sippican River (5.1%) and MEP-SE-003 in Beaverdam Creek (7.3%) The relatively higher tidal flushing in the outer Weweantic River locations (e.g., MEP-SE-005 and 004) corresponded to lower TOC (0.7% and 0.4%, respectively). Higher TOC values were associated with a higher percent silt, with the exception of the anomalous Beaverdam Creek station (MEP-SE-003; Figure 4).

Table 3. Results for the Weweantic River Estuary System sediment grain size and TOC in 2023.

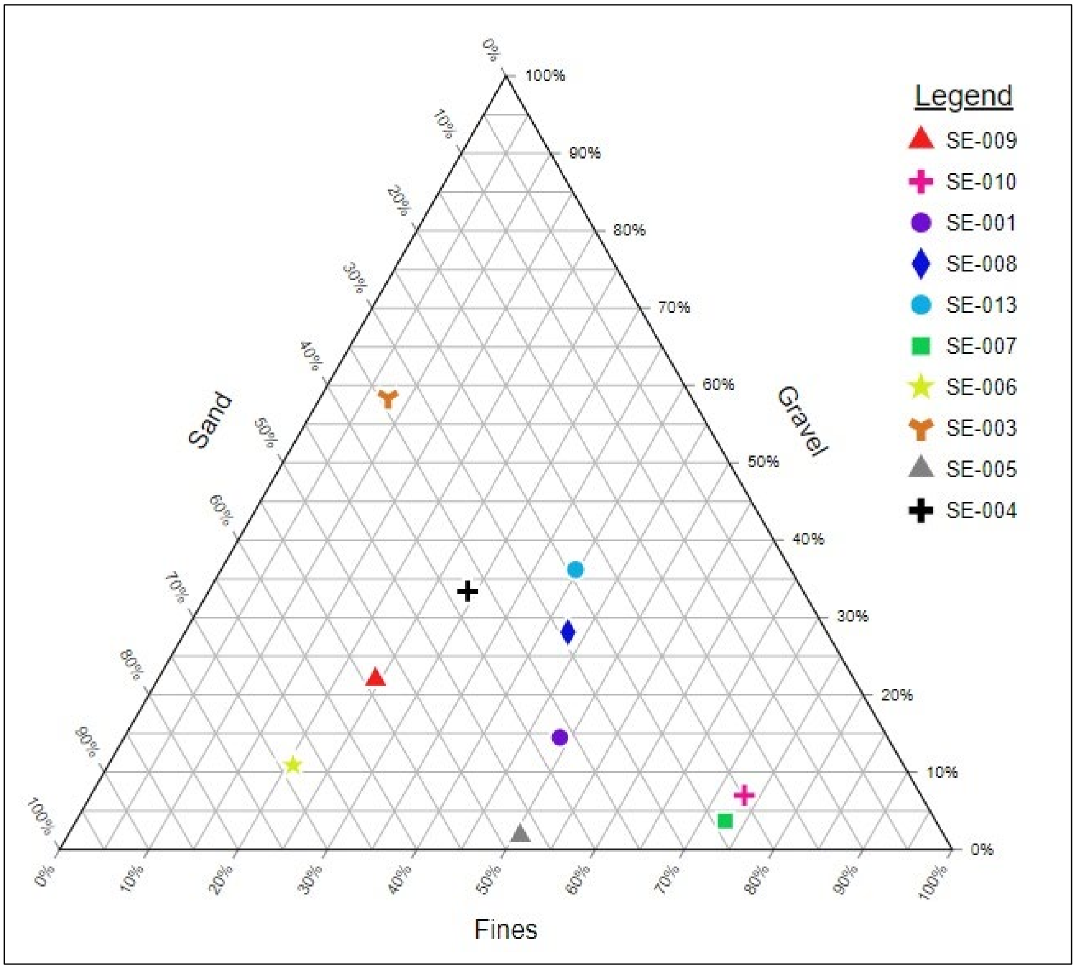
	Percent (%)									
	SE-009	**SE-010**	**SE-001**	**SE-008**	**SE-013**	**SE-007**	**SE-006**	**SE-003**	**SE-005**	**SE-004**
Gravel	22.0	7.0	14.5	28.1	36.2	3.7	10.9	58.4	1.8	33.4
Coarse Sand	11.3	11.7	11.5	16.7	13.9	7.2	9.7	21.8	2.1	7.6
Medium Sand	42.3	8.1	25.2	12.3	10.2	16.4	58.8	12.1	45.4	30.0
Very Fine Sand	19.1	21.6	20.3	7.5	12.2	32.7	17.4	7.1	44.3	25.8
Silt	5.3	51.6	28.5	35.4	27.5	40.1	3.3	0.5	6.4	3.2
TOC	2.3	6.8	2.2	6.9	5.1	3.2	0.4	7.3	0.7	0.4

Stations are organized from innermost (left) to outermost (right) within the Weweantic River Estuary System; basins are separated by solid black lines.



a.

Figure 3. Weweantic River Estuary System percent grain size analysis shown as a) a stacked bar graph and b) a ternary plot, fall 2023.



b.

Figure 3. Continued. The data are displayed on this ternary plot so that stations with higher gravel proportions are plotted towards the top of the triangle, stations with higher sand proportions are plotted near the bottom left of the triangle, and stations with higher fines are plotted towards the bottom right of the triangle. The stations in the legend are ordered from innermost to outermost in the Weweantic River Estuary System as shown in the sampling location map (Figure 2)

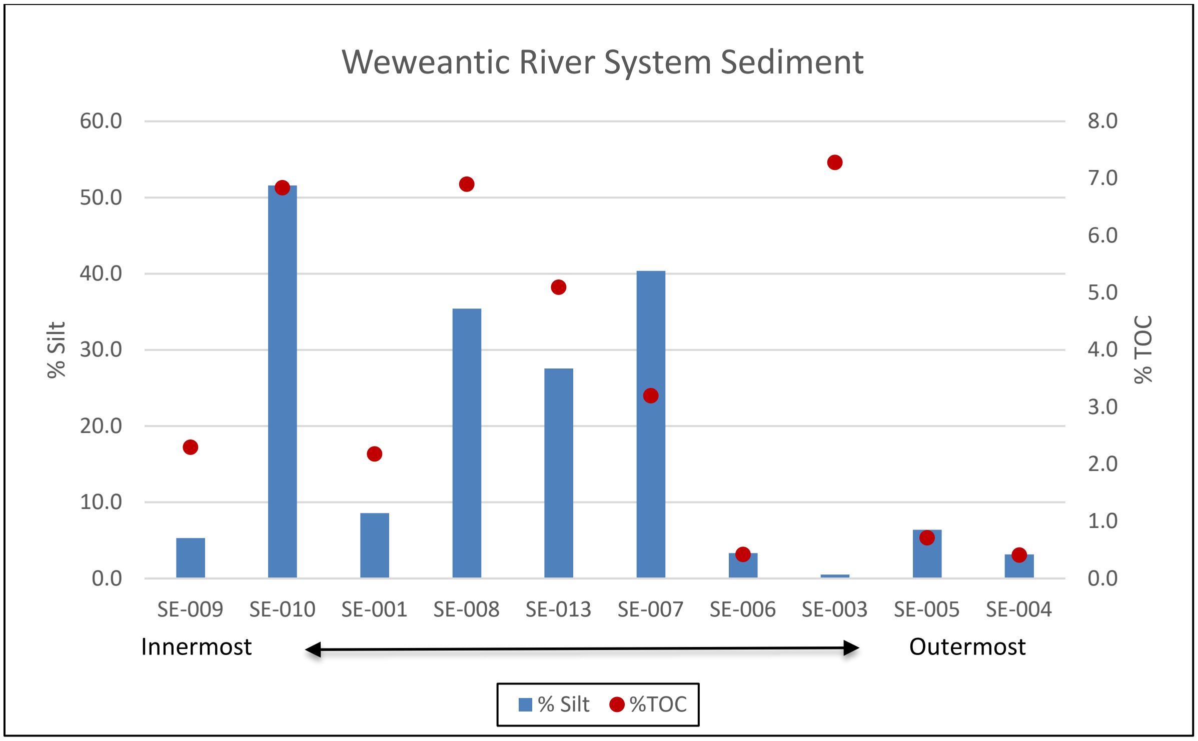


Figure 4. Weweantic River Estuary System sediment: percent silt and TOC, 2023.

3.3 Underwater Digital Images

Digital photographs and videos were taken at each station in the Weweantic River Estuary System. Underwater video quality was very poor on both sampling dates primarily due to the shallow water depth resulting in high turbidity, making the bottom indistinguishable from the water column. Images of representative habitat types found within the Weweantic are provided below in Figure 5. Eelgrass was not observed at any of the sampling locations in 2023. This is consistent with results from the MassDEP Eelgrass Mapping Project that indicate eelgrass has declined in most areas of the Weweantic River Estuary System from 1995 to 2017, the most recent year surveyed (Costello and Kenworthy 2011, MassDEP 2018, WHG 2021).

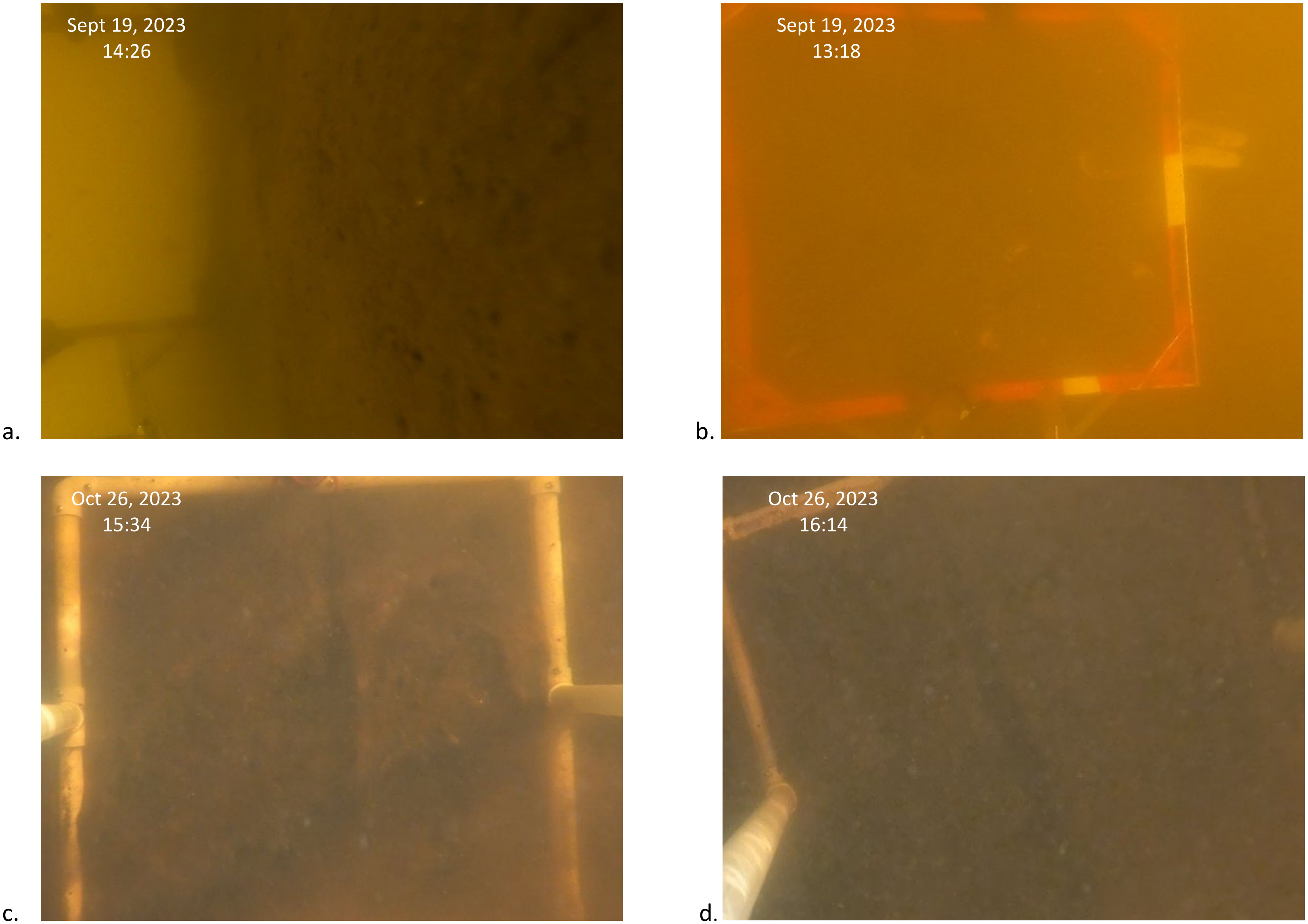


Figure 5. Images of Weweantic River bottom habitat: a) Station MEP-SE-005 (silty mud), b) Station MEP-SE-006 (silty sand with quahogs), c) Station MEP-SE-007 (silty sand), d) Station MEP-SE-013 (coarse sand).

3.4 Benthic Infauna Community

The 2023 Weweantic River Estuary System benthic samples contained a total of 144 taxa, representing nine phyla (Table 4). The benthic communities were characterized based on the following macroinvertebrate metrics: number of species (S), abundance (N), species richness (Margalef, D_{mg}), diversity (Shannon-Weiner [H’] and Simpson’s index [1-λ]), and evenness (Pielou, J’). In addition, Average Taxonomic Distinctness (ATD), cluster and non-metric multidimensional scaling (MDS) analyses, and US M-AMBI are presented to assess spatial and temporal trends in community composition within and between sub-embayments, and eventually between estuaries. Due to the complexity of the Weweantic River Estuary System, the cluster and MDS analyses are presented first to provide groups based on similarity for which the remaining metrics could be discussed in the report. Since US M-AMBI incorporates several of the above metrics (i.e., species number, Shannon-Weiner diversity H’, and BI score) and salinity category [see Methods section above]), US M-AMBI was used as an overall summary of the benthic habitat health status.

3.4.1 Dominant taxonomic groups and species

Among all stations, a total of 9,716 individuals from 144 taxa were identified in the 2023 Weweantic River Estuary System benthos (Table 4). These taxa represented the following nine phyla: Annelida (segmented worms), Mollusca (bivalves and gastropods), Arthropoda (amphipods, decapods, and insects), Echinodermata (sea cucumbers), Cnidaria (sea anemones), Platyhelminthes (flat worms), Nemertea (ribbon worms), Hemichordata (acorn worms), and Xenacoelomorpha (acoelomorph flatworms). The majority of taxa (71%) were polychaete annelids (bristle worms), followed by oligochaete annelids (aquatic earth worms; 18%) and molluscs (5%). Ten taxa comprised 80% of all individuals. The three most abundant taxa were the polychaete *Mediomastus ambiseta* (2,089 individuals), oligochaetes (1,788 individuals), and the polychaete *Streblospio benedicti* (1,340 individuals).

Table 4. Taxonomic list for Weweantic River Estuary System benthos, 2023.

