Presence or absence of amplicon sequence variants (ASVs) recovered from samples which are described in DATASET 01, Pseudo-nitzschia spp. from weekly samples and offshore cruises with the Northeast U.S. Shelf (NES) Long-Term Ecological Research (LTER)

Website: https://www.bco-dmo.org/dataset/847495
Data Type: Cruise Results
Version: 1
Version Date: 2021-04-05

Project
» RII Track-1: Rhode Island Consortium for Coastal Ecology Assessment, Innovation, and Modeling (C-AIM)

Contributors	Affiliation	Role
Jenkins, Bethany D.	University of Rhode Island (URI)	Principal Investigator
Bertin, Matthew	University of Rhode Island (URI)	Co-Principal Investigator
Sterling, Alexa	University of Rhode Island (URI)	Contact
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset is related to approximately weekly sampling of Narragansett Bay, RI in tandem with the University of Rhode Island (URI) Graduate School of Oceanography (GSO) Long-Term Plankton Time Series (LTPTS) and Fish Trawl Survey to examine species assemblages and toxicity of the diatom genus Pseudo-nitzschia spp. This dataset includes the presence or absence of amplicon sequence variants (ASVs) recovered from samples which are described in DATASET 01.

Table of Contents

- Coverage
- Dataset Description
  - Acquisition Description
  - Processing Description
- Related Publications
- Parameters
- Instruments
- Deployments
- Project Information
- Funding

Coverage

Spatial Extent: **N**:41.6716 **E**:-70.8626 **S**:40.206 **W**:-71.42
Temporal Extent: 2016-09-26 - 2019-11-25

Acquisition Description

For most samples, plankton biomass for Pseudo-nitzschia DNA identification was collected by passing an average of 270 mL of surface seawater with a peristaltic pump across a 25 mm 5.0 mm polyester

membrane filter (Sterlitech, Kent, WA, USA). Widths of some Pseudo-nitzschia spp. are < 5.0 mm (Lelong et al. 2012), but this size pore likely captured horizontally orientated cells and chains of cells, and was consistent with pore size used to examine toxicity. Filters were flash frozen in liquid nitrogen and stored at -80 °C until extraction. DNA was extracted using a modified version of the DNeasy Plant DNA extraction kit (Qiagen, Germantown, MD, USA) with an added bead beating step for 1 minute and QIA-Shredder column (Qiagen, Germantown, MD, USA) as reported in Chappell et al. 2019. Additionally, DNA was eluted in 30 µL with a second elution step of either 30 or 15 µL to maximize DNA yield. DNA was assessed for quality with a Nanodrop spectrophotometer (Thermo Fisher Scientific Inc., Waltham, MA, USA) and quantified using a Qubit fluorometer (Invitrogen, Carlsbad, CA, USA) with the Broad Range dsDNA and High Sensitivity dsDNA kits (Thermo Fisher Scientific Inc., Waltham, MA, USA). DNA yields reported by the Qubit ranged from below the limit of detection to 26.5, with an average of 2.0 ng DNA / mL eluent. Long-Term Plankton Time Series (LTPTS) samples from October 2016 and March 2017 had an average of 300 mL surface seawater passed over a 25 mm 0.2 mm filter, were extracted following existing LTPTS methods of DNA extraction using the DNeasy Blood and Tissue Kit (Qiagen, Germantown, MD, USA) with an added bead beating step (Canesi and Rynearson 2016), and yielded average 0.9 ng DNA / mL eluent as measured by the Qubit. Net tow samples had 50 mL of concentrate was passed across a 0.22 µm pore size Sterivex filter unit (MilliporeSigma, Burlington, MA, USA), and were extracted with the same modified DNeasy Plant DNA extraction protocol as above, with 4x volumes of AP1 buffer and RNase A and beads added to the unit to account for the larger sample surface area, extraction occurring within the capped unit itself to maximize yield, and then the lysate removed with a sterile syringe and subsequent steps with adjusted volumes as appropriate. As expected, DNA yields were higher from the Sterivex units ranging from 2.4 – 54.0 ng DNA / mL eluent with an average of 13.7 ng DNA/ mL elution as measured by the Qubit. For the March 13, 2017 NBay samples, 125 mL of surface seawater was passed across a HV filter and extracted with the DNeasy Plant DNA extraction kit with scissors and no beads. As measured by the Qubit, the average DNA yield was 3.7 ng DNA / mL eluent. A negative control sample was prepared of a blank 25 mm 5.0 mm polyester membrane filter using extraction reagents which had no detectable DNA using the Qubit. There were two positive controls of mock communities comprised of two known Pseudo-nitzschia species from monocultures. The two Pseudo-nitzschia cultures were P. subcurvata collected from the Southern Ocean and P. pungens isolated from NBay (provided by J. Rines). One positive control was made by combining equal concentrations of extracted DNA with 1.0 ng DNA of each culture. The second positive control was created of equal cell abundance estimated to be captured onto the filters of the cultures prior to extraction. These negative and positive controls were prepared for sequencing and sequenced on the same plate as the other environmental samples.

