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Abstracts

RI C-AIM and University of Rhode Island graduate student Teresa Mako instructs undergraduates at Bryant University how to create simple, paper-based sensors.

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Carbon Black Templated Gold Nanoparticles for Nitrate Capture and Detection by Surface Enhanced Raman Spectroscopy

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Surface-enhanced Raman scattering (SERS) spectroscopy is an ultra-sensitive spectroscopic technique carried out on nanostructured plasmonic materials such as gold nanoparticles. Upon excitation with the appropriate light, the nanoparticles intensify the electric field that couples with the vibrational modes of the molecule under study, increasing its characteristic Raman signals and making possible its ultrasensitive or even single-molecule detection.

We used this analytical technique for fast and reliable detection of nitrate, which in excess amount in water bodies can cause large increases in aquatic plant growth, leading to local hypoxia that negatively affects aquatic life.

A good SERS substrate is the essential prerequisite for reliable SERS measurements with high detection limits. We describe a simple strategy to grow gold with multiple hot spots on carbon black nanoparticles as highly effective SERS substrates for the detection of a wide range of analytes in aqueous solution. We show that this gold-carbon hybrid nanoparticle can improve the affinity of different analytes including nitrate to the surface of SERS substrate and produce strong signals.

Life at the Edge: Trait Variability at the Thermal Limits Can Drive Diatom Community Dynamics

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Organismal distributions are largely mediated by temperature, suggesting thermal trait variability plays a key role in defining species' niches. We employed a trait–based approach to better understand how interspecific thermal trait variability could explain and characterize diatom community dynamics. A culture library was generated consisting of 23 strains from 5 diatom species in the genus *Skeletonema*, isolated from Narragansett Bay (NB), RI, USA, where this genus can comprise up to 99 percent of microplankton. Growth rates were determined at temperatures ranging from -2 to 36°C to construct strain-specific thermal reaction norms. Comparison of performance curves revealed interspecific overlap at the thermal optima and significant divergence at the thermal limits. Cellular elemental composition was then examined in two thermally differentiated species and the most variation was again exhibited at the thermal limits.

To determine the potential impact of interspecific trait variation on community composition, a species succession model was formulated utilizing parameters from each species' empirically-determined reaction norm and historical temperature data from NB. Seasonal succession patterns in our modeled diatom community paralleled those observed in the field, indicating that thermal limits of growth are important determinants of diatom community dynamics and, ultimately, carbon flux and nutrient cycling through marine ecosystems. Here, characterization of thermal limits rather than thermal optima were the best predictors of community composition patterns, suggesting that thermal limit analysis be incorporated into both empirical and modeling efforts in the future.

The Rhode Island Consortium for Nanoscience and Nanotechnology: An Advanced Nanomaterial Characterization Center

Irene Andreu

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The Rhode Island Consortium for Nanoscience and Nanotechnology (RIN2) is a multi-user materials characterization facility that enables cutting-edge academic and industrial research and education through access to advanced material characterization equipment. It is the only materials characterization center in Rhode Island offering cryogenic scanning and transmission electron microscopy.

Specific objectives of RIN2 are:

- Offer advanced materials characterization to users at URI, other academic institutions, non-profits and industries
- Provide theoretical and hands-on training on these tools and related processes to the next generation of researchers at the pre-college, undergraduate, graduate and post-graduate level
- Connect researchers from different disciplines and foster collaboration to solve grand challenges

The instruments available at RIN2 are:

- Transmission electron microscope (TEM) with cryogenic and elemental analysis capabilities: JEOL JEM-2100 equipped with a Gatan cryotransfer holder and Oxford Instruments energy dispersive X-ray spectrometer (EDS)
- Scanning electron microscope (SEM) with cryogenic and elemental analysis capabilities: Zeiss Sigma-VP field emission SEM equipped with variable pressure, secondary electron, in-lens and backscattering detectors, a Gatan Alto cryogenic preparation and loading module, and Oxford Instruments energy dispersive X-ray spectrometer (EDS)
- X-ray diffraction (XRD): Rigaku Ultima IV X-ray diffractometer
- Confocal Raman microscope (CRM): WITec alpha 300 R equipped with motorized XYZ stage for large area acquisition, two excitation laser wavelengths (785 and 532 nm) and 10x to 100x objectives
- High-content screening system (HCS): Perkin Elmer Opera Phenix high-throughput confocal fluorescence microscope

This facility is supported by NSF EPSCoR #OIA-1655221. Contact Irene Andreu at iandreu@uri.edu and check out our website (https://web.uri.edu/nano/) for information on these characterization instruments.

Rhode Island Genomics and Sequencing Center

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The Rhode Island Genomics and Sequencing Center (RIGSC) was established to provide technical and analytical support for molecular biology and genomics research at the University of Rhode Island and all RI-EPSCoR institutions. The mission of the RIGSC is to facilitate interdisciplinary genomics research and undergraduate and graduate student training opportunities by providing researchers access to cutting-edge technologies in the field of genomics. The RIGSC offers services in robotic sample preparation, DNA sequencing (Sanger and Next Generation), fragment analysis and quantitative-PCR. We also provide imaging services using transmitted light, epifluorescence, and laser scanning confocal microscopy.

The RIGSC is available to students, staff, and faculty at URI, as well as RI-EPSCoR researchers. Detailed information on sample preparation, submission instructions, equipment use and any fees is available on our website at web.uri.edu/gsc/.

Preferences for Residential vs. Community Solar Programs in Rhode Island

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Innovation in energy technologies is necessary due to the growing impacts of climate change, especially for a coastal state such as Rhode Island. Household adoption of solar energy is an important piece of the transition from our fossil-fuel dominant energy system toward a more sustainable energy future, driving long-term growth of the state economy. Rhode Island has implemented a variety of statewide policies and incentives aimed at increasing the use of alternative energy at the household level by decreasing costs through grants and tax-incentives (DSIRE, 2018). More recently, they have designed the Community Renewables Program to promote solar adoption among low-to-moderate income (LMI) households, renters, and others who cannot install solar on their properties (Commerce RI, 2018).