Phylum	**Class/Order**	**Taxa**		**Phylum**	**Class/Order**	**Taxa**	
Annelida	Polychaete	Alitta	succinea	Annelida	Polychaete	Notomastus	sp.
		Ampharete	oculata			Odontosyllis	obscurus
		Aphelochaeta	sp.			Oxydromus	obscurus
		Arabella	iricolor			Parasabella	microphthalma
		Aricidea	catherinae			Pectinaria	gouldii
		Brania	wellfleetensis			Phyllodoce	arenae
		Cabira	incerta			Pista	mediterranea
		Carazziella	hobsonae			Podarkeopsis	levifuscina
		Caulleriella	sp.			Polycirrus	eximius
		Cirratulus	sp.			Polydora	aggregata
		Clymenella	torquata			Polydora	cornuta
		Dipolydora	concharum			Polydora	heterochaeta
		Dipolydora	socialis			Potamilla	neglecta
		Drilonereis	longa			Prionospio	heterobranchia
		Enoplobranchus	sanguineus			Prionospio	steenstrupi
		Eteone	longa			Sabellaria	vulgaris
		Euclymene	collaris			Salvatoria	brevipharyngea
		Eulalia	viridis			Salvatoria	clavata
		Eumida	sanguinea			Schistomeringos	rudolphi
		Eusyllis	lamelligera			Scoletoma	tenuis
		Exogone	dispar			Sphaerosyllis	perkinsi
		Fabricia	stellaris			Sphaerosyllis	taylori
		Glycera	americana			Spiochaetopterus	oculatus
		Glycera	dibranchiata			Sthenelais	limicola
		Glycinde	multidens			Streblospio	benedicti
		Heteromastus	filiformis			Streptosyllis	verrilli
		Hobsonia	florida			Tharyx	acutus
		Hypereteone	heteropoda			Tharyx	sp.
		Kirkegaardia	baptisteae			Tharyx A*	sp.
		Kirkegaardia	hampsoni	Annelida	Oligochaeta	Oligochaeta	
		Leitoscoloplos	robustus	Arthropoda	Amphipoda	Ampelisca	abdita
		Marenzelleria	neglecta			Ampelisca	vadorum
		Marphysa	sanguinea			Ampelisca	verrilli
		Mediomastus	ambiseta			Apocorophium	acutum
		Mediomastus	californiensis			Batea	catharinensis
		Mediomastus	sp.			Caprella	mutica
		Melinna	maculata			Cerapus	tubularis
		Microphthalmus	sczelkowii			Cymadusa	compta

Table 4. Continued.

Phylum	Class/Order	Taxa	
Arthropoda	Amphipoda	Deutella	incerta
		Eobrolgus	spinosus
		Ericthonius	brasiliensis
		Globosolembos	smithi
		Grandidierella	japonica
		Lysianopsis	alba
		Microdeutopus	gryllotalpa
		Monocorophium	acherusicum
		Paracaprella	tenuis
		Rudilemboides	naglei
		Unciola	serrata
Arthropoda	Cumacea	Cyclaspis	varians
		Leucon	americanus
	Decapoda	Callinectes	sapidus
		Dyspanopeus	sayi
		Pagurus	sp.
		Panopeidae	
		Penaeus	aztecus
		Portunidae	
	Diptera (Insect)	Chironomidae A*	
		Chironomidae B*	
	Isopoda	Cyathura	polita
		Edotia	triloba
		Ianiropsis	serricaudis
		Ptilanthura	tenuis
	Pycnogonida	Anoplodactylus	petiolatus
		Callipallene	brevirostris
Cnidaria	Actinaria	Actinothoe	sp.
		Edwardsia	elegans
		Urticina	crassicornis
	Anthoathecata	Euphysa	aurata
Echinodermata	Holothuroidea	Epitomapta	roseola
		Leptosynapta	tenuis
		Pentamera	pulcherrima
Hemichordata	Enteropneusta	Saccoglossus	kowalevskii
Xenacoelomorpha	Xenacoelomorpha		
Mollusca	Gastropoda	Acteocina	canaliculata
		Astyris	lunata
		Caecum	pulchellum
		Crepidula	fornicata
		Haminella	solitaria
		Hydrobiidae	
		Ilyanassa	obsoleta
		Japonactaeon	punctostriatus
		Lacuna	vincta
		Pyramidellidae	
		Turbonilla	interrupta
Mollusca	Bivalvia	Ameritella	agilis
		Ennucula	delphinodonta
		Gemma	gemma
		Laevicardium	mortoni
		Lyonsia	hyalina
		Macoma	petalum
		Mercenaria	mercenaria
		Mulinia	lateralis
		Mya	arenaria
		Nucula	proxima
		Nuculidae	
		Spisula	solidissima
		Tagelus	divisus
		Tellinidae	
Nemertea	Hoplonemertea	Amphiporus	cruentatus
	Hoplonemertea	Amphiporus	ochraceus
	Hoplonemertea	Correanemertes	bioculatus
	Hoplonemertea	Zygonemertes	virescens
	Paleonemertea	Carinoma	tremaphoros
	Paleonemertea	Cephalothrix	linearis
	Piliidiophora	Cerebratulus	lacteus
Platyhelminthes	Platyhelminthes 19*		
	Platyhelminthes 22*		
	Platyhelminthes 5*		

*Indicates specimens that were distinguishable from each other, but not identifiable to a lower level.

3.4.2 Cluster and non-metric multidimensional scaling (MDS)

The Weweantic River Estuary System is complex, comprising three relatively narrow bodies of water: the Weweantic River, Beaverdam Creek, and Sippican River, with a wide range of salinities ranging from tidal fresh to polyhaline with sand and mud sediments. The tidal fresh water (salinity = 0.2 ppt) was recorded at Station MEP-SE-009 in the upper Weweantic River, and thus above the reach of the saltwater incursion.

As indicated above, benthic infaunal grabs were collected at 10 stations within the System. Multivariate analyses were used to assess spatial patterns in the infaunal assemblages at the Weweantic River Estuary System sampling stations. The cluster analysis identified three assemblages in the benthos (Table 5, Figure 6). The patterns identified through cluster analysis were confirmed in the MDS ordination plot (Figure 7). Spatial patterns in the faunal assemblages of the System reflect a gradient from Group 1- the Lower Weweantic River (Stations MEP-SE-004, 005, and 006), to Group 2- the Mid-Weweantic River (Stations MEP-SE-001 and 007) and Beaverdam Creek (Station MEP-SE-003), and Group 3- the Upper Weweantic (Stations MEP-SE-008, 009, and 010) and Sippican River (Station MEP-SE-013; Table 5). The similarity among groups was 47% for Group 1, 51% for Group 3, and 70% for Group 3 (dark blue dashed lines in Figure 7).

Table 5. Summary of groupings identified in the cluster and MDS plots of the Weweantic River Estuary System benthic infauna, 2023.

Group	Station MEP-SE-	Section of Weweantic River Estuary System	Group	Station MEP-SE-	Section of Weweantic River Estuary System
1	004	Lower Weweantic	3	008	Upper Weweantic
	005			009	
	006			010	
2	001	Mid-Weweantic		013	Sippican River
	003	Beaverdam Creek			
	007	Mid-Weweantic			

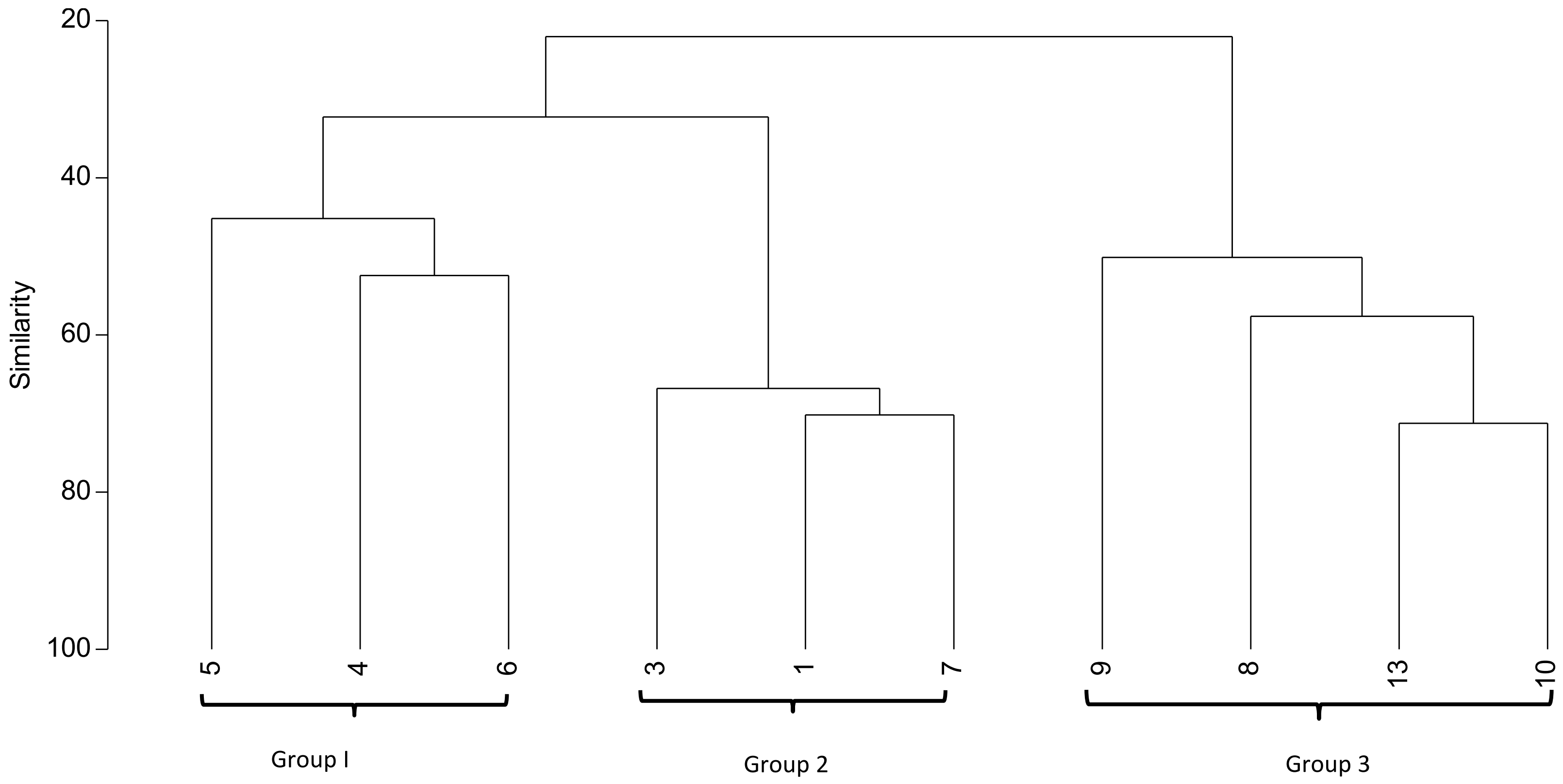


Figure 6. Cluster analysis results of the 2023 Weweantic River infaunal samples. The x-axis = each of the 10 stations (MEP-SE-00X).

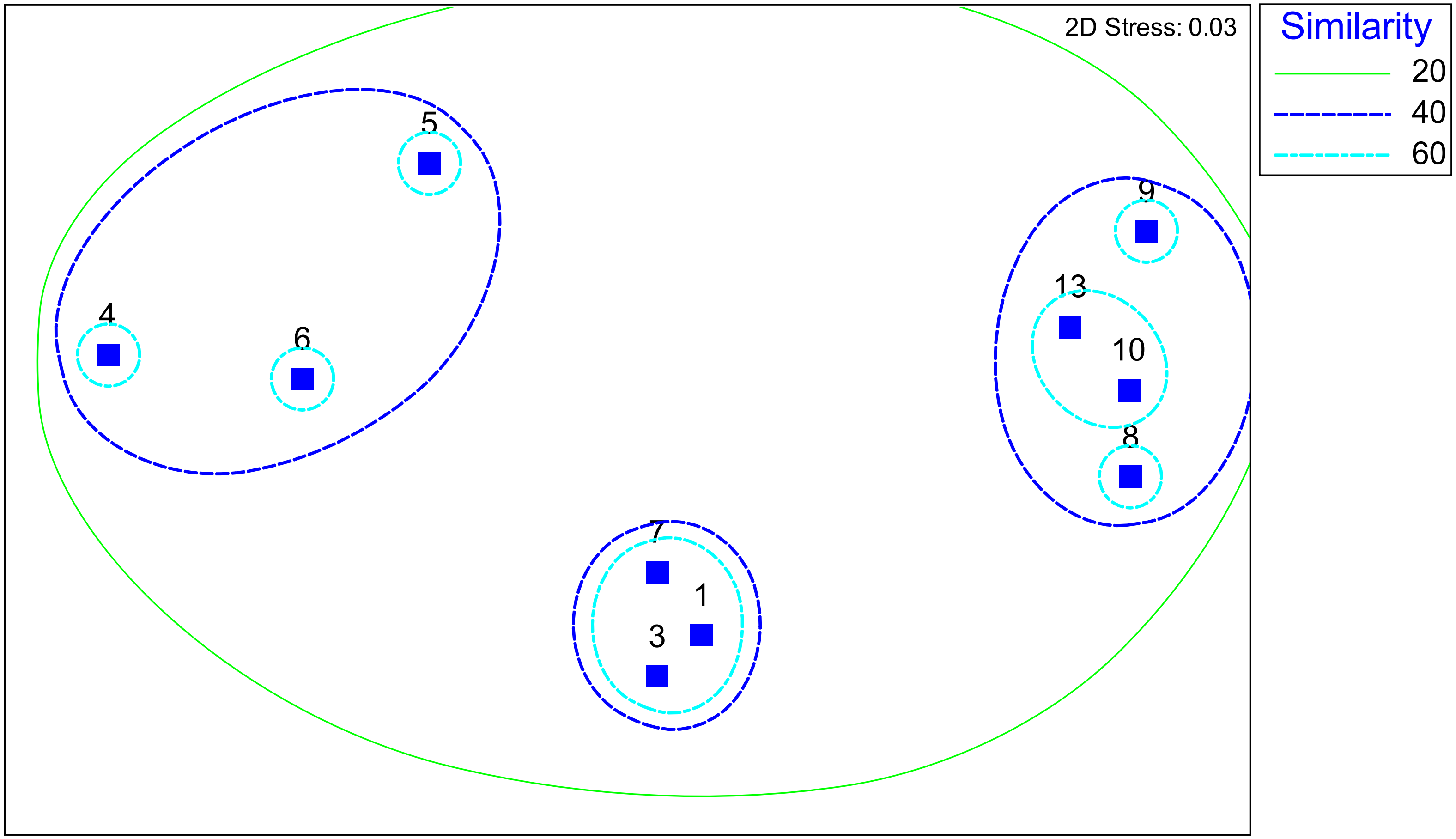


Figure 7. MDS ordination plot of Weweantic River 2023 infaunal benthic samples. Each blue square on the plot represents one of the 10 stations (MEP-SE-00X). Similarity circles are presented as minima.

3.4.3 Dominant taxonomic groups and species

The top five taxonomic groups for each of the three groups above are presented in Table 6 and Figure 8. Overall, benthic communities indicate a relatively poor habitat, with assemblages dominated by one or two taxonomic groups. Polychaetes were the most abundant group in the lower and mid-Weweantic River/Beaver Dam Creek and the second most abundant in the upper Weweantic River/Sippican River. Oligochaetes were the most abundant group in the upper Weweantic/Sippican River and second most abundant in the mid-Weweantic River/Beaverdam Creek and ranked fourth in the lower Weweantic River.

Table 6. Percent contribution of taxonomic groups in the Lower Weweantic, Mid-Weweantic/Beaverdam Creek, and Upper Weweantic/Sippican River areas, 2023.