The ITS1 has been targeted for amplification and analysis by ARISA previously for Pseudo-nitzschia identification in environmental samples (Hubbard, Rocap, and Armbrust 2008). A comparison of ITS1 appears to be much less conserved and is divergent enough across Pseudo-nitzschia that 41 different species can be identified using existing public sequencing data. The primers to target the ITS1 region of Pseudo-nitzschia used this existing forward primer sequence of the ITS1 region for eukaryotes: TCCGTAGGTGAACCTGCGG (White et al. 1990) and a custom reverse primer designed using 132 Pseudo-nitzschia ITS1 sequences from the NCBI nucleotide database (downloaded on 4/3/2019) from this nucleotide search: ((Pseudo-nitzschia[Organism]) AND internal transcribed spacer[Title]) NOT uncultured): CATCCACCGCTGAAAGTTGTAA. This reverse primer targets a conserved region in the 5.8S. All primer sequences are reported from 5' – 3'. MiSeq adapter sequences were added to the beginning of the primer sequences for these full sequences used in this study: forward primer TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCCGTAGGTGAACCTGCGG and reverse primer GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCATCCACCGCTGAAAGTTGTAA. When checking the specificity of these primers using the NCBI nt database, it became known that sequences beyond Pseudo-nitzschia would also be amplified in this study including other diatoms and dinoflagellates; however, the large number of sequencing reads recovered on the MiSeq platform would circumvent this non-specific characteristic of the primers.

The accession numbers of the sequences used in this primer design are reported in Table S2 of Sterling et al. (in prep), along with a summary of Pseudo-nitzschia species expected to amplify with these based on the in silico design. The expected ranges for PCR products were from 235 – 370 bp as the size of the ITS1 region differs for some Pseudo-nitzschia taxa. Primers (Integrated DNA Technologies, Coralville, IA, USA) were HPLC purified, resuspended in 1x Tris-Acetate-EDTA (TAE) buffer, and then working stocks created in

diethylpyrocarbonate (DEPC)-treated H2O. About 4 ng of extracted DNA was used for each PCR reaction. If, according to the Qubit quantification, the DNA concentration was less than 2 ng mL-1 or below the limit of detection, it was then used as is, and just 2 mL was added to the PCR reaction. PCR reactions were set up on ice, in a 1x reaction in 25 mL total volume. Final primer concentration was 0.5 mM and polymerase was Phusion Hot Start High-Fidelity Master Mix (Thermo Fisher Scientific Inc., Waltham, MA, USA). There were two cycles with different annealing temperatures, the first with an annealing temperature specific to the loci-specific region and the second set of cycles with an annealing temperature that also takes the MiSeq adapter sequence into account (Canesi and Rynearson 2016). PCR conditions used were initial denaturation for 30 seconds at 98 °C, 15 cycles of the following: denaturation for 10 seconds at 98 °C, annealing for 30 seconds at 64.1 °C , extension for 30 seconds at 72 °C, and 15 cycles with the same conditions except a higher annealing temperature of 72 °C , and then a final extension for 10 minutes at 72 °C , and a holding temperature of 10 °C until stored in the -20 °C freezer. PCR products were visualized on a 1% agarose gel before submission to the URI Genomics and Sequencing Center (Kington, RI, USA) where library preparation and sequencing were performed on a 2x300 bp MiSeq run (Illumina, Inc., San Diego, CA, USA). There were 193 environmental samples were sequenced, along with two positive controls of Pseudo-nitzschia DNA from cultures and one negative control, for a total of 196 samples using two sets of MiSeq indices on the same sequencing plate. It was deemed appropriate to multiplex this plate as estimated read depth to recover Pseudo-nitzschia sequences was predicted to be lower than usual.