By surveying Rhode Island residents, we will (1) examine the general drivers of household willingness and intention to switch to solar including demographic factors, environmental concern, novelty seeking, social and personal norms, and trust in the solar industry, (2) specifically examine what factors differ in leading residents to prefer installing solar panels at their home vs. subscribing to a community solar project, (3) examine how personal experience of climate change and land use preferences impact their decision-making.

Findings from this study will offer insights into whether policies supporting community solar would likely expand solar adoption in Rhode Island and which segments of the population would most benefit. Excerpts from ongoing research, including survey-sampling strategies from the representative town of North Providence and survey questionnaire, will be presented.

Towards the Development of a Low-Cost and Easily-Deployable Sensing Platform for Phosphate and Nitrate

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We will present results from our initial experiments leading to the development of a low-cost and easily- deployable sensing platform for phosphate and nitrate. The phosphate sensor is based on carboxylic acid functionalized carbon nanodots complexed with europium (III) ions.[1] Upon excitation at 370 nm, the native carbon nanodot fluorescence at 500 nm and quenched by the complexation with the europium (II) ions is restored upon interaction with phosphate ($H_2PO_4{}^-$ or $HPO_4{}^{2-}$). The nitrate sensor is based on a potential sensitive dye, diA [4-(4-dihexadecylaminostyryl)-N-methylpyridinium iodide], incorporated with a nitrate ionophore and a plasticizer in a PVC membrane.[2]

The diffusion of nitrate into the membrane results in changes in the local environment of the dye and an increase in fluorescence at 560 nm (λ_{ex} = 460 nm). At present, our LOD's for both phosphate and nitrate are 10^{-5} M (≈1ppm) and we are working to (i) improve sensitivity, (ii) alter the chemical composition to realize a common excitation wavelength, and (iii) fabricate paper-based devices.

[1] H X. Zhao, L. Q. Liu, Z. D. Liu, Y. Wang, X. J. Zhao, and C. Z. Huang. *Chem Comm*. 47, 2604-2606, 2011.

[2] G. Kim, K. A. Sudduth, S. A. Grant and N. R. Kitchen. *J. Biosystems Eng*, 37, 209-213, 2012.

Nanostructured Electrochemical Sensor for Detection of Seawater Nutrients

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Nitrite salts are widely used in industrial manufacturing process and can have detrimental effects to both human health and aquatic life. For example, nitrites can cause the transformation of normal hemoglobin to methemoglobin, leading to loss of hemoglobin's ability to transport oxygen. There is an unmet need for portable, reliable and economical sensor for nitrites due to its ubiquitous nature and toxicity.

Herein, we demonstrate the use of multi-wall carbon nanotubes screen printed electrodes (MWCNT-SPE) that have the capability for individual determination of nitrite anions at micromolar concentrations in aqueous solutions. Using cyclic voltammetry, the MWCNT-SPE displayed activity in the oxidation of nitrite ions at pH = 3.00 with increase in anodic peaks at 0.8 V vs. Ag/AgCl in vast concentrations with a linear range from 10mM to 400mM.

Microfluidic sample delivery systems coupled to amperometric detection are currently being explored to further lower the detection limits. This approach was used to measure nitrites in seawater samples. The disposable MWCNT-SPE offers a low cost, portable and economic approach for nitrite detection in sea water samples.

Microfluidic Paper-Based Devices for the Detection of Nitrate and Nitrite

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Interest in microfluidic paper-based devices for environmental monitoring and analysis has increased over the past several years due to the many advantages that these devices exhibit as compared to conventional analytical methods in use. Microfluidic paper-based devices allow for low-cost, easy-to-use, rapid and in-field detection of nutrients in water that would increase the frequency and geographic coverage of such environmental monitoring.

Of the several different nutrients of interest, detection of nitrate and nitrite has garnered much attention due to human health concerns and environmental problems resulting from the availability of excess amounts of these nutrients in water. Microfluidic paper-based devices make use of capillarity to flow fluids through paper without the need of a pump. This allows for a self-contained device that doesn't require any power source to operate. We present microfluidic paper-based devices that we are currently working on developing for the detection of nitrate and nitrite in the parts per billion range.

Advancements in Automated Nitrogen Detection via Surface Enhanced Raman Spectroscopy and Wavelet Transform Background Subtraction

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Nitrates and phosphates are vital macronutrients for plants and animals, and their levels in seawater provide important information when assessing the coastal ecosystem. At the moment, nitrate and phosphate levels are being measured, but their analyses are outdated. A self-sustaining sensor with a high sensitivity and selectivity for nitrate and phosphate would be beneficial. Surface Enhanced Raman Spectroscopy (SERS) is a well-known spectroscopic technique that utilizes surface roughened substrates to provide Raman enhancement to help detect analytes at a single molecule level. Due to its high sensitivity, SERS is a promising candidate for a nitrate or phosphate sensor when combined with a selective filter.

Our work has shown the advancements SERS coupled with selective chemical reactions to nitrate can make in the field of nitrate detection, along with a background subtraction method to be used for real time analysis.

GSO Dock Phytoplankton and Optics Observatory

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Continuous flow-through observations began at the University of Rhode Island, Graduate School of Oceanography's (GSO) dock in November 2017 and continue through today. Data include temperature, salinity, absorption, scattering and fluorescence, along with phytoplankton identification and enumeration for cells within 10-150 μm via an Imaging Flow CytoBot (IFCB). Real-time IFCB imagery is available at http://phyto-optics.gso.uri.edu:8888.