	Lower Weweantic River	**Mid-Weweantic/Beaver Dam Cr.**	**Upper Weweantic/Sippican Rivers**
Polychaeta	82.8	78.3	25.3
Oligochaeta	3.2	15.9	65.3
Arthropoda	4.6	3.1	4.8
Mollusca	8.2	2.1	1.2
Nemertea	0.4	0.3	3.2
Others	0.8	0.3	0.2

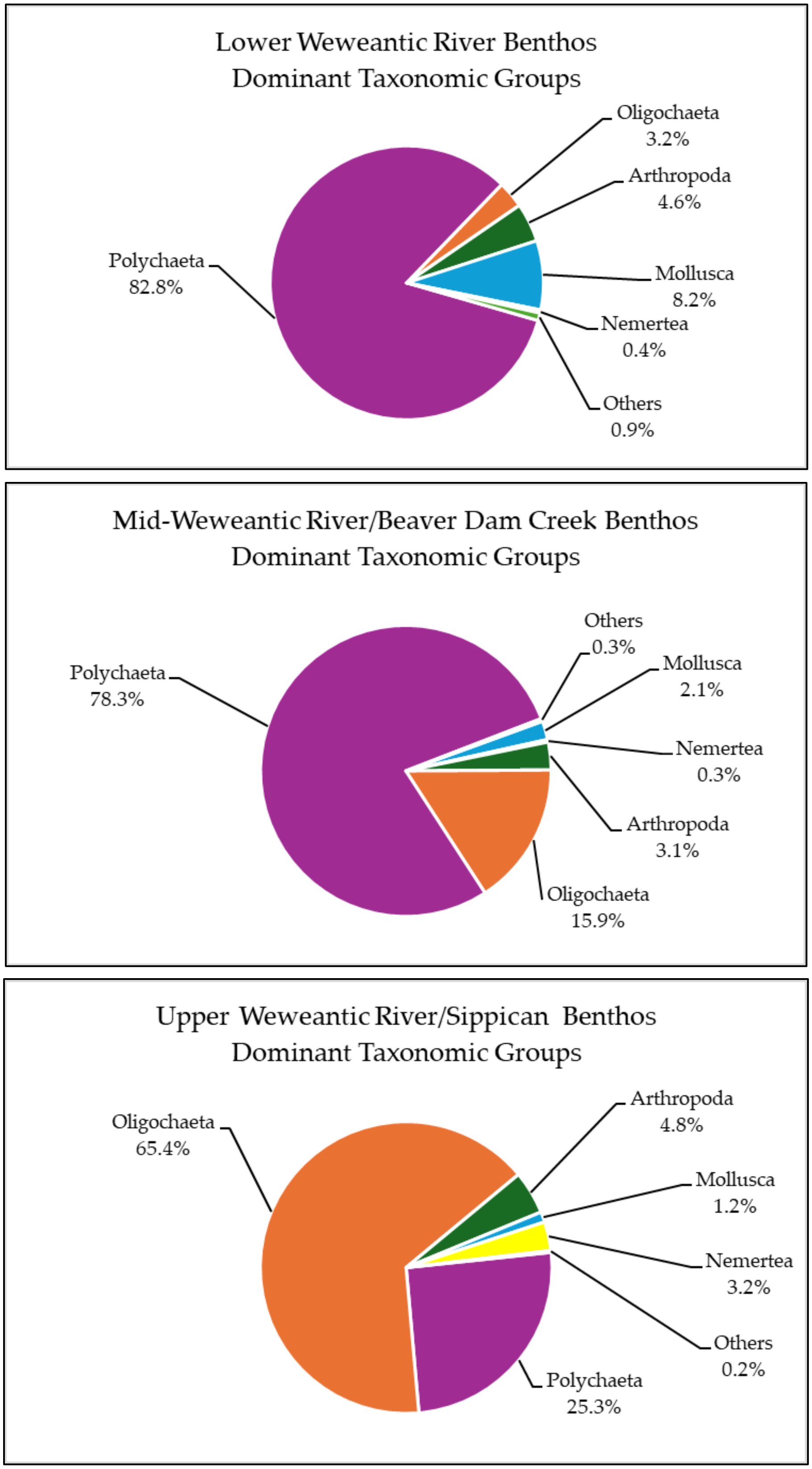


Figure 8. Percentage of benthic groups in the Lower Weweantic River (top), Mid-Weweantic/Beaverdam Creek (middle), and Upper Weweantic/Sippican Rivers (bottom), June 2023.

The top five dominant species were different among groupings in the Lower Weweantic, Mid-Weweantic/Beaverdam Creek, and Upper Weweantic/Sippican Rivers (Table 7, Figure 9). The most abundant taxon in the Lower Weweantic was the polychaete *Fabricia stellaris* contributing 17% to the total abundance, followed by polychaetes *Mediomastus ambiseta* (16%), *Exogone disbar* (14%), and *Polycirrus eximius* (10%), and the fifth ranking taxon bivalve *Nucula proxima* (6%; Figure 9). *F. stellaris* inhabits intertidal to shallow subtidal waters and can occur in high abundance (Artsdatabanken 2024). The relatively high percentage of *M. ambiseta,* a pollution-tolerant species in polyhaline mud capable of reproducing several times per year and develops rapidly (Caracciolo and Steimle 1983), suggests a relatively poor habitat quality.

Within the Mid-Weweantic and Beaverdam Creek stations, the most abundant taxa were *M. ambiseta* contributing 35% to the total, polychaete *Streblospio benedict*i (29%), followed by oligochaetes (16%), and polychaetes *Scoletoma tenuis* (6%), and *Leitoscoloplos robustus* (3%). *M. ambiseta* lives in vertical mucus tubes and has been recorded in association with *S. benedicti,* as was the case in these samples. *S. benedicti* occurs in mudflats and soft sediments of estuaries and coastal waters and tolerates a broad range of temperatures and salinities. *S. benedicti* is tolerant to high organic content and pollution, flourishes in disturbed environments, is considered an opportunistic pioneering species, and can reach very high densities (Kocheshkova and Matviy 2009, Detwiler et al. 2002). *S. tenuis* and *L. robustus* are commonly found in soft bottom/mud flats (Richards 1938, Fauchald et al. 2009).

Numerical dominants within Group 3 in the Upper Weweantic River and Sippican River indicated the least healthy habitat compared to Group 1 and 2 with the following contributions to the total: oligochaetes (65%), polychaetes *S. benedicti* (8%), *Microphthalmus sczelkowii* (7%), and *Heteromastus filiformis* (6%), and insect Chironomidae (B[3]; 3%; Figure 9). *H. filiformis,* is a complex of cryptic species in the family Capitellidae, which are among the most abundant polychaetes in soft-bottom communities (Blake and Ruff 2007).

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[3] The letter “B” indicates a different, but unidentifiable species of chironomid from Chironomidae A.

Table 7. Percent contribution of the top five benthic species in the Lower Weweantic, Mid-Weweantic/Beaverdam Creek, and Upper Weweantic/Sippican River areas, 2023.

Taxonomic Group	**Taxa**	**Lower Weweantic**	**Mid-Weweantic/ Beaverdam Creek**	**Upper Weweantic/ Sippican Rivers**
Polychaete	*Fabricia stellaris*	16.5%		
Polychaete	*Mediomastus ambiseta*	16.4%		
Polychaete	*Exogone dispar*	14.2%		
Polychaete	*Polycirrus eximius*	10.1%		
Polychaete	*Mediomastus ambiseta*		35.2%	
Polychaete	*Streblospio benedicti*		28.6%	7.9%
Polychaete	*Scoletoma tenuis*		6.2%	
Polychaete	*Leitoscoloplos robustus*		2.5%	
Polychaete	*Microphthalmus sczelkowii*			6.5%
Polychaete	*Heteromastus filiformis*			6.3%
Oligochaete	Oligochaeta		15.9%	65.4%
Insect	Chironomidae			3.2%
Bivalve	*Nucula proxima*	5.6%		
	Others	37.1%	11.6%	10.7%

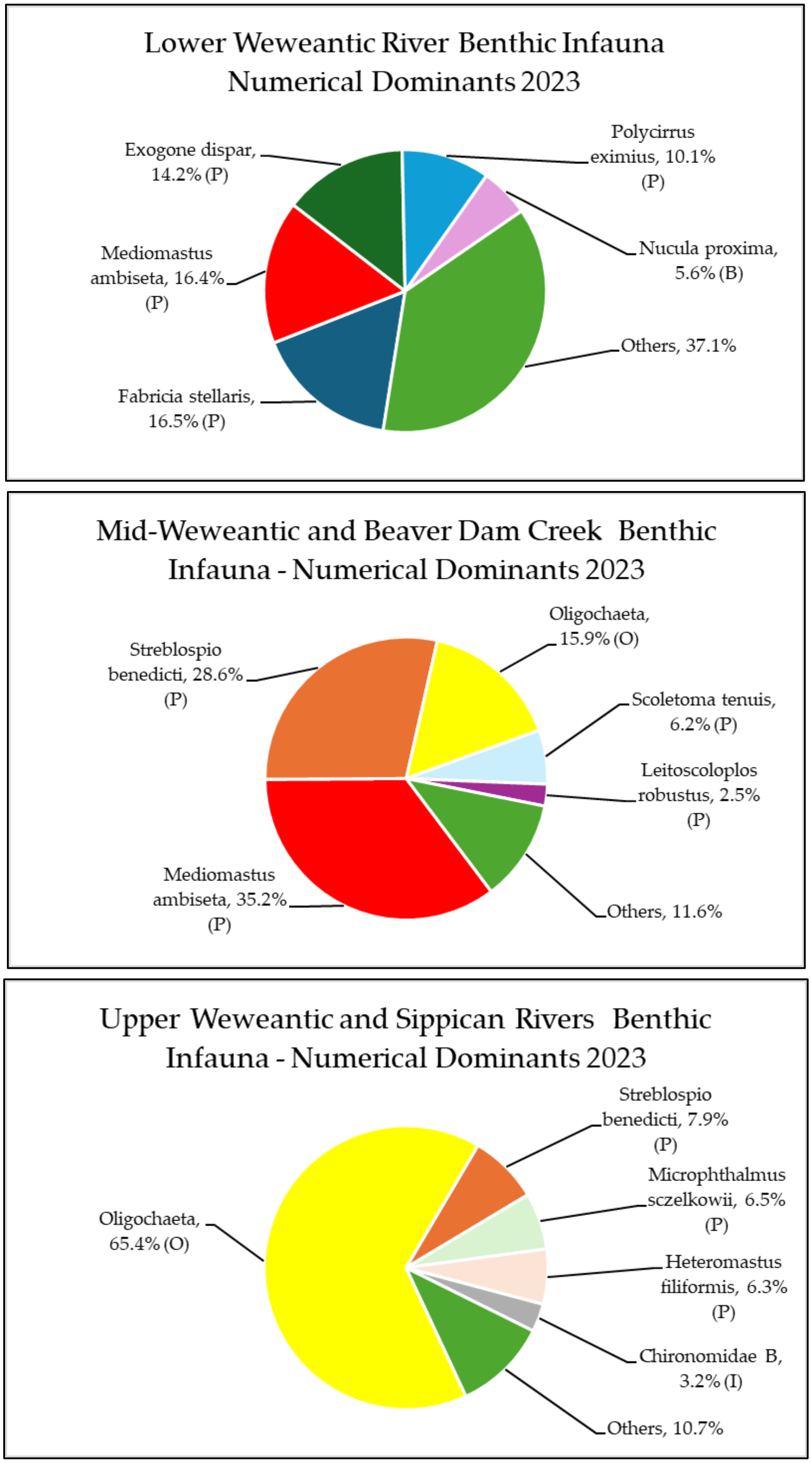

Figure 9. Top five taxa in the Lower, Mid-, and Upper Weweantic River Estuary System, 2023. P = Polychaete, B = Bivalve, I = Insect, and O = Oligochaete.

3.4.4 Diversity, richness, and evenness indices

When comparing the three groupings in terms of the number of species and abundance, the Lower Weweantic River appears to have relatively higher quality benthic habitat compared to the Mid-Weweantic/Beaverdam Creek and Upper Weweantic/Sippican River. The number of taxa was higher in the Lower Weweantic (mean of 66 taxa, ranging from 45 to 90 taxa per station) compared to the Mid-Weweantic/Beaverdam Creek (mean of 33 taxa, ranging from 29 to 35 taxa) and the Upper Weweantic/Sippican River (mean of 14 taxa, ranging from 11 to 17; Table 8, Figure 10). The mean number of individuals was also relatively higher in the Lower Weweantic (mean of 695 individuals, ranging from 238 to 1,223 individuals per station) compared to the Mid-Weweantic/Beaverdam Creek (mean of 664 individuals, ranging from 530 to 862 individuals) and the Upper Weweantic/Sippican River (mean of 195 individuals, ranging from 92 to 396 individuals; Table 8, Figure 11). As mentioned above, Group 3 is the least healthy benthic community with notably low numbers of taxa, abundance, and H'.

Table 8. Weweantic River Estuary System infaunal community parameters by station, 2023.

Area	**Assessment Units and Sub-segments**	**Group**	**Station**	**S**	**N**	**d**	**J'**	**H'(loge)**	**1-Lambda'**	**% Oligochaetes**
Lower Weweantic River	Weweantic R. - A	1	MEP_SE_004	90	1223	12.52	0.61	2.75	0.87	2.0
	Weweantic R. - B		MEP_SE_005	45	238	8.04	0.74	2.80	0.91	9.3
	Weweantic R. - C		MEP_SE_006	64	626	9.78	0.65	2.70	0.86	2.5
Mid-Weweantic River & Beaverdam Creek	Weweantic R. - F	2	MEP_SE_001	35	600	5.32	0.54	1.92	0.78	15.5
	Beaverdam Cr.		MEP_SE_003	34	862	4.88	0.48	1.70	0.71	14.2
	Weweantic R. - D		MEP_SE_007	29	530	4.46	0.52	1.76	0.75	18.3
Upper Weweantic and Sippican River	Weweantic R. - E	3	MEP_SE_008	11	396	1.67	0.36	0.88	0.38	72.2
	Weweantic R. - H		MEP_SE_009	12	184	2.11	0.69	1.71	0.73	47.3
	Weweantic R. - G		MEP_SE_010	17	111	3.40	0.54	1.52	0.62	59.3
	Sippican R.		MEP_SE_013	15	92	3.10	0.61	1.66	0.69	41.8

S = Total number of distinct taxa in both replicates, N = mean number of individuals, d = Margalef's species richness, J' = Pielou's evenness, H' = Shannon-Weiner diversity index, and 1-λ = Simpson diversity[4].

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[4] D, J', H', and 1-λ were calculated using station data.

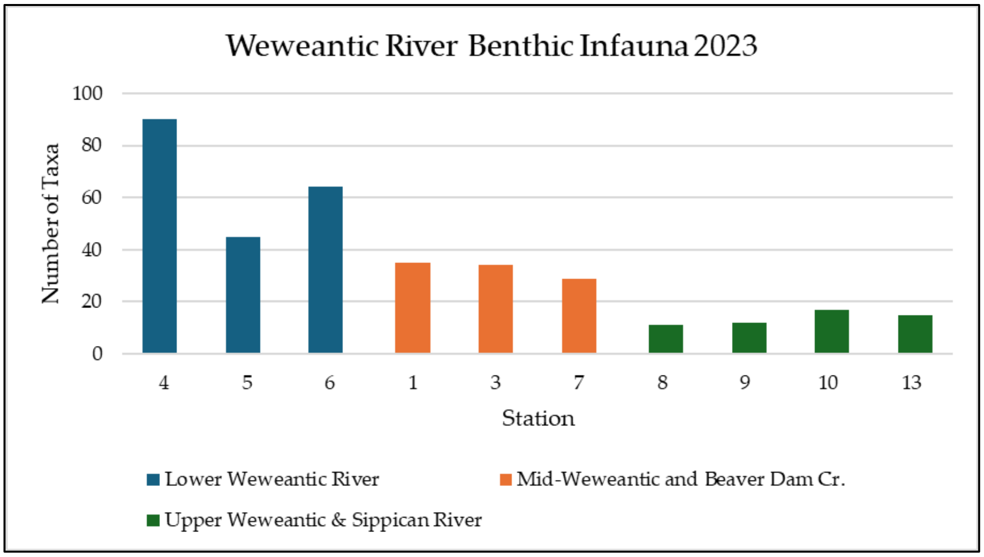

Figure 10. Total number of distinct taxa per station for the Weweantic River Estuary System Benthos, 2023: Lower River (blue bars), Mid- River (orange bars), and Upper River (green bars).