The columns are the library_ID as described in DATASET 01: the identifying sample number that connects the row of environmental data to the corresponding plankton biomass filter that was sequenced for the Pseudo-nitzschia species assemblages. The Sequence Sample ID connect to the sample_title, library_ID and file names in NCBI's Short Read Archive (SRA) under this related Bioproject #PRJNA690940.

The rows are the Sequence_of_ASV as described in DATASET 02: the DNA sequence of the internal transcribed spacer (ITS) 1 region used to identify the Pseudo-nitzschia [NCBI:txid41953] species. Only ASVs shown pass the threshold of accounting for > 1% relative abundance in a sample.

The matrix is filled in indicating whether or not that specific ASV sequence was present in that corresponding sample with 1 = Present and 0 = Absent.

Problem report: Sample #AS424 had no ASVs belonging to *Pseudo-nitzschia* sp. and was removed.

Processing Description

A custom bioinformatics pipeline was utilized. CutAdapt (Martin 2011) was used to trim Illumina MiSeq adapters and primer sequences. Primer sequences were trimmed from both ends of sequences, with the reverse complement of the other primer trimmed the end of the sequences. If reads did not have the ITS1 primer sequence, they were discarded. Reads needed to be one base pair (bp) or longer to continue in the pipeline. Trimmed sequences were inputted into DADA2 (v. 1.16) to determine amplicon sequence variants (ASVs; Callahan et al. 2016). ASVs were retained at that level, with some potentially having as few differences as one bp to each other, for the subsequent analysis. ASVs were identified as *Pseudo-nitzschia* taxa using a curated database from NCBI sequences (Table S2 in Sterling et al. in prep) which used to design primers to assign taxonomy for ITS1 ASVs trimmed of the primer sequences using the scikit-learn naïve Bayes machine learning classifier (Pedregosa et al. 2011) at default settings in QIIME2 (Bolyen et al. 2019). The scikit-learn naïve Bayes machine learning classifier identified 97 ASVs as *Pseudo-nitzschia* at the species level. Three of these ASVs belonged to *P. subcurvata* from the positive control mock community and were removed from analysis. All of the 6,503 ASVs recovered from the 192 non-control samples from the sequencing effort were run through a megablast search using BLAST+ version 2.9 with the nucleaotide (nt) database downloaded on October 4, 2020. There were 540 ASVs which had a known *Pseudo-nitzschia* taxa, including clones, vouchers, and environmental samples, as its top megablast hit. In addition to the 97 ASVs identified as a specific *Pseudo-nitzschia* species from the QIIME2 pipeline, there were 115 ASVs identified as a *Pseudo-nitzschia* taxa with greater than 75% query coverage were manually examined. It was determined by judgement call that the 11 ASVs which were identified as *P. pungens* PC50 were likely *Cylindrotheca* instead and the 85 ASVs which were closest related to *P. delicatissima* KJ22-0.2-69 environmental clone was most closely related to known *Nitzschia* isolate

sequence from subsequent BLAST searches. This left 19 ASVs of interest, with 9 of them have >98% query coverage and >98% identity with known *Pseudo-nitzschia* sequences so were referred to as the specific *Pseudo-nitzschia* species and 10 ASVs were identified as the genus with identifiers of similar groups of ASVs to each other. These genus level ASVs have < 96% identity to existing sequences in the database. In total, there were 113 ASVs from the 192 samples that appeared to be of reliable *Pseudo-nitzschia* origin. Sample #AS424 had none of the 113 ASVs and was removed. Read counts were transformed into relative abundance out of total *Pseudo-nitzschia* taxa reads. If an ASV accounted for < 1% relative abundance in a sample, then it was considered "not present" or absent to avoid potentially spurious results. This removed 60 ASVs which only occurred in < 1% of reads in samples. The remaining 53 ASVs were used in the analysis in a presence/absence matrix to avoid potential problems from inflating read numbers with cell counts. This threshold retained 46 of the 97 scikit-learn classifier identified ASVs, and seven of the ASVs added by the megablast curation. Of the seven ASVs added from megablast results, three ASVs where in a group together at the genus level, and around 95% identity with known *P. americana* sequences. The other megablast added ASVs were very closely related to *P. cuspidata* and *P. calliantha*.