Flow-through observations are supported by weekly laboratory measurements of chlorophyll-a concentration as well as particulate, phytoplankton, and CDOM absorption at 550 wavelengths. A sample valve has been installed to easily obtain the same water passing through the system for collaborative work. Our efforts have focused on developing a robust classifier of phytoplankton species observed by the IFCB by manually classifying over 13,000 individual phytoplankton images into 60 classes.

These data are used as a training set for a Random Forest classification algorithm that shows >90 percent accuracy for most classes. We present a discussion of classifier strengths and limitations along with strategies for improvement. We will also show results from the classified dataset illuminating species succession and changes in phytoplankton size distribution in Narragansett Bay over the time series. Combined with the optical measurements, these observations will be used for the development of satellite remote sensing algorithms for detecting phytoplankton composition. They are also helpful for harmful algal bloom monitoring, light availability, turbidity, CDOM variability, and real-time "view" of water column conditions.

Investigation into the Microbiome of the Little Skate, *Leucoraja erinacea*, and its Intersection with Toxicity Metabolism of the Host

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Microbes that inhabit the intestines of host animals have significant effects on physiology, development, and signaling systems of the host, including those aspects involved in processing environmental toxins. The core microbiome of the little skate, *Leucoraja erinacea*, a cartilaginous fish related to sharks and rays and a model for effects of pollutants on marine animals, was characterized by sequencing the spiral valve intestine. Samples were prepared from 11 skates captured in environments that include a polluted test site and control site in New Haven Harbor and from animals held in a lab setting with water from Narragansett Bay. 16s rRNA amplicons were generated from DNA in microbial communities. Primers followed the Earth Microbiome Project protocol (515F/806R). Greengenes database mining was used in the QIIME pipeline to identify 16s rRNA gene homologs.

Proteobacteria, Firmicutes, Bacteroidetes and Actinobacteria were the most prevalent genera; the control sample had the greatest diversity at the genus level, and the polluted sample the least, dominated by Proteobacteria. The bioinformatics software package PICRUSt and the KEGG database were employed to predict metabolic activity of the samples, with focus on environmental toxins. Bray-Curtis and UniFrac analysis in QIIME showed similar community content in the individual animals from the laboratory-setting environment, though an individual from a polluted site clustered near to both. Clustered samples had similar numbers of PICRUSt-predicted functional sequences.

While a greater range of individual samples is needed to assess differences between skate gut microbiomes with respect to environment, the similarity in top genera for each sample demonstrated the first representation of a core microbiome for the little skate.

Data Platforms and WebVR: Representations of the Buoy Experience

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WebVR is an experimental JavaScript application programming interface that allows internet browsers to render a three-dimensional scene without the use of any additional plug-ins. Visualizing data from an oceanographic research buoy in WebVR allows us to include the buoy in the representation. The goal is to create an online portal for information that reveals the sensing apparatus - in this case, an RI C-AIM buoy in Narragansett Bay - that is typically hidden or ignored in traditional visualizations of data.

The final project will be a WebVR representation of the buoy in its environment. Users will be able to manipulate 3D models of the buoys and learn more about the various technical components and their scientific applications. Users can also visualize what the buoy is sensing by querying the most recent data from the buoy hosted on the RI Data Discovery Center website. The data that is retrieved will be used to generate animations of the buoy “experience.”

Distribution, Diversity, and Drivers of Human Activities in and around Narragansett Bay

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To explore C-AIM Objective 2.4.2 on how human activity is influenced by the structure and function of coastal resources, an intercept survey of Narragansett Bay users was employed from June-August 2018. Data were collected from 580 users across 19 coastal sites (beaches, public parks, and coastal access points) in Rhode Island to improve understanding of human uses and attitudinal factors related to Narragansett Bay resources.

This study is exploring the distribution and diversity of human activities along the Bay and factors driving patterns of use by asking users how they interacted with a site (i.e. activities, frequency of visits, and travel information), their perceptions of site conditions (i.e. water quality, amenities and features, and connectedness to the site), and personal characteristics (i.e. income, gender, age, and race/ethnicity). Preliminary results indicate that user engagement, site conditions, and user characteristics vary across sites. Data collected from this project will be compared with water quality and ecological indicators to investigate how changes to the coastal environment impact human activities.

These results will provide insight on how people interact with the coastal environment and explore potential inequalities in resource use and access.

Understanding Mechanisms of Temperature Adaptation Through Genome-scale Modeling and Transcriptomics

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The adaptation of marine microbes to diverse temperature conditions plays an important role in niche selection and could influence the composition and functional diversity of microbial communities. However, significant knowledge gaps remain in the potential mechanisms underlying the metabolic changes induced by temperature variations. Here, integrating genome-scale modeling with transcriptomics, we investigate the metabolic and functional variations of the deep-sea bacteria *Shewanella psychrophila* WP2 under different temperature regimes. Through the incorporation of temperature, reaction thermodynamics, and metabolite concentrations into the modeling of metabolic flux, our model revealed significant variability within the pathways of amino acids metabolism, nucleotide metabolism, and some parts of co-factor biosynthesis, under non-optimal temperatures.

The model-based prediction was overall corroborated with transcriptome samples taken from the early, mid, and late exponential phases for WP2 cultivated under the optimal (15°C), low (4°C), and high temperature (20°C) conditions. Specifically, the increased expression of various amino acid metabolism genes shows a potential role for this pathway in responding to changes in reactive oxygen stress and membrane fluidity. This study provides an example for future studies of key microbes in the Narragansett Bay. With future accumulation of GEMs for various cultivated organisms and environmental microbiomes, we will explore the metabolic dynamics and evolution of diverse microbial communities under changing temperature.