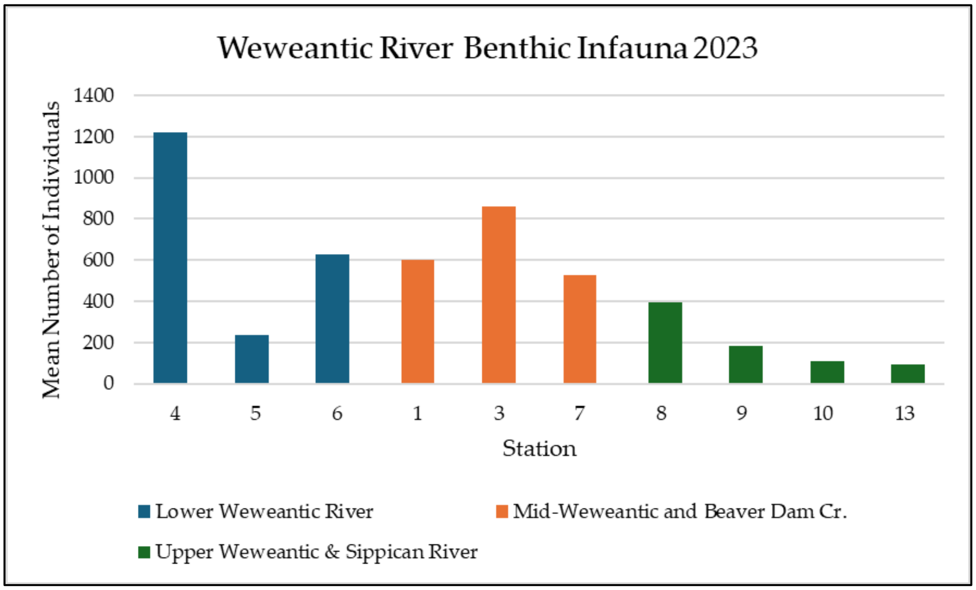

Figure 11. Mean number of individuals for the Weweantic River Estuary System Benthos, 2023: Lower River (blue bars), Mid- River (orange bars), and Upper River (green bars).

Overall, diversity, richness, and evenness indices indicated a gradient of habitat quality, with the Lower Weweantic River healthier relative to the Mid-Weweantic/Beaverdam Creek, and the lowest habitat conditions in the Upper Weweantic/Sippican River. The Shannon-Wiener diversity index (H’) is a function of the number of different taxa in a sample, the number of individuals per taxa, and the total number of individuals. H’ increases with the number of species in the community and when a more even distribution of numbers among taxa is found. H’ ranges from 0 when only one species is present to 5.0 when many taxa are found in equal numbers of individuals. Evenness is another expression of how individuals are distributed among different species or taxa. Pielou's evenness index (J') ranges from 0 to 1 and is essentially the reverse of dominance and therefore a sample with low evenness would be highly dominated by a small number of the taxa present.

The average Shannon Wiener diversity index (H') was higher in the Lower Weweantic River (2.75 with a range of 2.7 to 2.8) compared to Mid-Weweantic/Beaverdam Creek (mean of 1.8, range of 1.7 to 1.9) and the Upper Weweantic/Sippican River (mean of 1.4, range of 0.9 to 1.7; Table 8; Figure 12). Similarly, Margalef's species richness (D_{mg}), and Simpson's diversity (1-λ) indices indicated that the Lower Weweantic River had higher habitat quality (e.g., higher richness and diversity, and evenness) compared to the Mid-Weweantic/Beaverdam Creek and Upper Weweantic/Sippican River (Figure 13 and Figure 14, respectively). Average Pielou's evenness (J') was lowest in the Mid-Weweantic/Beaverdam Creek (0.51 with a range of 0.48 to 0.54) compared to the Lower Weweantic River (0.67 with a range of 0.61 to 0.74) and Upper Weweantic/Sippican River (0.55 with a range of 0.36 to 0.69; Figure 15). Station MEP-SE-008 had the lowest values in each of the four community parameters (Figure 12 – 15). This is not surprising due to the very low number of taxa (11 taxa), low number of individuals (mean = 396) and may be due to the proximity to the Wareham Marina. The marina is located on a landmass jutting out into the river which abuts Station MEP-SE-008 on the south, which may impact the currents, causing eddies and restricted flow to the area near where the samples were collected. However, more data are needed to clarify the ecological and bathymetric conditions in this area.

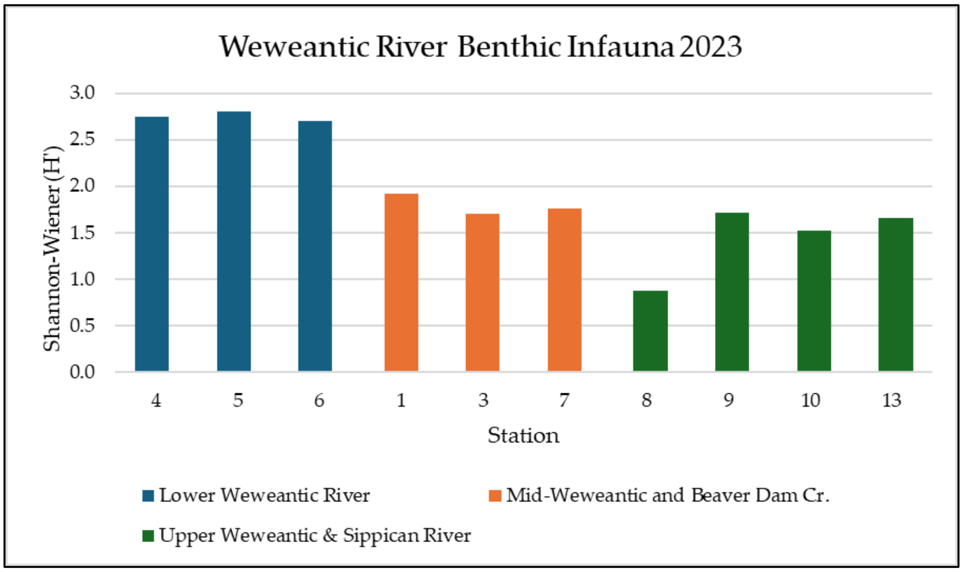

Figure 12. Shannon-Weiner diversity indices for the Weweantic River Estuary System Benthos, 2023: Lower River (blue bars), Mid-River (orange bars), and Upper River (green bars).

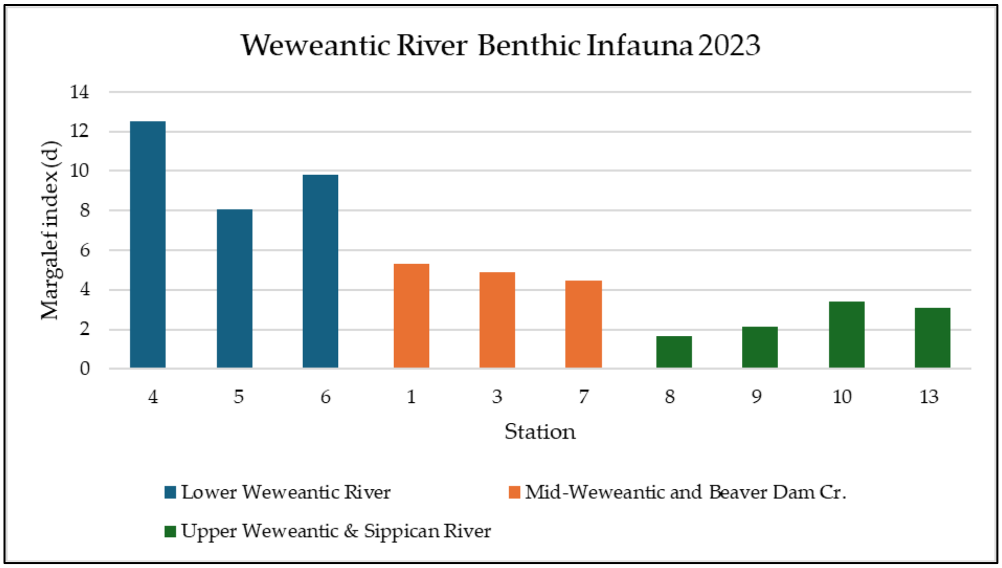

Figure 13. Margalef's species richness indices for Weweantic River Estuary System Benthos, 2023: Lower River (blue bars), Mid-River (orange bars), and Upper River (green bars).

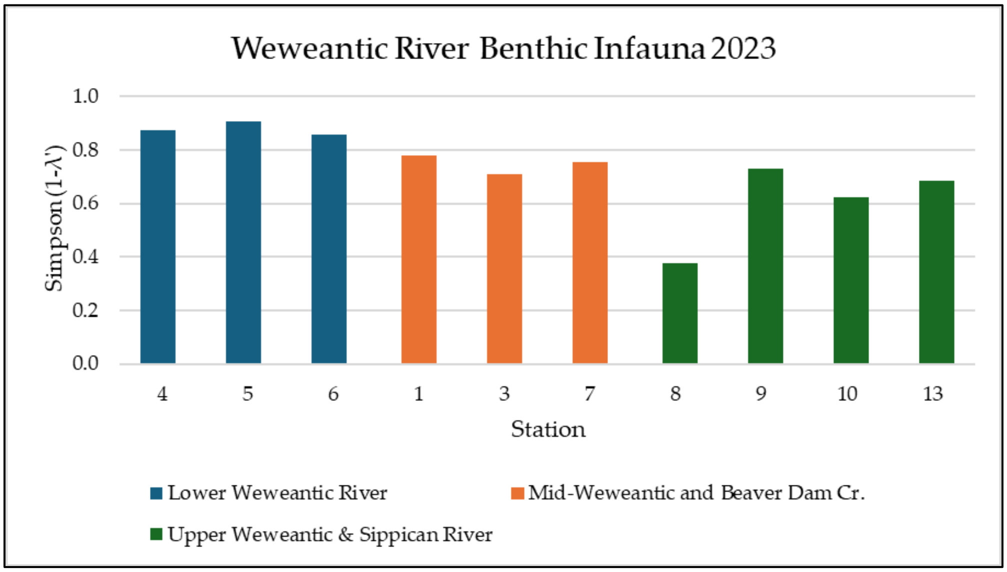

Figure 14. Simpson's diversity indices for the Weweantic River Estuary System Benthos, 2023: Lower River (blue bars), Mid-river (orange bars), and Upper River (green bars).

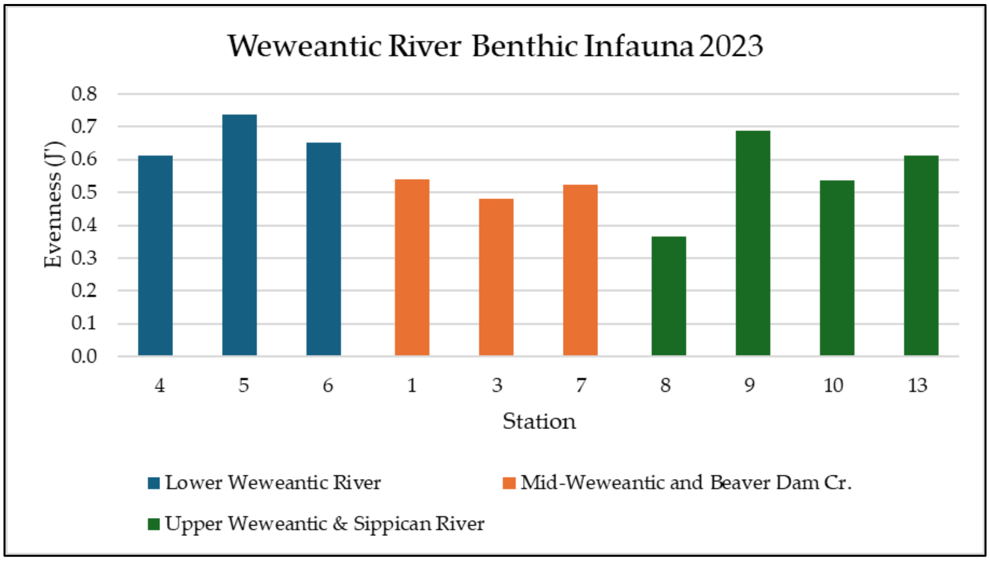

Figure 15. Pielou's evenness indices for the Weweantic River Estuary System Benthos, 2023: Lower River (blue bars), Mid-River (orange bars), and Upper River (green bars).

3.4.5 Pollution-tolerant and Pollution-sensitive species

Macroinvertebrates are valuable indicators of pollution due to their relatively sedentary life history and predictable responses to contaminants and eutrophication pollution (Scott 1990, Pelletier et al. 2010). Pelletier et al. (2010) identified benthic invertebrates that could be used as indicator species to detect the presence (pollution-tolerant species) or absence (pollution sensitive species) of pollution for various habitats including oligohaline tidal freshwater mud, low mesohaline mud, high mesohaline mud, polyhaline mud, and polyhaline sand that are present in the Weweantic River Estuary System. There were three pollution-tolerant indicator species identified: gastropod *Ceacum pulchellum* at Station MEP-SE-004, and polychaetes *Mediomastus ambiseta* and *Mediomastus californiensis* at Stations (MEP-SE-004, 005, and 006; Pelletier et al. 2010; Table 9). *M. ambiseta* and *M. californiensis* contributed 8% to the abundance in Station MEP-SE-004 and were numerically dominant species in Stations MEP-SE-005 and 006. When combined these two species contributed 20% and 34% to the total abundance in Station MEP-SE-005 and 006, respectively suggesting a stressed, low-quality habitat. Although these lower Weweantic River samples had relatively higher benthic community parameters (Figures 10-15) compared to the mid-Weweantic/Beaverdam Creek and upper Weweantic/Sippican River samples, the relatively high percentage of pollution-tolerant species implies a stressed habitat. In addition, no pollution-sensitive indicator species were identified, suggesting a relatively low-quality habitat throughout the System.

Table 9. Pollution-sensitive and pollution-tolerant indicator species recorded in the Weweantic River Estuary System, 2023.

Taxon	Taxonomic Group	Pollution Sensitive/Tolerant[1]	Habitat Type	Recorded in Station MEP-SE-	Location in Weweantic River Estuary System
Caecum pulchellum	Gastropod	Tolerant	Polyhaline sand	004	Lower Weweantic River
Mediomastus ambiseta	Polychaete	Tolerant	Polyhaline sand	004, 005, 006	Lower Weweantic River
Mediomastus californiensis	Polychaete	Tolerant	Polyhaline sand	004, 005, 006	Lower Weweantic River

1 -Pelletier et al. 2010.

Percent silt was superimposed on the MDS plot (Figure 16) to examine whether it was correlated with the relative benthic quality gradient indicated in the cluster and MDS plots. The correlation between the station location and percent silt was somewhat inconsistent. Percent silt in Group 1 stations tracked with the MDS plot with relatively low levels of silt (ranging from 3 to 6%). These three stations would be expected to have relatively low silt levels due to their location near the river mouth and corresponding greater tidal flushing compared to stations farther up the river. The percentages of silt in Group 2 stations were highly variable ranging from very low (0.5%) at Station MEP-SE-003 in Beaverdam Creek to moderate at Station MEP-SE-001 (9%) and high (40%) at Station MEP-SE-007 in the Mid-Weweantic. Station MEP-SE-007 is located just north of the mouth of the Sippican River and Route 6 Bridge, which may produce eddies and result in elevated sediment deposition. The relatively lower percent silt at Station MEP-SE-001, higher up the Weweantic River than Station MEP-SE-007, may be due to its proximity to the shore compared to Station MEP-SE-007 which is in the middle of the thalweg, with presumably more current. As mentioned above in Section 3.2.1, the lower percent silt level in the Beaverdam Creek (MEP-SE-003) compared to those in the lower Weweantic River is highly unusual, unexpected, and may indicate an error in the sediment grain size results.