BCO-DMO Processing Notes:
- data were submitted in file "DATA03_ASVTable_Sterling_NBay.csv".
- added conventional header with dataset name, PI name, version date
- columns and rows were flipped to allow better viewing (would be extremely wide if not pivoted)

[table of contents | back to top]

Related Publications

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., … Asnicar, F. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 37(8), 852–857. doi:10.1038/s41587-019-0209-9
Methods

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: High-resolution sample inference from Illumina amplicon data. Nature Methods, 13(7), 581–583. doi:10.1038/nmeth.3869
Methods

Canesi, K., & Rynearson, T. (2016). Temporal variation of Skeletonema community composition from a long-term time series in Narragansett Bay identified using high-throughput DNA sequencing. Marine Ecology Progress Series, 556, 1–16. doi:10.3354/meps11843
Methods

Chappell, P., Armbrust, E., Barbeau, K., Bundy, R., Moffett, J., Vedamati, J., & Jenkins, B. (2019). Patterns of diatom diversity correlate with dissolved trace metal concentrations and longitudinal position in the northeast Pacific coastal-offshore transition zone. Marine Ecology Progress Series, 609, 69–86. doi:10.3354/meps12810
Methods

Hubbard, K. A., Rocap, G., & Armbrust, E. V. (2008). Inter- and Intraspecific Community Structure within the Diatom Genuspseudo-Nitzschia(Bacillariophyceae). Journal of Phycology, 44(3), 637–649. doi:10.1111/j.1529-8817.2008.00518.x
Methods

Lelong, A., Hégaret, H., Soudant, P., & Bates, S. S. (2012). Pseudo-nitzschia (Bacillariophyceae) species, domoic acid and amnesic shellfish poisoning: revisiting previous paradigms. Phycologia, 51(2), 168–216. doi:10.2216/11-37.1
Methods

Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet.journal, 17(1), 10. doi:10.14806/ej.17.1.200
Software

Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., ... & Duchesnay, E. (2011). Scikit-learn: Machine learning in Python. the Journal of machine Learning research, 12, 2825-2830. https://www.jmlr.org/papers/volume12/pedregosa11a/pedregosa11a.pdf
Software

White, T. J., Bruns, T., Lee, S. J. W. T., & Taylor, J. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications, 18(1), 315-322. https://nature.berkeley.edu/brunslab/papers/white1990.pdf
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
ASV_sequence	DNA sequence of the amplicon sequence variants (ASVs)	unitless
AS301	presence (1) or absence (0) of the ASV in sample number AS301	unitless
AS302	presence (1) or absence (0) of the ASV in sample number AS302	unitless
AS303	presence (1) or absence (0) of the ASV in sample number AS303	unitless
AS304	presence (1) or absence (0) of the ASV in sample number AS304	unitless
AS305	presence (1) or absence (0) of the ASV in sample number AS305	unitless
AS306	presence (1) or absence (0) of the ASV in sample number AS306	unitless
AS307	presence (1) or absence (0) of the ASV in sample number AS307	unitless
AS308	presence (1) or absence (0) of the ASV in sample number AS308	unitless
AS309	presence (1) or absence (0) of the ASV in sample number AS309	unitless
AS310	presence (1) or absence (0) of the ASV in sample number AS310	unitless
AS311	presence (1) or absence (0) of the ASV in sample number AS311	unitless
AS312	presence (1) or absence (0) of the ASV in sample number AS312	unitless
AS313	presence (1) or absence (0) of the ASV in sample number AS313	unitless
AS314	presence (1) or absence (0) of the ASV in sample number AS314	unitless
AS315	presence (1) or absence (0) of the ASV in sample number AS315	unitless
AS316	presence (1) or absence (0) of the ASV in sample number AS316	unitless
AS317	presence (1) or absence (0) of the ASV in sample number AS317	unitless
AS318	presence (1) or absence (0) of the ASV in sample number AS318	unitless
AS319	presence (1) or absence (0) of the ASV in sample number AS319	unitless
AS320	presence (1) or absence (0) of the ASV in sample number AS320	unitless
AS321	presence (1) or absence (0) of the ASV in sample number AS321	unitless
AS322	presence (1) or absence (0) of the ASV in sample number AS322	unitless
AS323	presence (1) or absence (0) of the ASV in sample number AS323	unitless
AS324	presence (1) or absence (0) of the ASV in sample number AS324	unitless
AS325	presence (1) or absence (0) of the ASV in sample number AS325	unitless
AS326	presence (1) or absence (0) of the ASV in sample number AS326	unitless