Decreased Zooplankton in Narragansett Bay, RI (USA)

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The historically dominant copepod *Acartia spp.* was less abundant during the sampling period when compared to previous years. Weekly zooplankton samples were collected between February 19, 2018 and March 18, 2019 at Station 2 in Narragansett Bay in concurrence with the Long-Term Plankton Time Series. The sampling scheme involved 5-meter vertical tows using a 64-micron mesh net attached to a 30-centimeter diameter ring. Total zooplankton abundance and species composition were determined for the entire sampling period, and dry-weight calculations were preformed between May 28, 2018 and March 18, 2019. Total zooplankton numbers and copepods in the current year were greater than 50 percent less than in 2002 to 2004. The maximum *Acartia* adult and copepodite abundance was 57,918/m3 on April 30, 2018 compared to 30,957.22/m3 on May 1, 2002, 26,185.63/m3 on April 4, 2003 and 62,118.13/m3 on June 4, 2004. Average summer zooplankton biomass was 113.9845g/m3 in 2018.

A relationship between barnacle larvae and the winter-spring bloom can be discerned for both the earlier years and the current year. Overall numbers of barnacle larvae had not changed during the sample years. A correspondence analysis will be done to determine the relationship between the seasonal evolution of zooplankton and environmental drivers.

Patterns of Phytoplankton Community Composition within Narragansett Bay

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Diatoms are important phytoplankton in the marine environment, contributing 40-50 percent of primary production. The diversity and distribution of diatom communities is important for understanding the ecosystem in Narragansett Bay (NBay). Traditional methods for quantifying species diversity can be difficult. We are using a combination of microscopy and high- throughput sequencing (HTS) to determine seasonal patterns of phytoplankton within NBay, using six years of weekly water column samples obtained from the NBay Plankton Time Series.

Our initial focus was on the diversity within the abundant diatom genus *Thalassiosira*. HTS revealed the presence of seven small and abundant species of *Thalassiosira* that had not been previously identified in the count data from the NBay Plankton Time Series. For example, *Thalassiosira pseudonana* has not been observed using microscopy since 1999, but the frequent occurrence of this species in the HTS results suggests that it could be an important contributor to phytoplankton communities than previously recognized. We are now expanding our investigation to assess species diversity across all diatoms during the six-year sampling period (2008-2014).

By combining HTS with microscopy, we aim to examine diatom diversity within NBay to elucidate seasonal, annual and inter-annual patterns of community composition. In addition, diversity data will be correlated with various environmental factors (eg. nutrients and temperature) to investigate how community patterns may shift over time due to changing environmental conditions.

Distribution of Neuronal Proteins in Two North Atlantic Cnidarians

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Our C-AIM project aims to use advanced microscopy and imaging techniques to investigate the marine life of Narragansett Bay. Here, we use flash photography, confocal florescent light microscopy, and transmission electron microscopy to investigate the anatomy and nervous systems of two Cnidarian species from the Bay. Antibodies against neuronal proteins including the synaptic vesicle marker SV2, the post synaptic protein PSD95, and the Alzheimer's protein APP as well as the DNA marker DAPI help to define the location and distribution of neurons in these species.

Here, in preliminary findings, we visualize nerve terminals with yet undefined roles within these organisms. The positive antibody staining demonstrates that these neuronal proteins are conserved in species from Cnidarians to humans. Further work is need to understand how these neurons act in a coordinated fashion to control feeding, swimming, and other behaviors of these life forms.

Sugar Sensing by Native and Chemically Modified Silicon Nitride Nanopores

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Sugars are unavoidable in daily life, from the surface of our cells to the suggested masses displayed on the nutritional information labels of our food. The chemical structures of isolated polysaccharides are often highly varied and require complex and expensive analytical instrumentation to decipher. Because of this, it is desirable to develop more affordable devices that can still quickly and reliably reveal this information. Solid state nanopores are starting to demonstrate their potential to make this a reality. Further development of these devices could lead to advances in sensing capabilities for applications in glycomics.

In this work, nanopores are fabricated on thin film silicon nitride (SiNx) membranes by dielectric breakdown. In short, two wells containing an electrolyte solution with a voltage potential between them are isolated by an individual membrane, eventually resulting in a single pore with nanometer dimensions. Once formed, the conditions of the electrolyte solution are tuned to alter the chemical conditions on the surface of the pore and the analyte of interest to produce ideal parameters for translocation under an applied electric field. Achieving better selectivity and sensitivity to specific species is accomplished by surface chemical modification leading to unique and novel sensing abilities.

Robust methods of chemical functionalization have been developed for extensive customizability of the nanopore surface. These devices are currently being used to analyze polysaccharides, peptides, carboxylic acid capped gold nanoparticles, and the interactions between them.

Buoy Data Viewer: Search and Display Historical Narragansett Bay Buoy Data Using RI C-AIM's Buoy Data Viewer

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One goal of the Rhode Island Data Discovery Center is to be a central resource for sharing, searching and displaying historical environmental data related to Narragansett Bay, in particular time series data throughout the Bay.

We have identified numerous collections of historic data, many of which are well organized and well maintained by multiple scientists and groups in the state. The collections, however, are stored in different locations and/or in varying formats, making it time-consuming for students/researchers who are searching for specific data to quickly and easily find what they need.

We are working to address this situation by making any multi-site, time series data relevant to the Narragansett Bay ecosystem, available through the RI Data Discovery Center's website (http://ridatadiscoverycenter.org/index.html). In addition to making the search for a historical data set easier, we also offer additional features such as making online graphs, exporting data in various formats, etc.

For the past few months, we have collaborated with Rhode Island Department of Environmental Management's Office of Water Resources (RI DEM-OWR), the lead agency for the Narragansett Bay Fixed-Site Monitoring Network (NBFSMN), to incorporate the network's data into our database. We have successfully harvested quality-controlled, physical water quality time series data (2003,2005-2012) from the NBFSMN website (http://www.dem.ri.gov/programs/emergencyresponse/bart/stations.php) into our online database called the **Buoy Data Viewer**.