In Group 3, three of the four stations in the upper Weweantic including the Sippican River had a high percentage of silt ranging from 27 to 52%, while the fourth station (MEP-SE-009), the uppermost station in the System, was the exception with 5% silt. As mentioned above, the Horseshoe Pond Dam, approximately 0.5 miles upstream of Station MEP-SE-009, was removed in 2021. It is likely that the dam removal and subsequent flushing may have transported silty sediments downstream, thus leaving relatively low levels of silt in the upper portion of the Weweantic River and appears supported by the high silt percentage (52%) at the nearest station downstream (MEP-SE-010). Station MEP-SE-008 had a relatively high percentage of silt (35%) and the second highest TOC (6.9%), which is likely due to effects to the current and eddies that may result from the marina due south of the station location.

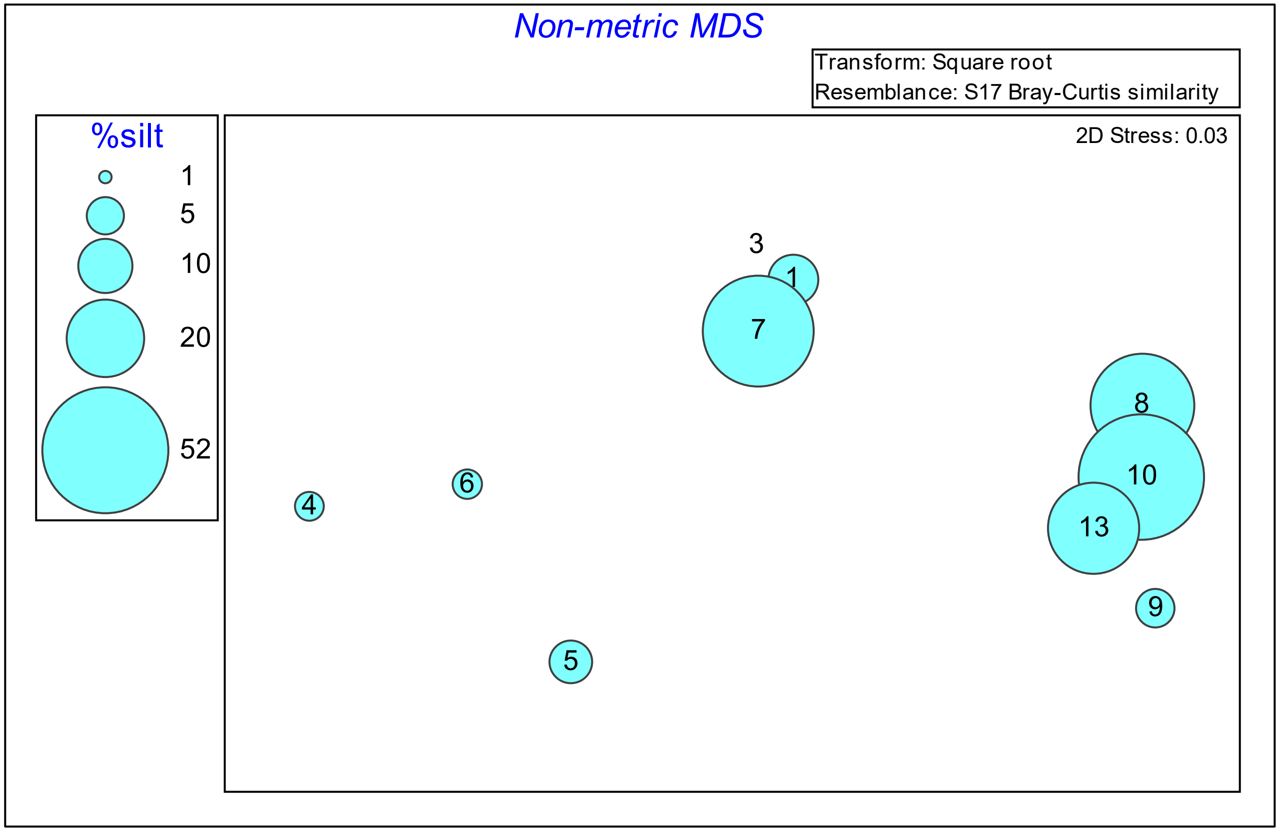

Figure 16. Percent fine sediments superimposed on the MDS ordination plot of the 2023 Weweantic River Estuary System infauna samples. Each point on the plot represents one of the 10 station numbers (MEP-SE-00X); similarity of species composition is indicated by proximity of points on the plot. The ordination and cluster analysis are both based on Bray-Curtis Similarity.

3.5 Average Taxonomic Distinctness (ATD)

Taxonomic distinctness is a biodiversity calculation used to indicate the relatedness of organisms based on Linnaean classification system. Average Taxonomic Distinctness (ATD, Delta+) is a relatedness measure that can only be calculated from simple species lists (e.g., Phylum, Class, Order, Family, Genus, and Species) but also possesses a robustness to the varying number of species in the lists. More specifically, mean values are unchanged in different-sized sub-lists generated by random sampling from a larger list. This suggests that it is valid to compare Delta+ over historic time or biogeographic space scales, under conditions of variable sampling effort.

Taxonomic data for ATD analysis are required to be at the same classification level. In this data set several taxa were only identified to the genus level, therefore that was the lowest level analyzed. Subsequently, any taxa that were identified to the family, class, order, or phylum were not included in this analysis. Most of these upper-level taxa were represented by only a few specimens except Oligochaeta, that were numerical dominants in Group 2 and 3 samples.

Average taxonomic distinctness (Delta+) for the Weweantic River Estuary System benthos is represented in the funnel plot showing the 95% upper and lower limits of the expected range of diversity (Figure 17). Results indicate that while most samples are within the expected range, four samples (Station MEP-SE-001 (replicate 3 presented in Figure 17 as 1-3), MEP-SE-003 (3-3), and MEP-SE-007 (7-3 in Group 2) and one sample (Station MEP-SE-004 (4-2 in Group 1) were below the expected range of biodiversity. Although Sample 4-2 had a relatively high number of taxa (n = 46), there was a disproportionate level of representation from two polychaete species (*Exogone dispar* and *Fabricia stellaris*). The three other samples in Group 2 had a relatively low number of taxa (n = 16, 18, and 16 taxa, respectively), of which two taxa (Sample 3-3 and 7-3; *S. benedicti* and *M. ambiseta*) and three taxa (Sample 1-3; *S. benedicti*, *M. ambiseta*, and *Scoletoma tenuis*) contributed 83% to the overall abundance. Dominance of two to three taxa would account for the reduced taxonomic distinctness at these stations. These ATD results appear to be slightly inconsistent with the other community parameters examined (i.e., Shannon-Weiner diversity and Pielou's evenness [Table 8]) for the above stations. However, since community parameters for each station were calculated using the mean of two samples, results by sample could be different. In addition, the removal of the upper-level taxa (i.e., those identified to family, class, order, or phylum) would also decrease the diversity in the ATD compared to the community parameters.

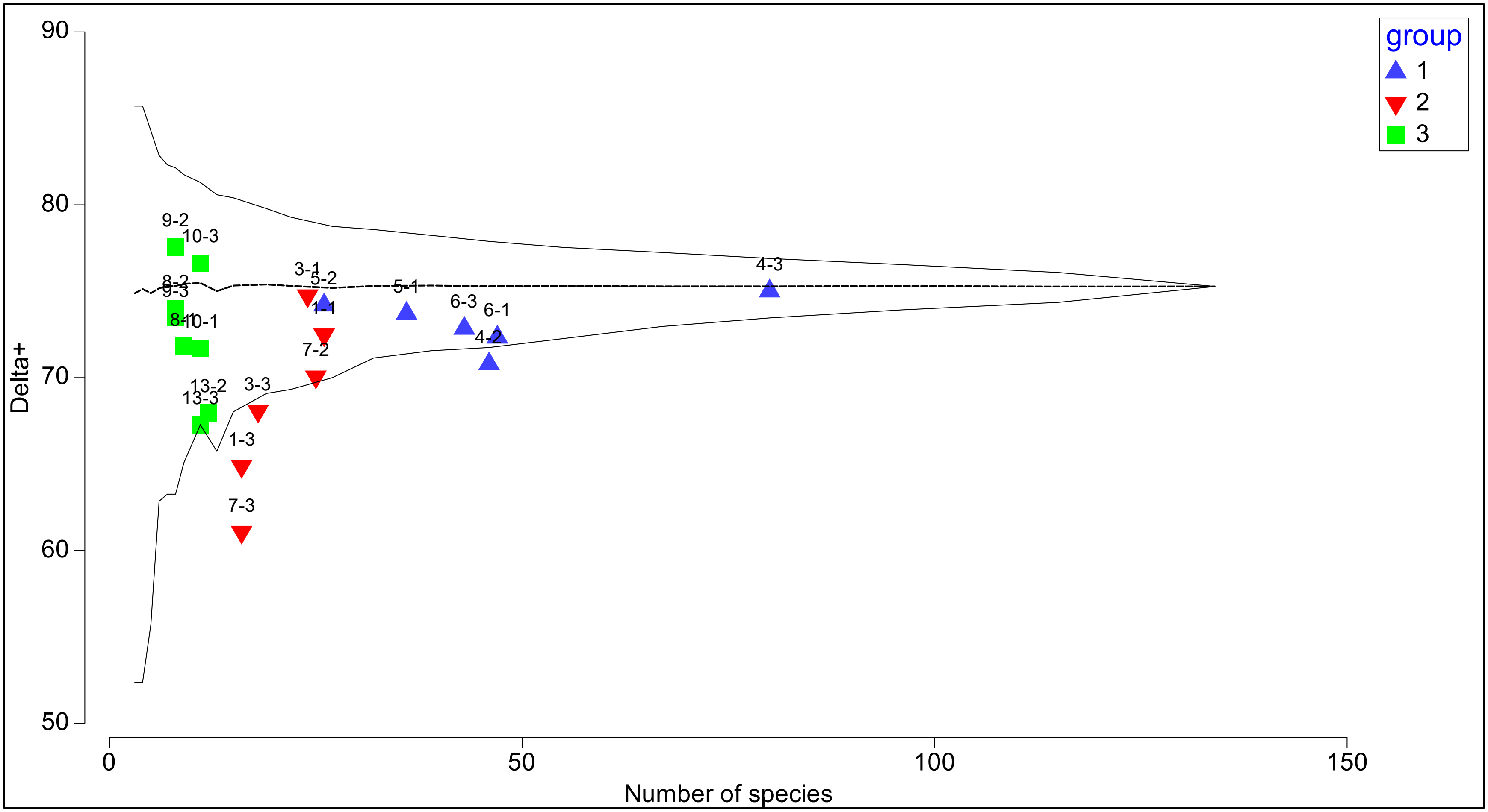

Figure 17. Weweantic River Estuary System Average Taxonomic Distinctness (Delta+) for all stations and samples, 2023. Labels indicate sample number and replicate number separated by a dash.

3.6 US M-AMBI

A summary of parameters including sediment characterization, percent silt, salinity, salinity categories used to calculate US M-AMBI, and water depth is presented in Table 10. US M-AMBI results for the Weweantic River Estuary System indicate that the health of the benthic community ranges from Poor to High (Table 11, Figure 18). US M-AMBI scores in the lower Weweantic (Group 1; all polyhaline sandy habitat) ranged from Good (33% of the stations) to High (67% of the stations). The US M-AMBI scores are consistent with the sediment grain size and TOC results observed at these stations that indicated a relatively healthy habitat with adequate tidal flushing.

The mid-Weweantic and Beaver Dam Creek (Group 2) habitat consisted of mesohaline and polyhaline mud, with US M-AMBI scores ranging from Moderate (50%) to Good (50%). Station MEP-SE-003 in the Beaver Dam Creek had the highest TOC among all stations (7%), which corresponded to Moderate US M-AMBI scores for both replicates. The two stations in the mid-Weweantic (MEP SE-001 and 007) had moderate TOC levels (2% and 3%, respectively) and US M-AMBI categories that tracked these results (MEP-SE-001 was scored as Good and MEP-SE-007 was scored as Moderate/Good [replicate 2 and 3]).

Within Group 3, the US M-AMBI values were consistent among sample replicates and with corresponding community parameters at some stations, but inconsistent among replicates and community parameters at others. The upper Weweantic River (tidal freshwater and mesohaline mud) and Sippican River (mesohaline mud) samples ranged from Poor to Good. Both of the Poor samples were at Station MEP-SE-008. The Poor US M-AMBI categorization is consistent with the community parameters (mean number of taxa = 10, mean number of individuals = 396; Table 11), high percentage of EG code V organisms (representing low quality; 65% and 82%, respectively for each replicate), high percentage of silt (35%), and the second highest TOC (6.9%).

Results for Station MEP-SE-009 were variable between replicates. Replicate 2 was categorized as Moderate with a US M-AMBI score of 0.53 and replicate 3 was characterized as Good with a score of 0.55 (Table 11). Replicate 2 was consistent with the other community data, however the community parameters for replicate 3 (11 taxa, 164 individuals, etc.; Table 11) suggest a Moderate (or lower) categorization. In this case, the AMBI score was considered to clarify the results. The AMBI score for replicate 3 (4.60) was extremely close to the score for replicate 2 (4.61), both corresponding with a Moderately Disturbed classification. As mentioned above, the AMBI score, based solely on a weighted abundance by pollution tolerance, characterized the sample on the percentage of organisms that were pollution tolerant or sensitive, and weighted the more pollution tolerant species higher compared to pollution sensitive species. For Sample MEP-SE-009 (replicate 3), the AMBI score was more consistent with a depauperate sample with very few taxa and high percentage of oligochaetes (48%). Due to the location in the upper estuary, and proximity to elevated currents from the Horseshoe Dam removal, the percent silt and TOC were relatively low (5% and 2%, respectively). The high flushing rate likely resulted in removal of benthic habitat and infauna, which are expected to return, but may still be somewhat different to those downstream due to the freshwater habitat. Overall, although the US M-AMBI score indicated a Good habitat, the other ecological data suggest a less healthy habitat consistent with the AMBI Moderately Disturbed category.

US M-AMBI results between replicates at Station MEP-SE-010 were consistent amongst samples, both categorized as Moderate. Both samples had a low number of taxa (13 and 12, respectively), very low number of individuals (136 and 85, respectively), and relatively low H’ diversity index (1.4 and 1.5, respectively; Table 11). These data are consistent with the high silt content (52%) and TOC (6.8%) of a low quality, disturbed habitat.

US M-AMBI categories were also variable between replicates at Station MEP-SE-013. Replicate 2 (0.42) fell within the Moderate category while replicate 3 was scored as Good (0.58; Table 11). The Moderate classification for replicate 2 is consistent with the data, however the community parameters (12 taxa, 35 individuals), high silt and TOC (28% and 5%, respectively) are not consistent with a Good habitat. As with Station MEP-SE-009, in this case, the AMBI score (3.81), categorized as Moderately Disturbed, is consistent with the habitat and benthic metrics.

Table 10. Summary of habitats in the Weweantic River Estuary System benthos, 2023.

Station	Group Name	Group Number	Sediment from survey notes	% silt	Salinity	Salinity/sediment category*	Depth (m)
4	Lower Weweantic River	1	sandy	3.2	23	Polyhaline sand	1.3
5			sandy	6.4	23-28	Polyhaline sand	1.4
6			sandy	3.3	20-26	Polyhaline sand	2.3
1	Mid-Weweantic River & Beaver Dam Cr.	2	hard-packed silt	8.6	10-11	Mesohaline mud	1.1
3			mud	0.5	21	Polyhaline mud	0.5
7			silt	40.4	17	Mesohaline mud	0.5
8	Upper Weweantic & Sippican Rivers	3	soft silt	35.4	16	Mesohaline mud	0.5
9			soft silt	5.3	0.2	Tidal Fresh mud	0.4
10			soft silt	51.6	9	Mesohaline mud	0.5
13			soft silt	27.5	16	Mesohaline mud	0.5

*Source: Pelletier et al. 2010.