AS327	presence (1) or absence (0) of the ASV in sample number AS327	unitless
AS328	presence (1) or absence (0) of the ASV in sample number AS328	unitless
AS329	presence (1) or absence (0) of the ASV in sample number AS329	unitless
AS330	presence (1) or absence (0) of the ASV in sample number AS330	unitless
AS331	presence (1) or absence (0) of the ASV in sample number AS331	unitless
AS332	presence (1) or absence (0) of the ASV in sample number AS332	unitless
AS333	presence (1) or absence (0) of the ASV in sample number AS333	unitless
AS334	presence (1) or absence (0) of the ASV in sample number AS334	unitless
AS335	presence (1) or absence (0) of the ASV in sample number AS335	unitless
AS336	presence (1) or absence (0) of the ASV in sample number AS336	unitless
AS337	presence (1) or absence (0) of the ASV in sample number AS337	unitless
AS338	presence (1) or absence (0) of the ASV in sample number AS338	unitless
AS339	presence (1) or absence (0) of the ASV in sample number AS339	unitless
AS340	presence (1) or absence (0) of the ASV in sample number AS340	unitless
AS341	presence (1) or absence (0) of the ASV in sample number AS341	unitless
AS342	presence (1) or absence (0) of the ASV in sample number AS342	unitless
AS343	presence (1) or absence (0) of the ASV in sample number AS343	unitless
AS344	presence (1) or absence (0) of the ASV in sample number AS344	unitless
AS345	presence (1) or absence (0) of the ASV in sample number AS345	unitless
AS346	presence (1) or absence (0) of the ASV in sample number AS346	unitless
AS347	presence (1) or absence (0) of the ASV in sample number AS347	unitless
AS348	presence (1) or absence (0) of the ASV in sample number AS348	unitless
AS349	presence (1) or absence (0) of the ASV in sample number AS349	unitless
AS350	presence (1) or absence (0) of the ASV in sample number AS350	unitless
AS351	presence (1) or absence (0) of the ASV in sample number AS351	unitless
AS352	presence (1) or absence (0) of the ASV in sample number AS352	unitless
AS353	presence (1) or absence (0) of the ASV in sample number AS353	unitless
AS354	presence (1) or absence (0) of the ASV in sample number AS354	unitless
AS355	presence (1) or absence (0) of the ASV in sample number AS355	unitless
AS356	presence (1) or absence (0) of the ASV in sample number AS356	unitless
AS357	presence (1) or absence (0) of the ASV in sample number AS357	unitless
AS358	presence (1) or absence (0) of the ASV in sample number AS358	unitless
AS359	presence (1) or absence (0) of the ASV in sample number AS359	unitless
AS360	presence (1) or absence (0) of the ASV in sample number AS360	unitless
AS361	presence (1) or absence (0) of the ASV in sample number AS361	unitless
AS362	presence (1) or absence (0) of the ASV in sample number AS362	unitless
AS363	presence (1) or absence (0) of the ASV in sample number AS363	unitless
AS364	presence (1) or absence (0) of the ASV in sample number AS364	unitless