The network's dataset with multiple points throughout the Bay has high value to the modeling community. NBFSMN data is also valuable to many other investigators because it can provide a rich context upon which other types of data can be overlaid, such as a time series of DNA sequences of marine species.

The **Buoy Data Viewer** can be used to quickly display multiple parameters from multiple NBFSMN buoys for a given date range as graph or export graph/data (additional formats under construction).

Towards Continuous *in situ* Sensing of Marine Pollutants Using Surface Enhanced Raman Spectroscopy (SERS)

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Excess concentrations of nitrate and phosphate in seawater can lead to harmful algae blooms that damage coastal ecosystems, pose health risks and adversely impact commercial activity. Early *in situ* detection of over-nutrification is necessary for rapid response and mitigation plans.

Commercial nitrate and phosphate sensors utilize UV-Vis spectroscopy and are generally incapable of detecting at limits set by the U.S. Environmental Protection Agency (EPA), necessitating new approaches for *in situ* monitoring. Surface enhanced Raman spectroscopy (SERS) is a technique theoretically capable of single molecule detection, and therefore may be a promising approach for nitrate and phosphate detection. However, there are clear challenges as SERS sensing is negatively affected by interference in complex media and in situ sensing in a solution phase reduces accuracy and resolution. It is because of these challenges, in part, why much of the data reported in the literature are taken for purified samples that are then dried on a SERS substrate.

Our goal is to address the engineering challenges for a SERS *in situ* seawater nutrient concentration measurement system. Batch and flow-through devices have been designed to incorporate commercially available, nanostructured gold SERS substrates. By benchmarking against 4-nitrobenzenethiol/ethanol solutions, our results show that SERS devices can be used as a development platform for a seawater nutrient sensor. They also depict the challenges associated with complex media and provide insight into surface modification strategies needed to selectively detect nitrate and phosphate.

Isolation and Characterization of Marine Microorganisms in Narragansett Bay

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The marine hydrosphere covers over two-thirds of the planet, however only 0.1 percent of marine microorganisms have been successfully cultivated within a lab. With the vast majority of microorganisms remaining uncultivable, the ocean contains untapped potential for new antibiotics, enzymes, and compounds from these microorganisms. In order to combat this great plate anomaly, novel techniques have emerged to more closely simulate growth conditions experienced by these microorganisms in their natural habitat.

The goal of this study was to identify sampling and isolation conditions conducive to the *in situ* growth of marine microorganisms from Narragansett Bay. Raw seawater was collected from facilities at Roger Williams University and the University of Rhode Island Bay Campus. Microbes were collected by water filtration over a 0.2μm pore size filter or centrifugation, then plated on oligotrophic media (Actinomycete isolation agar and R2A agar) under aerobic and anaerobic growth conditions.

Filtration produced a greater abundance and diversity of colonies than centrifugation of the equivalent volume of water. In comparing media, Actinomycete isolation agar was found to recover a greater diversity of colonies than R2A agar, as assessed by colony morphology. Fifteen isolates were prepared for polymerase chain reaction (PCR) amplification of the 16S rRNA and ITS regions for identification of bacteria and fungi respectively. The purified PCR products were Sanger sequenced and isolates were identified to the genus level using nucleotide BLAST. Future research will focus on further subculturing to isolate additional colonies as well as comparing aerobic and anaerobic growth.

In summary, through the use of filtration and centrifugation of seawater samples and cultivation on low-nutrient media, bacterial and fungal isolates from Narragansett Bay were cultured and characterized. This research will help to establish protocols for the cultivation of microorganisms that will enable monitoring of changes in marine ecosystems geographically, seasonally, and in response to climate change.

Bio-Reporter to Sense Nitrate in Narragansett Bay

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The concentrations of nitrate (NO^{3-}) and phosphate (PO_4^{3-}) in Narragansett Bay have been shown to undergo considerable temporal and spatial variation. However, the dynamics of these fluxes have never been monitored on a fine-scale (<100 m, < 1 day) or in real-time. Continuous monitoring of estuarine systems, such as Narragansett Bay, remains in its infancy and requires a new and innovative approach to analysis. Additionally, bioavailable nutrients often constitute only a small fraction of the chemically measured element (in some cases only about 1%).

Whole-cell bio-reporters are promising candidates for low cost, continuous environmental sensing of bioavailable nutrients. In this poster, the creation and validation of a sensor using a self-bioluminescent strain of the cyanobacteria *Synechococcus elongatus pcc* 7942 for the direct measurement of bioavailable nitrate will be described. For this analysis bio-reporters were constructed by fusing the promoters of glnA to the luxAB operon. This allowed for the measurement of nitrate bioavailability through the measurement of light emission. Studies confirmed gene sequence as well as transformation into *Synechococcus elongatus*. Validations of bio-reporter specificity, sensitivity and longevity are reported for both known nitrate standards and estuarine water. Proposed sensor designs are also presented with a specific focus on storage, longevity and cell viability.

The specificity, sensitivity, and low cost of these bio-sensors make them ideal candidates for continuous monitoring of biological nitrates in estuaries such as Narragansett Bay.

Effect of Temperature on Muscle Mechanics and Metabolism in Fish Species of Narragansett Bay

Anabela Maia, Amina Chamanlal, Megan Hatcher & Nicholas Saygeh

Biology, Rhode Island College, Providence, RI

The effects of climate change are particularly strong in estuarine habitats where animals are already exposed to a variety of stressors, including other anthropogenic pressures and changes in salinity.