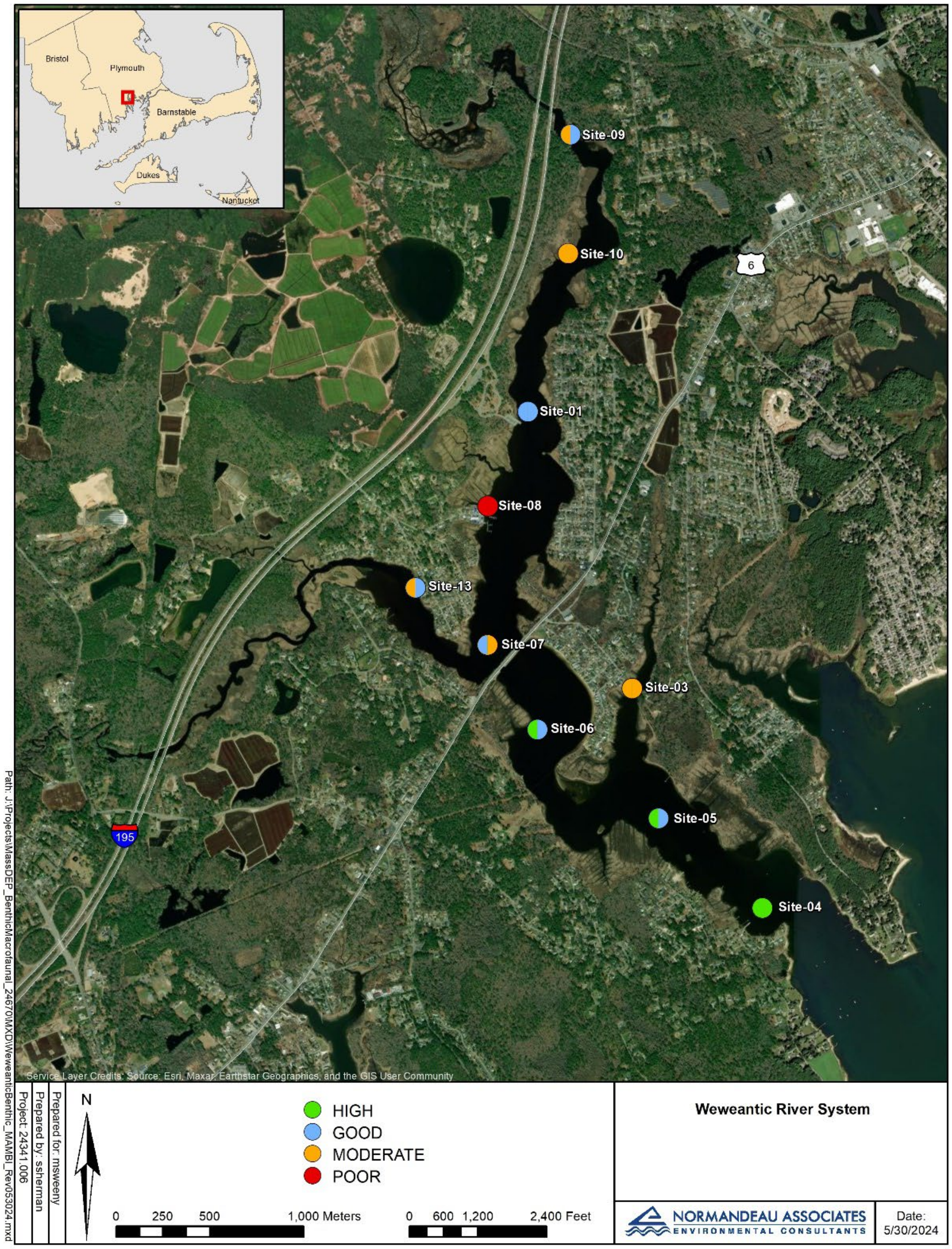

Figure 18. Summary of US M-AMBI results for Weweantic River Estuary System benthos, 2023. The circles at each station location represent qualitative US M-AMBI scores Poor, Moderate, Good, and High for each station. Each circle represents the two replicate samples at each station, Replicate 1 on the left and Replicate 2 on the right half of each circle.

Table 11. US M-AMBI score and category for Weweantic River Estuary System benthic samples.

Sample	Group Name	Group Number	S	H'	% Oligochaetes	AMBI*	AMBI Categories	M-AMBI**	M-AMBI Category
MEP_SE_004_2	Lower Weweantic River	1	48	2.53	1.4	2.10	Slightly disturbed	0.856	High
MEP_SE_004_3			83	2.77	2.6	2.13	Slightly disturbed	1.000	High
MEP_SE_005_1			38	2.71	10.4	2.85	Slightly disturbed	0.773	High
MEP_SE_005_2			27	2.57	8.2	2.40	Slightly disturbed	0.739	Good
MEP_SE_006_1			50	2.60	2.4	3.11	Slightly disturbed	0.796	High
MEP_SE_006_3			44	2.63	2.5	3.18	Slightly disturbed	0.765	Good
MEP_SE_001_1	Mid-Weweantic River & Beaver Dam Cr.	2	29	1.90	14.5	4.03	Moderately disturbed	0.720	Good
MEP_SE_001_3			18	1.87	16.6	3.93	Moderately disturbed	0.608	Good
MEP_SE_003_1			26	1.65	17.6	4.34	Moderately disturbed	0.464	Moderate
MEP_SE_003_3			22	1.61	10.8	4.32	Moderately disturbed	0.442	Moderate
MEP_SE_007_2			27	1.95	14.6	4.11	Moderately disturbed	0.702	Good
MEP_SE_007_3			18	1.57	22.0	4.49	Moderately disturbed	0.525	Moderate
MEP_SE_008_1	Upper Weweantic & Sippican Rivers	3	10	1.31	62.0	5.02	Heavily disturbed	0.365	Poor
MEP_SE_008_2			10	0.71	82.4	5.33	Heavily disturbed	0.255	Poor
MEP_SE_009_2			11	1.63	47.1	4.61	Moderately disturbed	0.529	Moderate
MEP_SE_009_3			11	1.76	47.6	4.60	Moderately disturbed	0.547	Good
MEP_SE_010_1			13	1.40	61.0	5.07	Heavily disturbed	0.406	Moderate
MEP_SE_010_3			12	1.50	57.6	4.75	Moderately disturbed	0.432	Moderate
MEP_SE_013_2			13	1.44	60.8	5.02	Heavily disturbed	0.415	Moderate
MEP_SE_013_3			12	2.07	22.9	3.81	Moderately disturbed	0.582	Good

AMBI = Calculated Biological Index (see methods section), S = number of individuals, H’ = Shannon-Wiener diversity index.

*AMBI is an abundance-weighted, tolerance value index that assesses habitat condition based upon the relative abundance of taxa in different tolerance value groups (i.e., EG codes) but does not account for salinity.

**M-AMBI factors in diversity, species richness, AMBI, and salinity.

3.7 Current Factors Contributing to Habitat Health

This section provides an explanation of the relatively low habitat health based on current, available information. Studies and data on the Weweantic River Estuary System's benthic community health are scarce. However, summaries of recent environmental data are provided in the MassDEP Embayment-specific Study Plan: Weweantic River Estuary System (MassDEP 2023f) and include the following:

- Final 2022 Integrated List of Waters for the Clean Water (MassDEP 2023c),
- Shellfish classification area BB35 - Weweantic River, MA (MA DMF 2013)
- Buzzards Bay Coastal Drainage Area Assessment and Listing Decision Summary (MassDEP 2022),
- Buzzards Bay Coalition (BBC) Bay Health Index scores (BBC 2022b), and
- The Horseshoe Pond Dam – Weweantic River Restoration Project (NOAA 2017).

The BBC and Marine Biological Laboratory in Woods Hole have collected and analyzed nitrogen (organic and inorganic), dissolved oxygen, algal pigments, and water clarity data in several embayments in Buzzards Bay including the Weweantic River for over 30 years. The five parameters are summed into a single Bay Health Score ranging from 0 to 100 with a score of 0 indicating waters severely polluted with nitrogen and a score of 100 representing pristine waters. The Bay Health Scores support the benthic results in this report.

The Upper Bay Health Index scores (comparable to Stations MEP-SE-001 and 007 in Group 2 and Station MEP-SE-008 in Group 3 in this report) from 1996 through 2022 ranged from 27 (Poor) to 37 (Fair), with a majority (69%) of the scores ranked as Poor. The most recent 5-year average available based on data collected from 2018 to 2022, continues to indicate the Bay water quality as Poor at an Index of 30 (a slight improvement compared to the 2017 – 2021 average of 29; BBC 2022ba). The Bay Health Index score for the lower Weweantic River (comparable to Stations MEP-SE-004, 005, and 006 in Group 1) is relatively healthier than the upper estuary, with a 5-year average Index from 2018 through 2022 of 39 (Fair; a slight decline compared to the 2017 – 2021 average of 40). The 2022 score (40), was the lowest of the 25-year series (BBC 2022a). The Bay Health Index scores in the lower Weweantic have been consistently "Fair", ranging from 40 to 51, indicating an impaired ecosystem in transition (BBC 2022a).

Nitrogen is one of the greatest threats to coastal water quality in the US (Costa 2013). Most of the nitrogen pollution that reaches Buzzards Bay comes from septic systems, wastewater treatment plants, and road runoff (Jakuba et al. 2023). Cranberry bogs can also contribute significant amounts of nutrients in watershed areas with a high density of cranberry bogs like the Weweantic River (Figure 19; Jakuba et al. 2023). There are more than 9,000 acres of cranberry bogs in the Weweantic River and Wareham River Watersheds that contribute approximately 30% of the nitrogen pollution to the Weweantic River and 20% to the Wareham River (residential septic systems are the primary source of nitrogen to both rivers; Jakuba et al. 2023). The Weweantic River has an estimated TN load of 73,394.2 kilogram per year (kg/yr), with about 28,047.8 kg/yr attributed to wastewater and 10,206.4 kg/yr to fertilizer. The total areal load of nitrogen in the Weweantic River is estimated to be 458.7 kilogram per hectare per year (kg/ha/yr; WHG 2021, MassDEP 2023f). Ninety-six percent of the Weweantic River watershed (40,638 acres) is unsewered, relying on septic systems to treat wastewater (MassDEP 2023f).

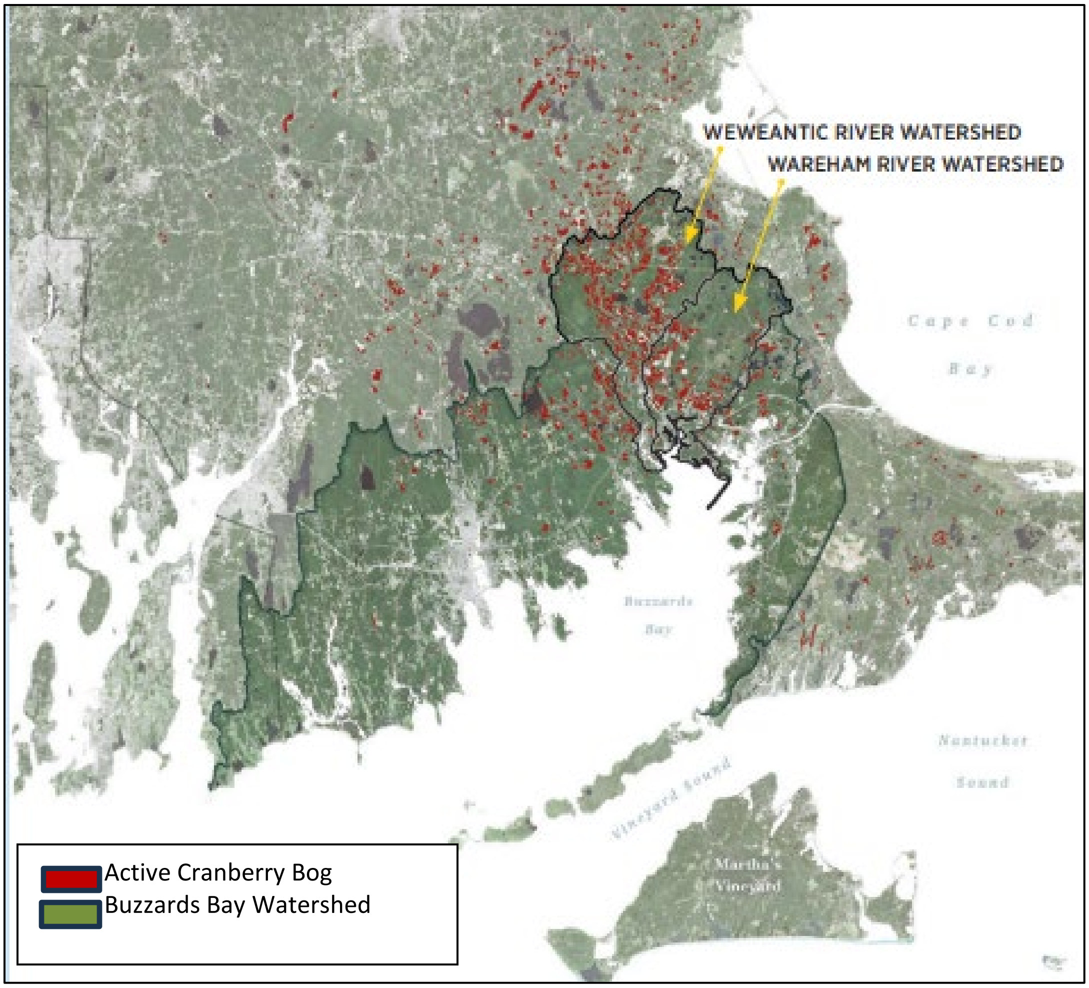

Figure 19. High density of cranberry bogs in the Weweantic River Watershed (Jakuba et al. 2023).

In 2011, the Buzzards Bay Coalition (and others[5]) began a study to examine and quantify how cranberry bogs contribute to eutrophication of coastal watersheds and to determine what management actions could be used to minimize the level of nutrients discharges and maximize its removal. The study included three research topics: 1) measurement of nutrient releases from cranberry bogs, 2) modeling the contribution of cranberry bogs to overall watershed nutrients, and 3) potential benefits to water quality from restoring natural wetlands at existing cranberry bogs. There are two types of bogs in southeast Massachusetts, flow-through bogs, in which a river channel flows through the bog and wetland-type bogs that are in areas that were formerly wetlands, often on the edges of forest or near ponds, and are connected to streams by ditches or channels. Since about 80% of the bogs in Buzzards Bay are the wetland-type, the study included only wetland-type bogs.

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[5] Other contributors included the U.S. Department of Agriculture Agricultural Research Service (USDA), Woodwell Climate Research Center, University of Massachusetts (UMass) Cranberry Station, Cape Cod Cranberry Growers' Association, Marine Biological Laboratory, Southeastern Regional Planning & Economic Development District, and the Town of Carver.

Measuring Nutrient Releases

Prior to the study, information regarding amounts of nitrogen released from cranberry bogs was limited to only two studies, DeMoranville and Howes (2005) and Howes and Teal (1995). One study focused on flow-through bogs and the other examined 6 traditional wetland-type bogs. Results of these studies indicated that nitrogen loss was higher in the flow-through bogs compared to traditional wetland bogs, but there was a wide range of outputs across bogs making it difficult to develop management strategies to reduce eutrophication (Jakuba et al. 2023).

In the 2011 study, six bogs were monitored for one-and-a-half years from the bog inlets and outlets. Because previous research suggested that flood events accounted for most of the annual nutrient loss, the initial study focused on flood events, and subsequent sampling at three bogs included collecting water during both flood releases and low flows between floods.

The study found that the differences in nitrogen concentrations discharging from the bogs were influenced more by nitrogen sources in the watershed and how much water flowed through a bog, than by specific farming practices; and the amount of water flowing through was influenced by where the bog sits in the landscape (Jakuba et al. 2023). For example, the large amount of water flowing through one of the bogs that was fed by a large amount of groundwater input from springs resulted in higher overall amounts of nutrients washing downstream compared to other bogs with ditches that were mostly dry or with water that was not flowing.