AS365	presence (1) or absence (0) of the ASV in sample number AS365	unitless
AS366	presence (1) or absence (0) of the ASV in sample number AS366	unitless
AS367	presence (1) or absence (0) of the ASV in sample number AS367	unitless
AS368	presence (1) or absence (0) of the ASV in sample number AS368	unitless
AS369	presence (1) or absence (0) of the ASV in sample number AS369	unitless
AS370	presence (1) or absence (0) of the ASV in sample number AS370	unitless
AS371	presence (1) or absence (0) of the ASV in sample number AS371	unitless
AS372	presence (1) or absence (0) of the ASV in sample number AS372	unitless
AS373	presence (1) or absence (0) of the ASV in sample number AS373	unitless
AS374	presence (1) or absence (0) of the ASV in sample number AS374	unitless
AS375	presence (1) or absence (0) of the ASV in sample number AS375	unitless
AS376	presence (1) or absence (0) of the ASV in sample number AS376	unitless
AS377	presence (1) or absence (0) of the ASV in sample number AS377	unitless
AS378	presence (1) or absence (0) of the ASV in sample number AS378	unitless
AS379	presence (1) or absence (0) of the ASV in sample number AS379	unitless
AS380	presence (1) or absence (0) of the ASV in sample number AS380	unitless
AS381	presence (1) or absence (0) of the ASV in sample number AS381	unitless
AS382	presence (1) or absence (0) of the ASV in sample number AS382	unitless
AS383	presence (1) or absence (0) of the ASV in sample number AS383	unitless
AS384	presence (1) or absence (0) of the ASV in sample number AS384	unitless
AS385	presence (1) or absence (0) of the ASV in sample number AS385	unitless
AS386	presence (1) or absence (0) of the ASV in sample number AS386	unitless
AS387	presence (1) or absence (0) of the ASV in sample number AS387	unitless
AS388	presence (1) or absence (0) of the ASV in sample number AS388	unitless
AS389	presence (1) or absence (0) of the ASV in sample number AS389	unitless
AS390	presence (1) or absence (0) of the ASV in sample number AS390	unitless
AS391	presence (1) or absence (0) of the ASV in sample number AS391	unitless
AS392	presence (1) or absence (0) of the ASV in sample number AS392	unitless
AS393	presence (1) or absence (0) of the ASV in sample number AS393	unitless
AS394	presence (1) or absence (0) of the ASV in sample number AS394	unitless
AS395	presence (1) or absence (0) of the ASV in sample number AS395	unitless
AS396	presence (1) or absence (0) of the ASV in sample number AS396	unitless
AS397	presence (1) or absence (0) of the ASV in sample number AS397	unitless
AS398	presence (1) or absence (0) of the ASV in sample number AS398	unitless
AS399	presence (1) or absence (0) of the ASV in sample number AS399	unitless
AS400	presence (1) or absence (0) of the ASV in sample number AS400	unitless
AS401	presence (1) or absence (0) of the ASV in sample number AS401	unitless
AS402	presence (1) or absence (0) of the ASV in sample number AS402	unitless

AS403	presence (1) or absence (0) of the ASV in sample number AS403	unitless
AS404	presence (1) or absence (0) of the ASV in sample number AS404	unitless
AS405	presence (1) or absence (0) of the ASV in sample number AS405	unitless
AS406	presence (1) or absence (0) of the ASV in sample number AS406	unitless
AS407	presence (1) or absence (0) of the ASV in sample number AS407	unitless
AS408	presence (1) or absence (0) of the ASV in sample number AS408	unitless
AS409	presence (1) or absence (0) of the ASV in sample number AS409	unitless
AS410	presence (1) or absence (0) of the ASV in sample number AS410	unitless
AS411	presence (1) or absence (0) of the ASV in sample number AS411	unitless
AS412	presence (1) or absence (0) of the ASV in sample number AS412	unitless
AS413	presence (1) or absence (0) of the ASV in sample number AS413	unitless
AS414	presence (1) or absence (0) of the ASV in sample number AS414	unitless
AS415	presence (1) or absence (0) of the ASV in sample number AS415	unitless
AS416	presence (1) or absence (0) of the ASV in sample number AS416	unitless
AS417	presence (1) or absence (0) of the ASV in sample number AS417	unitless
AS418	presence (1) or absence (0) of the ASV in sample number AS418	unitless
AS419	presence (1) or absence (0) of the ASV in sample number AS419	unitless
AS420	presence (1) or absence (0) of the ASV in sample number AS420	unitless
AS421	presence (1) or absence (0) of the ASV in sample number AS421	unitless
AS422	presence (1) or absence (0) of the ASV in sample number AS422	unitless
AS423	presence (1) or absence (0) of the ASV in sample number AS423	unitless
AS425	presence (1) or absence (0) of the ASV in sample number AS425	unitless
AS426	presence (1) or absence (0) of the ASV in sample number AS426	unitless
AS427	presence (1) or absence (0) of the ASV in sample number AS427	unitless
AS428	presence (1) or absence (0) of the ASV in sample number AS428	unitless
AS429	presence (1) or absence (0) of the ASV in sample number AS429	unitless
AS430	presence (1) or absence (0) of the ASV in sample number AS430	unitless
AS431	presence (1) or absence (0) of the ASV in sample number AS431	unitless
AS432	presence (1) or absence (0) of the ASV in sample number AS432	unitless
AS433	presence (1) or absence (0) of the ASV in sample number AS433	unitless
AS434	presence (1) or absence (0) of the ASV in sample number AS434	unitless
AS435	presence (1) or absence (0) of the ASV in sample number AS435	unitless
AS436	presence (1) or absence (0) of the ASV in sample number AS436	unitless
AS437	presence (1) or absence (0) of the ASV in sample number AS437	unitless
AS438	presence (1) or absence (0) of the ASV in sample number AS438	unitless
AS439	presence (1) or absence (0) of the ASV in sample number AS439	unitless
AS440	presence (1) or absence (0) of the ASV in sample number AS440	unitless
AS441	presence (1) or absence (0) of the ASV in sample number AS441	unitless