Summer temperatures in Narragansett Bay have seen a steady increase in the last decades, with even more pronounced temperature increases over winter months. Most fish are not able to regulate their body temperature, and their metabolism is likely to be strongly affected by temperature fluctuations. In general, higher temperatures accelerate biological processes and can lead to faster growth, however they can also induce stress and leave less energy available for maintenance, immune response and reproduction. Temperature optima vary widely between different species and increases in temperature are likely to change the fish composition of Narragansett Bay. We are already seeing changes in population dynamics of black sea bass and scup, which have been increasing in abundance. Species like summer flounder and little skate have been identified as more likely to be negatively impacted, while the effects of warming temperatures in spiny and smooth dogfish populations are complex.

We aim to understand how the metabolic demands of these six species change under different temperatures by measuring basal and standard metabolic rates, that is the oxygen consumed during both rest and normal swimming activity. Swimming for fish is a costly activity and is powered by body undulations and fin musculature. We will also look at muscle contraction through electromyography to determine changes in muscle recruitment that are likely affecting overall metabolism. Preliminary muscle physiology data from summer flounder and spiny dogfish show shifts in muscle properties with increased temperatures.

The next step would be to look at the remainder of the species and to determine oxygen demands of swimming for the six species under different temperatures.

C-AIM Career Development Program: Preparing Graduate Students and Post-Docs for Career Success

Sunshine Menezes[1], Katharine McDuffie[1], Julia Rei[2] & Jordanne Feldman[3]

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[3]Geology, University of Rhode Island, Kingston, RI

Most PhD graduates pursue careers outside of academia. While these graduates bring important skills to their jobs, such as the ability to analyze problems and critical thinking, employers have noted the absence of some essential professional skills such as team management, effective communication with diverse audiences, effective mentorship, and time management. Indeed, these skills are valuable for graduate students and post-doctoral fellows whether they pursue academic *or* non-academic careers. There are few opportunities for early career researchers to gain many of these skills, however.

RI C-AIM will address this gap through the creation of a new Career Development Program, led by the University of Rhode Island's Metcalf Institute in collaboration with C-AIM partner institutions. The Career Development Program (CDP) will provide a suite of training programs and learning experiences designed to build career readiness among C-AIM participants. The CDP's primary audience will be graduate students and post-docs, but C-AIM faculty and staff, as well as advanced undergraduates from all eight C-AIM partner institutions, also will be able to participate in CDP programs.

Participants can opt to pursue a Certificate in Career Development by attending specific required programs and additional electives. The certificate requirements are intended to address topics and skills that are generally absent from formal degree programs but are increasingly necessary for professional success in STEM fields. An online opportunities catalog will list existing career development opportunities at all C-AIM partner institutions as well as new offerings developed by Metcalf Institute. Participants may attend programs from the catalog for points toward CDP certification.

Metcalf Institute will conduct programmatic and longitudinal surveys to assess the effectiveness and outcomes of the CDP. This program will amplify C-AIM's workforce development efforts while building new collaborations between C- AIM partner institutions. Most importantly, the CDP will prepare C-AIM participants for successful careers.

A DNA Barcode and Photographic Library of the Organisms of Narragansett Bay

Mollie Mikulski, Catherine Keable, John Petrick, Alex Rosado, Laura Landen, Christopher Deacutis & Joseph DeGiorgis

Biology, Providence College, Providence, RI

As part of the C-AIM mission, we have begun to develop a photographic library and a DNA barcode for each species that lives in Narragansett Bay. To this end, we have collected organisms through a variety of techniques, including trawler tows, dip netting, plankton tows, piling scraping, and hook and line fishing. We have also obtained samples previously collected or cultured by many other C-AIM participants.

Each species is photographed in their native environment or in the laboratory/studio setting using a wide variety of techniques from flash photography to electron microscopy. Genomic DNA samples are obtained for each species and used for PCR and sequence analysis. To date, we have more than 60 species in total. We have begun to develop a website (http://www.speciesofnb.com/) to disseminate the data we collect.

This spring and summer we hope to add 100 species to our database in collaboration with other C-AIM investigators.

Constraining Biological Rates Governing the Western North Atlantic Annual Cycle in Phytoplankton Biomass

Françoise Morison[1], Gayantonia Franzè[1], Jason Graff[2], Elizabeth Harvey[3] &
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Interactions between phytoplankton and their grazers have been hypothesized to be a major ecological factor governing dynamics of phytoplankton biomass accumulation over the annual cycle, including when the North Atlantic spring bloom initiates (Behrenfeld & Boss 2014). A major goal of the North Atlantic Aerosols and Marine Ecosystems Study (NAAMES) was to define environmental and ecological controls on plankton communities, to build a predictive understanding of the structure and function of plankton systems.

During the four NAAMES field campaigns conducted in November 2015, May 2016, September 2017, and March 2018 in the Western North Atlantic (38-48 W, 40-55 N), we measured phytoplankton growth and grazer/virus-induced mortality rates in a total of 193 two-point dilution experiments. Concurrent measurements of physical, chemical, and biological properties provided an environmental context for the rate measurements. Some stations sampled at different seasons overlapped in their physical and chemical properties, reflecting the latitudinal extent and the mesoscale physical complexity of the study region. Seasonal and geographical variability in grazing impact on primary production remains to be investigated; yet phytoplankton biomass accumulation rates were overall generally positive, implying a prolonged growth period and a relatively shorter period of net biomass loss.

Consequently, seasonal biogeochemical fluxes and the transfer of matter and energy through the western North Atlantic food web may be processes that are sustained over the yearly cycle, rather than defined by short bloom events.

Systematic Differences Between Eulerian and Surface Drifter Statistics in the Gulf of Mexico

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Lagrangian instruments are frequently deployed throughout the global ocean to estimate regional oceanic statistics. Previous work paired with observations suggests that drifters tend to collect in convergent regions. This prevents drifters from sampling the entire velocity field, and may lead to biased statistics. Modeling work has confirmed that structure functions calculated with synthetic surface drifters are systematically different from Eulerian counterparts at scale separations below 10km in the Gulf of Mexico.