Results indicated that although there was variability among the six bogs, the nitrogen outputs were close to estimates for wetland bogs from other studies (Town of Carver 2015). Results from the more detailed sampling of three bogs were similar with average net stream transport of nitrogen ranging from -0.1 to 11.3 lb/ac; Jakuba et al. 2023). The range of phosphorus concentrations among bogs was smaller compared to nitrogen concentrations (1.9 to 4.0 lb/ac, average of 2.7 lb/ac) and were similar or slightly higher than previous studies (Jakuba et al. 2023). The study provided improved estimates of nitrogen and phosphorus outputs from cranberry bogs, which could thus be more confidently used in effectively developing nitrogen reduction management plans (Jakuba et al. 2023). MassDEP generally uses 0.5 mg/L total nitrogen as the target for benthic habitat restoration.

These results also indicated that since most of the annual nitrogen [and phosphorus] losses occurred during non-flooding times, targeting nutrient removal management measures during non-flood periods with small but steady outflows could be beneficial (Jakuba et al. 2023). Suggested practices could include additional storage time in ponds or increased naturalization of stream channels to enhance nitrogen uptake and denitrification. Jakuba et al. (2023) also suggested that bogs with higher flow are good targets for nutrient removal measures because larger amounts of nitrogen and phosphorus are passing through them.

Modeling How Cranberry Bogs Impact Watershed Nutrients

Two models were used in the Wareham River (in the adjacent watershed southeast of the Weweantic River watershed; Figure 19) to examine how nutrients entering the watershed from cranberry bogs contribute to overall nutrient pollution downstream in the estuary. The Nutrient Loading Model (NLM), used to estimate how much nitrogen reaches surface waters (Valiela et al. 1997), was paired with a stream channel model (Wollheim et al. 2006), which uses information about the size of different stream and river stretches to estimate how much nitrogen will be assimilated by plants and microbes as the water moves in stream channels filled with plants and organic matter (Jakuba et al. 2023).

The revised NLM model indicated that cranberry bogs contributed approximately 20% to the nitrogen flowing into the Wareham River (Kennedy et al. 2023), which is similar to the previous estimates (Howes et al. 2014; Williamson et al. 2017). However, the amount of nitrogen each bog contributed was not uniform (Jakuba et al. 2023). More specifically, higher levels of nitrogen were released from flow-through bogs that line river channels compared to wetland bogs that connect the bogs to larger water bodies via streams of ditches. This is due to the uptake of some nitrogen by aquatic plants and bacteria during transport through the streams and ditches (Jakuba et al. 2023). The model estimated that approximately two-thirds of the nitrogen flowing from the bogs in the Wareham River Watershed is currently removed by plants and bacteria as the water moves through natural streams and wetlands (Neill et al. 2021).

Cranberry bogs are a significant source of nitrogen to the Wareham River, and management strategies to reduce nitrogen should be considered (Jakuba et al. 2023). Some suggestions include promoting practices that prevent nitrogen from washing downstream from bogs by creating storage ponds, naturalizing stream channels, or avoiding fertilizer application prior to predicted rain.

Potential Water Quality Benefits of Restoring Natural Wetlands at Current Cranberry Bogs

Current cranberry economics are causing some growers to retire portions of the bogs that are less profitable; and simultaneously the Massachusetts Division of Ecological Restoration has developed techniques for restoring retired cranberry bogs to naturalized wetlands. Jakuba et al (2023) examined how nitrogen reduction was achieved by restoration of a cranberry bog to a naturalized wetland in the Wareham River Watershed.

Results indicated that the potential amount of nitrogen removal from bog restoration depends on both the location and type of bog (Jakuba et al. 2023). For example, if all the flow-through bogs in the Wareham River Watershed were restored, a 10% reduction of overall nitrogen to the watershed would be achieved (Jakuba et al. 2023). Conversely, restoration of less than half the acreage of flow-through bogs that intercept high nitrogen groundwater would result in a 12% reduction in nitrogen to the estuary (Kennedy et al. 2023). The difference is that if bogs that are located at intercepts with surface and groundwater flowing from residential areas that contains high amounts of nitrogen are restored to wetlands, the natural nitrogen removal process from the wetlands would yield a higher nitrogen removal rate for the downstream estuarine waters (Jakuba et al. 2013; Neill et al. 2020). In summary, restoring flow-through bogs close to the estuary, and intercepting high nitrogen groundwater would maximize nutrient removal benefits for the estuary (Jakuba et al. 2023).

4 Summary

The Weweantic River Estuary System is an ecologically complex system with several biological and physical factors influencing the benthic community assemblages and health status. Factors include a salinity range of tidal fresh to polyhaline water, the removal of Horseshoe Dam, long, narrow reaches, and elevated nutrient concentrations. These factors have likely contributed to the inconsistencies between the community parameters and US M-AMBI results.

Overall, due to these inconsistencies, rather than summarizing the Weweantic River Estuary System's benthic health exclusively from the US M-AMBI results, a summary of the health condition for the Weweantic River Estuary System was based on a combination of the following seven factors: percent contribution from a single taxonomic group or species, presence of pollution-sensitive or pollution-tolerant species, percent silt, percent TOC, AMBI classification, and US M-AMBI classification (Table 12).

These results indicate a clear transition from relatively healthy benthic habitat in the lower Weweantic River (Group 1), to a moderately disturbed habitat in the mid-Weweantic River/Beaver Dam Creek (Group 2), and moderately to heavily disturbed, low-quality habitat in the upper Weweantic River/Sippican River (Group 3). The progression from relative health to moderate and then poor habitat is consistent among all factors (except pollution sensitive species which were zero in all groups) summarized in Table 12.

Table 12. Summary of ecological data and benthic indices.

	Percent contribution from single taxonomic group or species (%)	Pollution Sensitive Species	Pollution Tolerant Species	Percent silt (%)	Percent TOC (%)	Indicator based on TOC[1]	AMBI (range)	US M-AMBI (range)
Group 1	17	0	3	4	0.5	Minimally impaired	2.1 - 3.2 Slightly Disturbed	0.74 - 1.00 Good - High
Group 2	35	0	0	17	4.2	Degraded	3.9 - 4.5 Moderately Disturbed	0.44 - 0.72 Good -Moderate
Group 3	65	0	0	30	5.3	Degraded	3.8 - 5.3 Moderately - Heavily Disturbed	0.26 - 0.58 Poor - Good

[1] Pelletier et al. 2011; Hyland et al. 2005

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Appendix A. Water Quality Measurements in the Weweantic River Estuary System, 2023.

Station	AU-ID	Depth (m)	Temp (°C)	DO (mg/L)	pH	Salinity (ppt)
MEP-SE-009	MA 95-05	0.1	sample missing			
		0.39	19.06	8.28	8.49	0.23
MEP-SE-010	MA 95-05	0.1	sample missing			
		0.52	15.61	6.77	7.38	8.98
MEP-SE-001	MA 95-05	0.1	sample missing			
		0.49	15.78	7.68	7.46	10.33
		1.05	15.60	7.11	7.24	11.35
MEP-SE-008	MA 95-05	0.1	sample missing			
		0.5	17.92	7.24	7.47	15.60
MEP-SE-013	MA 95-07	0.1	sample missing			
		0.5	17.62	7.09	7.56	15.51
MEP-SE-007	MA 95-05	0.1	sample missing			
		0.5	17.34	7.34	7.58	17.03
MEP-SE-006	MA 95-05	0.1	sample missing			
		0.5	21.73	6.70	8.31	19.97
		1.02	21.22	6.47	8.25	21.51
		2.01	20.55	5.75	8.26	25.61
		2.28	20.51	5.73	8.28	26.41
MEP-SE-003	MA 95-53	0.1	sample missing			
		0.5	21.06	6.09	8.11	20.91
MEP-SE-005	MA 95-05	0.1	sample missing			
		0.5	20.97	6.26	8.28	22.87
		1.02	20.74	5.98	8.30	27.01
		1.4	20.67	5.90	8.34	27.97
MEP-SE-004	MA 95-05	0.1	sample missing			
		0.51	21.05	6.16	8.27	23.07
		1.03	21.05	6.15	8.26	23.10
		1.26	21.04	6.14	8.26	23.13

Appendix B. US M-AMBI Code Documentation.

(continued next page)

MassDEP Massachusetts Estuaries Project (MEP) Benthic Monitoring Report

Weweantic River 2023 Survey: M-AMBI Calculations

Normandeau Associates, Inc.

2024-05-29

Benthic Monitoring Report: Weweantic River 2023 Survey

U.S. Multivariate AMBI (M-AMBI) Calculations

Prepared for: Massachusetts Department of Environmental Protection (MassDEP)

Prepared by: Normandeau Associates, Inc.

- *A. Villarreal 29 May 2024*

Resources:

- 'M-AMBI revisited: looking inside a widely-used benthic index' (Sigovini et al., 2013)
- 'Effect of ecological group classification schemes on performance of the AMBI benthic index in US coastal waters' (Gillett et al., 2015)
- 'Adaptation and application of multivariate AMBI (M-AMBI) in US coastal waters' (Pelletier et al., 2018)
- AZTI Marine Biotic Index species list
  - Updated June 2022
  - Downloaded May 2024
- New_mambi_script.R
  - Provided by Marguerite Pelletier on 17 May 2024

Comments:

- Original script for calculating M-AMB: mambisimpl.R
- The following code uses the updated M-AMBI script: New_mambi_script.R
  - Provided by Marguerite Pelletier on 17 May 2024
  - Does not depend on external packages to run M-AMBI

```
knitr::opts_chunk$set(echo = TRUE)
```

packages for markdown file creation

```
# packages for markdown file creation
library(knitr)
library(tinytex)
library(rmarkdown)
```

R version and session information

```
# session information
sessionInfo()

## R version 4.4.0 (2024-04-24 ucrt)
## Platform: x86_64-w64-mingw32/x64
## Running under: Windows 11 x64 (build 22621)
```

```
##
## Matrix products: default
##
##
## locale:
## [1] LC_COLLATE=English_United States.utf8
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] rmarkdown_2.27 tinytex_0.51   knitr_1.47
##
## loaded via a namespace (and not attached):
##  [1] compiler_4.4.0    fastmap_1.2.0     cli_3.6.2         tools_4.4.0
##  [5] htmltools_0.5.8.1 rstudioapi_0.16.0 yaml_2.3.8        xfun_0.44
##  [9] digest_0.6.35     rlang_1.1.3       evaluate_0.23
```

setup and data import

```
# set working directory
setwd("I:\\MADEP\\Weweantic\\M_AMBI\\R")

# read in data
NCA_raw<-read.table("I:\\MADEP\\Weweantic\\M_AMBI\\R\\WR23_MAMBI_SAMPLE_IMPORT_REV.csv",
sep=",", header=TRUE)

# print input data
print.data.frame(NCA_raw)
```

```
##          Sample       BC  S        H1   olig Sbin_cd
## 1  MEP_SE_001_1 4.029412 29 1.8959547 14.533       M
## 2  MEP_SE_001_3 3.930723 18 1.8683793 16.566       M
## 3  MEP_SE_003_1 4.342691 26 1.6479602 17.585   P_RUS
## 4  MEP_SE_003_3 4.317073 22 1.6088987 10.783   P_RUS
## 5  MEP_SE_004_2 2.096126 48 2.5294894  1.435   P_RUS
## 6  MEP_SE_004_3 2.130721 83 2.7745562  2.632   P_RUS
## 7  MEP_SE_005_1 2.849462 38 2.7052062 10.394   P_RUS
## 8  MEP_SE_005_2 2.403061 27 2.5651930  8.163   P_RUS
## 9  MEP_SE_006_1 3.106280 50 2.6042220  2.415   P_RUS
## 10 MEP_SE_006_3 3.178288 44 2.6253898  2.536   P_RUS
## 11 MEP_SE_007_2 4.106436 27 1.9537295 14.604       M
## 12 MEP_SE_007_3 4.486260 18 1.5748415 21.985       M
## 13 MEP_SE_008_1 5.022152 10 1.3099973 62.048       M
## 14 MEP_SE_008_2 5.332800 10 0.7066417 82.400       M
## 15 MEP_SE_009_2 4.610294 11 1.6300287 47.059      TF
## 16 MEP_SE_009_3 4.600610 11 1.7561749 47.561      TF
## 17 MEP_SE_010_1 5.073529 13 1.4008841 61.029       M
## 18 MEP_SE_010_3 4.747059 12 1.4953524 57.647       M
## 19 MEP_SE_013_2 5.016892 13 1.4359189 60.811       M
## 20 MEP_SE_013_3 3.814286 12 2.0734207 22.857       M
```

salinity binning

```
#### salinity binning  ####

TF_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='TF'),]
# O_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='O'),]
M_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='M'),]
P_RUS_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='P_RUS'),]
```

```
# P_WEST_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='P_WEST'),]
# E_RUS_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='E_RUS'),]
# E_WEST_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='E_WEST'),]
# Hyper_raw <- NCA_raw[which(NCA_raw$Sbin_cd=='Hyper'),]

# print binned data
print(TF_raw)

##          Sample       BC  S       H1   olig Sbin_cd
## 15 MEP_SE_009_2 4.610294 11 1.630029 47.059      TF
## 16 MEP_SE_009_3 4.600610 11 1.756175 47.561      TF

# print(O_raw)
print(M_raw)

##          Sample       BC  S        H1   olig Sbin_cd
## 1  MEP_SE_001_1 4.029412 29 1.8959547 14.533       M
## 2  MEP_SE_001_3 3.930723 18 1.8683793 16.566       M
## 11 MEP_SE_007_2 4.106436 27 1.9537295 14.604       M
## 12 MEP_SE_007_3 4.486260 18 1.5748415 21.985       M
## 13 MEP_SE_008_1 5.022152 10 1.3099973 62.048       M
## 14 MEP_SE_008_2 5.332800 10 0.7066417 82.400       M
## 17 MEP_SE_010_1 5.073529 13 1.4008841 61.029       M
## 18 MEP_SE_010_3 4.747059 12 1.4953524 57.647       M
## 19 MEP_SE_013_2 5.016892 13 1.4359189 60.811       M
## 20 MEP_SE_013_3 3.814286 12 2.0734207 22.857       M

print(P_RUS_raw)

##          Sample       BC  S       H1   olig Sbin_cd
## 3  MEP_SE_003_1 4.342691 26 1.647960 17.585   P_RUS
## 4  MEP_SE_003_3 4.317073 22 1.608899 10.783   P_RUS
## 5  MEP_SE_004_2 2.096126 48 2.529489  1.435   P_RUS
## 6  MEP_SE_004_3 2.130721 83 2.774556  2.632   P_RUS
## 7  MEP_SE_005_1 2.849462 38 2.705206 10.394   P_RUS
## 8  MEP_SE_005_2 2.403061 27 2.565193  8.163   P_RUS
## 9  MEP_SE_006_1 3.106280 50 2.604222  2.415   P_RUS
## 10 MEP_SE_006_3 3.178288 44 2.625390  2.536   P_RUS

# print(P_WEST_raw)
# print(E_RUS_raw)
# print(E_WEST_raw)
# print(Hyper_raw)
```