AS442	presence (1) or absence (0) of the ASV in sample number AS442	unitless
AS443	presence (1) or absence (0) of the ASV in sample number AS443	unitless
AS444	presence (1) or absence (0) of the ASV in sample number AS444	unitless
AS445	presence (1) or absence (0) of the ASV in sample number AS445	unitless
AS446	presence (1) or absence (0) of the ASV in sample number AS446	unitless
AS447	presence (1) or absence (0) of the ASV in sample number AS447	unitless
AS448	presence (1) or absence (0) of the ASV in sample number AS448	unitless
AS449	presence (1) or absence (0) of the ASV in sample number AS449	unitless
AS450	presence (1) or absence (0) of the ASV in sample number AS450	unitless
AS451	presence (1) or absence (0) of the ASV in sample number AS451	unitless
AS452	presence (1) or absence (0) of the ASV in sample number AS452	unitless
AS453	presence (1) or absence (0) of the ASV in sample number AS453	unitless
AS454	presence (1) or absence (0) of the ASV in sample number AS454	unitless
AS455	presence (1) or absence (0) of the ASV in sample number AS455	unitless
AS456	presence (1) or absence (0) of the ASV in sample number AS456	unitless
AS457	presence (1) or absence (0) of the ASV in sample number AS457	unitless
AS458	presence (1) or absence (0) of the ASV in sample number AS458	unitless
AS459	presence (1) or absence (0) of the ASV in sample number AS459	unitless
AS460	presence (1) or absence (0) of the ASV in sample number AS460	unitless
AS461	presence (1) or absence (0) of the ASV in sample number AS461	unitless
AS462	presence (1) or absence (0) of the ASV in sample number AS462	unitless
AS463	presence (1) or absence (0) of the ASV in sample number AS463	unitless
AS464	presence (1) or absence (0) of the ASV in sample number AS464	unitless
AS465	presence (1) or absence (0) of the ASV in sample number AS465	unitless
AS466	presence (1) or absence (0) of the ASV in sample number AS466	unitless
AS467	presence (1) or absence (0) of the ASV in sample number AS467	unitless
AS468	presence (1) or absence (0) of the ASV in sample number AS468	unitless
AS469	presence (1) or absence (0) of the ASV in sample number AS469	unitless
AS470	presence (1) or absence (0) of the ASV in sample number AS470	unitless
AS471	presence (1) or absence (0) of the ASV in sample number AS471	unitless
AS472	presence (1) or absence (0) of the ASV in sample number AS472	unitless
AS473	presence (1) or absence (0) of the ASV in sample number AS473	unitless
AS474	presence (1) or absence (0) of the ASV in sample number AS474	unitless
AS475	presence (1) or absence (0) of the ASV in sample number AS475	unitless
AS476	presence (1) or absence (0) of the ASV in sample number AS476	unitless
AS477	presence (1) or absence (0) of the ASV in sample number AS477	unitless
AS478	presence (1) or absence (0) of the ASV in sample number AS478	unitless
AS479	presence (1) or absence (0) of the ASV in sample number AS479	unitless