In this study, we use a series of surface drifter launches as well as X-Band radar in a comparable location to the modeling study to test for the presence of these biases in observations. We compare structure functions from coincident Lagrangian (drifter) and Eulerian (radar) data, and investigate whether differences are related to the local divergence and vorticity.

Taxonomic and Functional Profiling of the Microbiome of the Eastern Oyster, *Crassostrea virginica*

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As an ecosystem engineer in marine environments, the reef-forming eastern oyster, *Crassostrea virginica*, provides habitat to other organisms and is involved in the deposition of organic matter to the surrounding sediments. Therefore, oyster population dynamics have profound impacts on the nutrient cycling and carbon flow to coastal sediments and higher trophic levels. Despite their high filtration rate (and hence high rate of encountering microbes from the water column), eastern oysters harbor a distinct microbiota from the surrounding seawater. While the taxonomic composition of the microbiota has been explored in prior studies, little is known about the tissue-specific composition of oyster microbiomes and the potential functional roles they play in mediating the health of oyster populations.

Using 16S rRNA sequencing to profile tissue-specific microbial communities of individual oysters carrying varying loads of the protozoan pathogen *Perkinsus marinus*, we first identified core taxa associated with different tissue types and observed potential correlations between taxa abundance and *P. marinus* infections. Global analysis of the taxonomic profiles also revealed a more distinct microbiome in the digestive tract compared to the gill, mantle, shell, hemolymph, and pallial fluid. In order to probe the functional roles of the digestive tract microbiome, shotgun metagenomic sequencing was then performed which led to the identification of over 200 metagenomic bins, including two high quality metagenome assembled genomes (MAGs) representing uncultured strains of Mollicutes and Chlamydiae. Detailed functional analysis of the MAGs revealed genes involved in potential host associations, with machinery in the Mollicutes MAG mediating binding to the host epithelium layers and genes in the Chlamydiae MAG mediating interactions with the host immune system.

Further study of host-microbe interactions will enable our understanding of host physiology, population dynamics, and ecosystem processes related to oyster microbiome functions in Rhode Island's coastal waters.

Colorimetric, Paper-Based Detection of Phosphate in Marine Environments

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In marine ecosystems, high concentrations of certain nutrients such as phosphate lead to undesired algal growth and low levels of dissolved oxygen. Such conditions are deadly for fish, shellfish and other marine organisms. The rapid and robust detection of these nutrients using a colorimetric, paper-based system that can be applied on-site, is of high interest to individuals monitoring marine environments. The spectrophotometric molybdenum blue method is a well-established method for detecting phosphate that involves the formation of molybdophosphoric acid from ortho phosphate and an excess of molybdate in acidic solution followed by reduction to give a molybdenum blue complex. Phosphate detection systems that use the molybdenum blue method have already been developed, but most of them suffer from high detection limits, reagent instability and require the user to handle highly toxic reagents. For these reasons, the development of a new and improved detection system is necessary.

Reported herein, is the development of a paper-based, colorimetric detection system for phosphate with improved stabilization of the molybdenum blue reagent. The colorimetric response of the system was analyzed and quantified using RGB analyses (ImageJ), allowing for more precise analysis than naked-eye detection permits.

Identification and Analysis of Bacteria Associated with *Ulva* Macroalgae in Narragansett Bay

Sara Chlastawa & Anna Radovic

Biology & Biomedical Sciences, Salve Regina University, Newport, RI

For the last several years, a team from Salve Regina University led by Professor JD Swanson studied an important component of the Narragansett Bay ecosystem, the green macroalgae from the *Ulva* Genus, by following the bloom identity of the two species (*Ulva compressa* and *Ulva rigida*), as well as analyzing the bacterial populations associated with either species at various locations. The collected data follow the seasonal fluctuations of these organisms, which we are now correlating with multiple biotic and abiotic factors.

Here we describe the analysis of bacteria collected on *Ulva* species during the May-September blooming season of 2018 with the goal to establish correlation between excessive growth of the algae followed by increased toxicity for other species in the Bay, and the specific bacteria. We have identified 20 different bacterial colonies, and tested their resistance to various conditions, including hypoxia, presence of probiotics, and increased temperature, all addressing their survival capacity during the most excessive blooming period in July.

We hope our data will contribute to the global effort of fighting toxic algal blooms that threaten many aquatic ecosystems.

Macro Photogrammetry for Small Biological Specimens

Georgia Rhodes, Benedict Gagliardi, III & Neal Overstrom

Edna Lawrence Nature Lab, Rhode Island School of Design, Providence, RI

The adaptation of digital photogrammetric techniques to create detailed 3D models of biological specimens includes methods of macro photography, focus-stacking, and the use of Agisoft Photoscan Standard software. In comparison with other methods of 3D scanning, macro photogrammetry allows for imaging of biological specimens that are small in size or have delicate structures. Three-dimensional models of *Palaemonetes* sp. (Grass Shrimp) and *Chondrus crispus* (Irish Moss) are included to demonstrate methods of specimen preparation and digital techniques used.

The implications of modeling biological specimens include the building of teaching materials and insights into spatial information, as well as shape and surface details.

Who's on First: Temporal Analysis of PDMS Biofouling in a Marine Environment

Keyana Roohani[1], Kayla Kurtz[2], Vinka Craver[2] & Christopher W. Reid[1]

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Biofouling on instrumentation deployed in the marine environment is one of the biggest challenges of long-term monitoring activities. As part of the RI C-AIM sensor development effort, microfluidics- based devices are currently in development. Understanding the dynamics of biofilm formation is essential to design antibiofuling strategies.

