LISMaRC Phase II Epifauna Sample Block and Site Diversity Measures in the Long Island Sound Cable Fund Initiative Phase II area of eastern Long Island Sound Collected during SEABOSS Operations (2018)

METADATA

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Dataset Title: *LISMaRC Phase II Epifauna Sample Block and Site Diversity Measures in the Long Island Sound Cable Fund Initiative Phase II area of eastern Long Island Sound Collected during SEABOSS Operations (2018)*

Filename: LISMaRC_BenthicEcology_2018_EpifaunaSeaBossBlockSite_Diversity.shp

Online Linkage: *http://www.marine-geo.org/portals/lis/*

Abstract: *The shapefile includes mean sample block- (SB) and site-specific (NB) diversity measures determined using analyzed images collected during USGS SEABed Observation and Sampling System (SEABOSS) operations in May 2018. Shapefile data includes block and site ID and diversity measures taxonomic and feature richness (S'), evenness (J), and Shannon-Weiner diversity (H_{log10}). These are the complete records of block- and site-level diversity.*

Dataset purpose: *This dataset provides detailed information on the epifaunal communities in the Phase II study area which can be used to map the spatial characteristics of these communities relative to several environmental features to meet the Long Island Sound Cable Fund's goal of ecological characterization of the Long Island Sound sea floor in conjunction with habitat mapping efforts.*

Time period of content: *These data were collected during May 2018.*

Dataset Status: *Complete*

Update Frequency: *None Planned*

Theme Keywords: *Benthic ecology, Epifauna, diversity, habitat, seafloor imaging, SEABOSS, Connecticut, New York, Long Island Sound, Fishers Island Sound, estuary, Long Island Sound Mapping and Research Collaborative, LISMaRC*

Access Constraints: *none*

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Dataset Credit: *The Long Island Sound Mapping and Research Collaborative (LISMaRC). LISMaRC is the University of Connecticut, the University of New Haven and the US Geological Survey. Funding provided by the Long Island Sound Seafloor Mapping Fund administered cooperatively by the EPA Long Island Sound Study and the Connecticut Department of Energy and Environmental Protection (DEEP).*

Data Quality Considerations: *see below*

Attribute accuracy: *All attributes were evaluated during data processing and analysis as standard quality control to ensure attributes contain accurate and relevant information and values.*

Completeness: *The information provided on epifaunal communities is complete*

Positional accuracy: *Shapefile object locations correspond to sample sites (NB) and the centroids of sample blocks (SB). Block and site locations were selected with the overall objective to sample as many of the different seafloor habitats that were evident in the side scan mosaic that had been previously developed for the study area.*

Process Steps: *Diversity indices were summarized as block- and site-specific mean values of taxonomic and feature richness (S'), evenness (J), and Shannon-Weiner diversity (H_{log10}) calculated at the scale of each analyzed image (n=595). Images were captured using the United States Geological Survey's (USGS) Seabed Observation and Sampling System (SEABOSS; Valentine et al. 2000) between May 8 and 15, 2018 on the RV Connecticut.*

SEABOSS captured orthogonal images of the seafloor. These images were analyzed for percent cover of all living seafloor species (excluding fish) and biogenic features. Percent cover was quantified using a grid of square cells overlaid on each image (n=216 grid cells). Within each grid square, organisms and biogenic features were identified to lowest possible taxonomic level. The sum of these grid cells for each image and organism or biogenic feature is reported in this dataset. Within-image measures of diversity and richness of taxa and biogenic features were determined per image.

Attributes:

Name: Sample block or site.

S_taxa: Taxa richness (S).

J_taxa: Taxa evenness (J').

Hlg10_t: Taxa Shannon-Weiner diversity index (H' log_{10}).

S_feat: Biogenic feature richness (S).

S_tx_ft: Combined taxa and biogenic feature richness (S).

J_tx_ft: Combined taxa and biogenic feature evenness (J').

Hlg10_tx_f: Combined taxa and biogenic feature Shannon-Weiner diversity index (H' log_{10}).

sm_2018: Sample blocks and sites sampled in May 2018.

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