AS480	presence (1) or absence (0) of the ASV in sample number AS480	unitless
AS481	presence (1) or absence (0) of the ASV in sample number AS481	unitless
AS482	presence (1) or absence (0) of the ASV in sample number AS482	unitless
AS483	presence (1) or absence (0) of the ASV in sample number AS483	unitless
AS484	presence (1) or absence (0) of the ASV in sample number AS484	unitless
AS485	presence (1) or absence (0) of the ASV in sample number AS485	unitless
AS486	presence (1) or absence (0) of the ASV in sample number AS486	unitless
AS487	presence (1) or absence (0) of the ASV in sample number AS487	unitless
AS488	presence (1) or absence (0) of the ASV in sample number AS488	unitless
AS489	presence (1) or absence (0) of the ASV in sample number AS489	unitless
AS493	presence (1) or absence (0) of the ASV in sample number AS493	unitless
AS494	presence (1) or absence (0) of the ASV in sample number AS494	unitless
AS495	presence (1) or absence (0) of the ASV in sample number AS495	unitless
AS496	presence (1) or absence (0) of the ASV in sample number AS496	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina MiSeq Next Generation Sequencing (University of Rhode Island Genomics and Sequencing Center)
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

[table of contents | back to top]

Deployments

EN608

Website	https://www.bco-dmo.org/deployment/848016
Platform	R/V Endeavor
Start Date	2018-01-31
End Date	2018-02-06
Description	C-AIM project

EN617

Website	https://www.bco-dmo.org/deployment/848018
Platform	R/V Endeavor
Start Date	2018-07-20
End Date	2018-07-25

EN627

Website	https://www.bco-dmo.org/deployment/848056
Platform	R/V Endeavor
Start Date	2019-02-01
End Date	2019-02-06

EN644

Website	https://www.bco-dmo.org/deployment/848020
Platform	R/V Endeavor
Start Date	2019-08-20
End Date	2019-08-25

[table of contents | back to top]

Project Information

RII Track-1: Rhode Island Consortium for Coastal Ecology Assessment, Innovation, and Modeling (C-AIM)

Coverage: Narragansett Bay, Rhode Island

NSF Award Abstract:

Non-technical Description
The University of Rhode Island (URI) will establish the Consortium for Coastal Ecology Assessment, Innovation, and Modeling (C-AIM) to coordinate research, education, and workforce development across Rhode Island (RI) in coastal marine science and ecology. C-AIM addresses fundamental research questions using observations, computational methods, and technology development applied to Narraganset Bay (NB), the largest estuary in New England and home to important ecosystem services including fisheries,

recreation, and tourism. The research will improve understanding of the microorganisms in NB, develop new models to predict pollution and harmful algal bloom events in NB, build new sensors for nutrients and pollutants, and provide data and tools for stakeholders in the state. Observational capabilities will be coordinated in an open platform for researchers across RI; it will provide real-time physical, chemical, and biological observations ? including live streaming to mobile devices. C-AIM will also establish the RI STEAM (STEM + Art) Imaging Consortium to foster collaboration between artists, designers, engineers, and scientists. Research internships will be offered to undergraduate students throughout the state and seed funding for research projects will be competitively awarded to Primarily Undergraduate Institution partners.

Technical Description
C-AIM will employ observations and modeling to assess interactions between organisms and ecosystem function in NB and investigate ecological responses to environmental events, such as hypoxia and algal blooms. Observations of the circulation, biogeochemistry, and ecosystem will be made using existing and new instrument platforms. The Bay Observatory ? a network of observational platforms around NB - will be networked to trigger enhanced water sampling and sensing during specific environmental events, such as hypoxic conditions or phytoplankton blooms. Biogeochemical, ecological, and coastal circulation models will be integrated and coupled to focus on eutrophication and pollutant loading. Data and models will be integrated on multiple scales, from individual organisms and trophic interactions to food-web responses, and from turbulence to the regional ocean circulation. New sensing technologies for nutrients and pollutants will be developed, including affordable, micro-fluidic (Lab-on-a-Chip) devices with antifouling capabilities. The results will be synthesized and communicated to stakeholders.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1655686
NSF Division of Ocean Sciences (NSF OCE)	OIA-1655221
National Oceanic and Atmospheric Administration (NOAA)	NA18OAR4170094
National Oceanic and Atmospheric Administration (NOAA)	NA14OAR4170082

[table of contents | back to top]