---

subset appropriate metrics and run M-AMBI

Tidal Freshwater

```
## Tidal Freshwater
TF_model<-TF_raw[,-1]
rownames(TF_model)<- TF_raw[,1]
AMBI_var <- c("BC","olig","H1")
metrics.ex <- TF_model[AMBI_var]

good_TF<-c(0.15,0,1.93)
bad_metric<-c(6,100,0)

# Note: for the scores to be the right sign, and the eventual M-AMBI scores calculated
correctly, the bad metric needs to be above the good metric
metrics.tot<-rbind(metrics.ex,bad_metric,good_TF)
B_no<-nrow(metrics.tot)-1
H_no<-nrow(metrics.tot)
rownames(metrics.tot)[B_no]<-"B"
rownames(metrics.tot)[H_no]<-"H"
```

```
## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software -from fun.mambisimple.R program but uses base
principle components analysis in R rather than psych
options(warn = -1)
METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
options(warn = 0)
METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
diag(sqrt(eigen(cor(metrics.tot))$values))
METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
colnames(METRICS.scores) <- c("x","y","z")
METRICS.tr<-METRICS.scores*-1

## this code was pulled from the fun.mambisimple.R program. This projects the scores onto the
pollution vector
EQR <- function(data) {
  segm <- data[nrow(data),] - data[(nrow(data)-1),]
  vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
  for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
  vett <- data - vett
  ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
  return(ris)
}
eqr <- EQR(METRICS.tr)
colnames(eqr)<- "M-AMBI"

mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
write.csv(mambi_output, "mambi_olig_TF.csv")

# print m-ambi metrics
print.data.frame(mambi_output)

##                     BC    olig       H1 M-AMBI           x          y
## MEP_SE_009_2 4.610294  47.059 1.630029  0.529  0.13407269 -0.2345849
## MEP_SE_009_3 4.600610  47.561 1.756175  0.547  0.08899295 -0.3592185
## B            6.000000 100.000 0.000000  0.000  2.24571892  2.5405991
## H            0.150000   0.000 1.930000  1.000 -2.46878456 -1.9467956
##                         z
## MEP_SE_009_2 -0.002152513
## MEP_SE_009_3 -0.001888456
## B             0.045104079
## H            -0.041063111
```

Oligohaline

```
# ## Oligohaline
# O_model<-O_raw[,-1]
# rownames(O_model)<- O_raw[,1]
# AMBI_var <- c("BC","S","H1")
# metrics.ex <- O_model[AMBI_var]
#
# good_O<-c(0.53,16.0,2.12)
# bad_metric<-c(6,0,0)
#
# #Note: for the scores to be the right sign, and the eventual M-AMBI scores calculated
correctly, the bad metric needs to be above the good metric
# metrics.tot<-rbind(metrics.ex,bad_metric,good_O)
# B_no<-nrow(metrics.tot)-1
# H_no<-nrow(metrics.tot)
# rownames(metrics.tot)[B_no]<-"B"
# rownames(metrics.tot)[H_no]<-"H"
#
# ## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software
```

```
# options(warn = -1)
# METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
# options(warn = 0)
# METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
# METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
diag(sqrt(eigen(cor(metrics.tot))$values))
# METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
# METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
# colnames(METRICS.scores) <- c("x","y","z")
# METRICS.tr<-METRICS.scores*-1
#
# ## this code was pulled from the fun.mambisimple.R program
# EQR <- function(data) {
#   segm <- data[nrow(data),] - data[(nrow(data)-1),]
#   vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
#   for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
#   vett <- data - vett
#   ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
#   return(ris)
# }
# eqr <- EQR(METRICS.tr)
# colnames(eqr)<- "M-AMBI"
#
# mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
# write.csv(mambi_output, "mambi_S_O.csv")
#
# # print m-ambi metrics
# print.data.frame(mambi_output)
```

Mesohaline

```
## Mesohaline
M_model<-M_raw[,-1]
rownames(M_model)<- M_raw[,1]
AMBI_var <- c("BC","S","H1")
metrics.ex <- M_model[AMBI_var]

good_M<-c(0.85,26.0,2.48)
bad_metric<-c(6,0,0)

# Note: for the scores to be the right sign, and the eventual M-AMBI scores calculated
correctly, the bad metric needs to be above the good metric
metrics.tot<-rbind(metrics.ex,bad_metric,good_M)
B_no<-nrow(metrics.tot)-1
H_no<-nrow(metrics.tot)
rownames(metrics.tot)[B_no]<-"B"
rownames(metrics.tot)[H_no]<-"H"

## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software
options(warn = -1)
METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
options(warn = 0)
METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
diag(sqrt(eigen(cor(metrics.tot))$values))
METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
colnames(METRICS.scores) <- c("x","y","z")
METRICS.tr<-METRICS.scores*-1

## this code was pulled from the fun.mambisimple.R program
EQR <- function(data) {
  segm <- data[nrow(data),] - data[(nrow(data)-1),]
  vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
  for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
```

```
  vett <- data - vett
  ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
  return(ris)
}
eqr <- EQR(METRICS.tr)
colnames(eqr)<- "M-AMBI"

mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
write.csv(mambi_output, "mambi_S_M.csv")

# print m-ambi metrics
print.data.frame(mambi_output)

##                      BC  S        H1 M-AMBI          x          y            z
## MEP_SE_001_1 4.029412 29 1.8959547  0.720  1.0781047 -1.7518923 -1.01114392
## MEP_SE_001_3 3.930723 18 1.8683793  0.608  0.6244649 -0.6013255 -0.63613920
## MEP_SE_007_2 4.106436 27 1.9537295  0.702  1.0425508 -1.5618658 -0.92256555
## MEP_SE_007_3 4.486260 18 1.5748415  0.525  0.1306659 -0.2555162 -0.05007358
## MEP_SE_008_1 5.022152 10 1.3099973  0.365 -0.6506893  0.9066504  0.80983051
## MEP_SE_008_2 5.332800 10 0.7066417  0.255 -1.4374559  1.4043805  1.44777115
## MEP_SE_010_1 5.073529 13 1.4008841  0.406 -0.4367617  0.5413600  0.66535122
## MEP_SE_010_3 4.747059 12 1.4953524  0.432 -0.2780855  0.4973736  0.41449332
## MEP_SE_013_2 5.016892 13 1.4359189  0.415 -0.3804793  0.5025646  0.60199317
## MEP_SE_013_3 3.814286 12 2.0734207  0.582  0.6500879 -0.1423003 -0.62972005
## B            6.000000  0 0.0000000  0.000 -2.8500848  3.1166728  2.78611480
## H            0.850000 26 2.4800000  1.000  2.5076824 -2.6561018 -3.47591187
```

Polyhaline-Rest of US

```
## Polyhaline-Rest of US
P_RUS_model<-P_RUS_raw[,-1]
rownames(P_RUS_model)<- P_RUS_raw[,1]
AMBI_var <- c("BC","S","H1")
metrics.ex <- P_RUS_model[AMBI_var]

good_P_RUS<-c(0.72,44.0,2.96)
bad_metric<-c(6,0,0)

# Note: for the scores to be the right sign, and the eventual M-AMBI scores calculated
correctly, the bad metric needs to be above the good metric
metrics.tot<-rbind(metrics.ex,bad_metric,good_P_RUS)
B_no<-nrow(metrics.tot)-1
H_no<-nrow(metrics.tot)
rownames(metrics.tot)[B_no]<-"B"
rownames(metrics.tot)[H_no]<-"H"

## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software
options(warn = -1)
METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
options(warn = 0)
METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
diag(sqrt(eigen(cor(metrics.tot))$values))
METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
colnames(METRICS.scores) <- c("x","y","z")
METRICS.tr<-METRICS.scores*-1

## this code was pulled from the fun.mambisimple.R program
EQR <- function(data) {
  segm <- data[nrow(data),] - data[(nrow(data)-1),]
  vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
  for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
  vett <- data - vett
  ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
```

```
  return(ris)
}
eqr <- EQR(METRICS.tr)
colnames(eqr)<- "M-AMBI"

mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
write.csv(mambi_output, "mambi_S_P_RUS.csv")

# print m-ambi metrics
print.data.frame(mambi_output)

##                    BC  S       H1 M-AMBI          x          y          z
## MEP_SE_003_1 4.342691 26 1.647960  0.464 -0.7944783  1.0666454 -1.3182379
## MEP_SE_003_3 4.317073 22 1.608899  0.442 -0.8644859  1.2444032 -1.3933209
## MEP_SE_004_2 2.096126 48 2.529489  0.856  0.5604754 -0.8076108  0.9947500
## MEP_SE_004_3 2.130721 83 2.774556  1.048  1.1429770 -2.3619688  1.6969940
## MEP_SE_005_1 2.849462 38 2.705206  0.773  0.4122888 -0.2982924  0.5104638
## MEP_SE_005_2 2.403061 27 2.565193  0.739  0.2740670  0.1157380  0.5061140
## MEP_SE_006_1 3.106280 50 2.604222  0.796  0.4290628 -0.6829619  0.4740166
## MEP_SE_006_3 3.178288 44 2.625390  0.765  0.3583171 -0.4282171  0.3515378
## B            6.000000  0 0.000000  0.000 -2.6234821  3.3338944 -3.8819969
## H            0.720000 44 2.960000  1.000  1.1052583 -1.1816300  2.0596794
```

Polyhaline-West

```
# ## Polyhaline-West
# P_WEST_model<-P_WEST_raw[,-1]
# rownames(P_WEST_model)<- P_WEST_raw[,1]
# AMBI_var <- c("BC","S","H1")
# metrics.ex <- P_WEST_model[AMBI_var]
#
# good_P_WEST<-c(0.18,76.8,3.30)
# bad_metric<-c(6,0,0)
#
# # Note: for the scores to be the right sign, and the eventual M-AMBI scores calculated
correctly, the bad metric needs to be above the good metric
# metrics.tot<-rbind(metrics.ex,bad_metric,good_P_WEST)
# B_no<-nrow(metrics.tot)-1
# H_no<-nrow(metrics.tot)
# rownames(metrics.tot)[B_no]<-"B"
# rownames(metrics.tot)[H_no]<-"H"
#
# ## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software
# options(warn = -1)
# METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
# options(warn = 0)
# METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
# METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
diag(sqrt(eigen(cor(metrics.tot))$values))
# METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
# METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
# colnames(METRICS.scores) <- c("x","y","z")
# METRICS.tr<-METRICS.scores*-1
#
# ## this code was pulled from the fun.mambisimple.R program
# EQR <- function(data) {
#   segm <- data[nrow(data),] - data[(nrow(data)-1),]
#   vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
#   for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
#   vett <- data - vett
#   ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
#   return(ris)
# }
# eqr <- EQR(METRICS.tr)
# colnames(eqr)<- "M-AMBI"
```

```
#
# mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
# write.csv(mambi_output, "mambi_S_P_WEST.csv")
#
# # print m-ambi metrics
# print.data.frame(mambi_output)
```

Euhaline-Rest of US

```
# ## Euhaline-Rest of US
# E_RUS_model<-E_RUS_raw[,-1]
# rownames(E_RUS_model)<- E_RUS_raw[,1]
# AMBI_var <- c("BC","S","H1")
# metrics.ex <- E_RUS_model[AMBI_var]
#
# good_E_RUS<-c(0.56,61.0,3.29)
# bad_metric<-c(6,0,0)
#
# # Note: for the scores to be the right sign, and the eventual M-AMBI scores  calculated
correctly, the bad metric needs to be above the good metric
# metrics.tot<-rbind(metrics.ex,bad_metric,good_E_RUS)
# B_no<-nrow(metrics.tot)-1
# H_no<-nrow(metrics.tot)
# rownames(metrics.tot)[B_no]<-"B"
# rownames(metrics.tot)[H_no]<-"H"
#
# ## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software
# options(warn = -1)
# METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
# options(warn = 0)
# METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
# METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
diag(sqrt(eigen(cor(metrics.tot))$values))
# METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
# METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
# colnames(METRICS.scores) <- c("x","y","z")
# METRICS.tr<-METRICS.scores*-1
#
# ## this code was pulled from the fun.mambisimple.R program
# EQR <- function(data) {
#   segm <- data[nrow(data),] - data[(nrow(data)-1),]
#   vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
#   for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
#   vett <- data - vett
#   ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
#   return(ris)
# }
# eqr <- EQR(METRICS.tr)
# colnames(eqr)<- "M-AMBI"
#
# mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
# write.csv(mambi_output, "mambi_S_E_RUS.csv")
#
# # print m-ambi metrics
# print.data.frame(mambi_output)
```

Euhaline-West

```
# ## Euhaline-West
# E_WEST_model<-E_WEST_raw[,-1]
# rownames(E_WEST_model)<- E_WEST_raw[,1]
# AMBI_var <- c("BC","S","H1")
# metrics.ex <- E_WEST_model[AMBI_var]
#
# good_E_WEST<-c(0.66,92.0,3.62)
# bad_metric<-c(6,0,0)
```

```
#
# # Note: for the scores to be the right sign, and the eventual M-AMBI scorescalculated
correctly, the bad metric needs to be above the good metric
# metrics.tot<-rbind(metrics.ex,bad_metric,good_E_WEST)
# B_no<-nrow(metrics.tot)-1
# H_no<-nrow(metrics.tot)
# rownames(metrics.tot)[B_no]<-"B"
# rownames(metrics.tot)[H_no]<-"H"
#
# ## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software
# options(warn = -1)
# METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
# options(warn = 0)
# METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
# METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
diag(sqrt(eigen(cor(metrics.tot))$values))
# METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
# METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
# colnames(METRICS.scores) <- c("x","y","z")
# METRICS.tr<-METRICS.scores*-1
#
# ## this code was pulled from the fun.mambisimple.R program
# EQR <- function(data) {
#   segm <- data[nrow(data),] - data[(nrow(data)-1),]
#   vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
#   for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
#   vett <- data - vett
#   ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
#   return(ris)
# }
# eqr <- EQR(METRICS.tr)
# colnames(eqr)<- "M-AMBI"
#
# mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
# write.csv(mambi_output, "mambi_S_E_WEST.csv")
#
# # print m-ambi metrics
# print.data.frame(mambi_output)
```

Hyperhaline

```
# ## Hyperhaline
# Hyper_model<-Hyper_raw[,-1]
# rownames(Hyper_model)<- Hyper_raw[,1]
# AMBI_var <- c("BC","S","H1")
# metrics.ex <- Hyper_model[AMBI_var]
#
# good_Hyper<-c(0.32,55.0,3.45)
# bad_metric<-c(6,0,0)
#
# # Note: for the scores to be the right sign, and the eventual M-AMBI scores calculated
correctly, the bad metric needs to be above the good metric
# metrics.tot<-rbind(metrics.ex,bad_metric,good_Hyper)
# B_no<-nrow(metrics.tot)-1
# H_no<-nrow(metrics.tot)
# rownames(metrics.tot)[B_no]<-"B"
# rownames(metrics.tot)[H_no]<-"H"
#
# ## direct calculation, which produces the factor scores with the same signs of the scores
produced by the AZTI-Tecnalia AMBI software
# options(warn = -1)
# METRICS.fa <- princomp(metrics.tot, cor = T, covmat = cov(metrics.tot))
# options(warn = 0)
# METRICS.fa.load <- loadings(METRICS.fa) %*% diag(METRICS.fa$sdev)
# METRICS.fa.load <- eigen(cor(metrics.tot))$vectors %*%
```

```
diag(sqrt(eigen(cor(metrics.tot))$values))
# METRICS.fa.load.varimax <- loadings(varimax(METRICS.fa.load))
# METRICS.scores <- scale(metrics.tot) %*% METRICS.fa.load.varimax
# colnames(METRICS.scores) <- c("x","y","z")
# METRICS.tr<-METRICS.scores*-1
#
# ## this code was pulled from the fun.mambisimple.R program
# EQR <- function(data) {
#   segm <- data[nrow(data),] - data[(nrow(data)-1),]
#   vett <- matrix(NA, nrow = nrow(data), ncol = ncol(data))
#   for (k in 1: ncol(data)) {vett[, k] <- data[(nrow(data)-1), k]}
#   vett <- data - vett
#   ris <- round((vett %*% segm / sqrt(sum(segm*segm))) / sqrt(sum(segm*segm)), 3)
#   return(ris)
# }
# eqr <- EQR(METRICS.tr)
# colnames(eqr)<- "M-AMBI"
#
# mambi_output <- cbind(metrics.tot,eqr,METRICS.tr)
# write.csv(mambi_output, "mambi_S_Hyper.csv")
#
# # print m-ambi metrics
# print.data.frame(mambi_output)
```