To investigate the biofouling of microfluidic devices, we have developed an *in vitro* biofouling assay and metagenomics pipeline to assess colonization and development of biofilm in polymers commonly used for microfluidics manufacturing. Initial experiments have employed a 1 cm^2 PDMS polymer incubated in Narragansett Bay seawater over a three-week time course. Total genomic DNA was extracted from incubated PDMS chips and 16srDNA amplified by PCR, library preparation, and sequencing performed on an Oxford Nanopore MinION. The initial pioneers (first 48 hours) of the PDMS polymer were predominantly alkane-degrading bacteria from the genus *Alcanivorax* and *Marinobacter* in addition to *Pseudomonas* and *Acrobacter*. Temporal changes in the microbial community were observed in the biofilm. While the pioneer species was a constant presence in the community after three days, increased microbial diversity was observed with colonization by *Aerobactium* and *Spongiibacter*. By the end of the three weeks, the biofilm presented a high diversity of gamma- and alpha- proteobacteria with a high abundance of chemoorganotrophic and photoheterotrophic Rhodobacteriaceae.

Wind Direction Drives Shelf-water Intrusions into Narragansett Bay

Kevin Rosa

Graduate School of Oceanography, University of Rhode Island, Narragansett, RI

The purpose of this study is to understand the physics that drive intrusions of high-nutrient shelf-water into Narragansett Bay and, for the first time, to be able to predict these events. Water mass exchange between Narragansett Bay and Rhode Island Sound is an active area of research, with recent findings showing that episodic intrusions of shelf water could be an even bigger source of nutrients than all of Narragansett Bay's rivers and wastewater treatments plants combined.

A monitoring station will be deployed at the mouth of the Bay in 2019 to measure the magnitude and chemical properties of the inflowing shelf water, but a key question remains: what causes these sporadic intrusions? To find out, I use a state-of-the-art 3D ocean model and run a set of experiments using different wind speeds and wind directions. The results so far show that these events are triggered by westerly winds. This result agrees well with the observed intrusions from the summer 2018 currents data. Westerly winds are an uncommon wind direction for this region, which would also explain why these intrusions are so rare.

With chemical data from the new monitoring station, we hope to link these flux estimates with chemical concentrations to develop an accurate Narragansett Bay nutrient budget.

Nanopore Sensing via Microfluidic Devices and Data Handling

Brian Sheetz, Robert B. Chevalier, James T. Hagan, Mellissa Morris & Jason R. Dwyer

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The ability to detect or sense the presence of a specific molecule is employed by almost every scientific field in some way. The sensitivity of these measurements is relative to the work being done, and for analytical sciences the limits of detection are constantly being tested and improved. The employment of nanopores to the sensing field has greatly increased the limit of detection and it has been proven that single molecules can be detected as they translocate nanopores[1]. Currently, analysis is carried out in "bulk" solution with channels leading to the pores. The scale of a nanopore is such that, nano, and does not require samples to be in a bulk form. Microfluidic methods have shown tremendous versatility when it comes to the manipulation of micro-scale fluids[2].

Combination of microfluidics and nanopores eliminates the bulk solution from the nanopore sensing methods and allows for single molecule sensitive detection to be implemented into the microfluidics realm. Secondly, the detection of single molecule translocations calls for fast and sensitive detection electronics. Currently, the most accurate method to analyze translocation data is to do it manually. The extensive time requirements needed to manually analyze data has created a need for a faster and less energy intensive method. A computer program capable of analyzing translocation data with the same or greater accuracy as manual analysis solves this problem and is explored.

[1] Ghosal, S., Sherwood, J. D. & Chang, H.-C. Solid-state nanopore hydrodynamics and transport. *Biomicrofluidics* 13, 11301 (2019).
[2] Chiu, D. T. *et al.* Small but Perfectly Formed? Successes, Challenges, and Opportunities for Microfluidics in the Chemical and Biological Sciences. *Chem* 2, 201–223 (2017).

Response of *Synechococcus elongatus* PCC 7942 to Microplastics

Tania Silva de Oliveira & Arijit Bose

Chemical Engineering, University of Rhode Island, Kingston, RI

About 80 percent of all plastic produced nowadays accumulates in the rivers and landfills. Including that, 95 percent of the plastics thrown in the rivers end up in the oceans. These are highly concerning statistics, since plastics, in fresh and salt water, do not degrade easily and can impact living organisms for over a hundred years. In our laboratory, we have been examining how a specific fresh water bacterium, *Synechococcus elongatus* PCC 7942, responds when exposed to microplastics.

We have exposed PCC 7942 to polystyrene and polyethylene particles of diameters varying from 0.2 μm to 10 μm and examined these samples using fluorescence microscopy and cryogenic scanning electron microscopy. The bacteria attached to the particles within 24 hours. Biofilm formation was detected within 72 hours of contact, and after 12 days of exposure it increased drastically, followed by an increase in the hetero-aggregates size. The control sample within this timeline showed spread cells and few small agglomerations. We reveal yet another pathway by which microplastics affect fresh water life.

Annual Time-Series of *Pseudo-nitzschia* spp and Domoic Acid Production in Narragansett Bay, Rhode Island, USA

Alexa R. Sterling[1], Erin M. Tully[2], Samantha B. Vaverka[3], Jacob P. Strock[4], Riley D. Kirk[5], Matthew J. Bertin[5] & Bethany D. Jenkins[1,4]

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Some strains of the diatom *Pseudo-nitzschia* produce the neurotoxin domoic acid (DA) which can bioaccumulate in shellfish. Toxic shellfish consumption has deleterious impacts on higher trophic levels, including mortality in marine animals and amnesic shellfish poisoning in humans. In 2016 and 2017, DA toxicity closed shellfish harvest in Narragansett Bay (NB), Rhode Island, USA. While *Pseudo-nitzschia* has been detected in NB for over 50 years, these were the first DA closures in RI, threatening local economies and potentially human health. It is unknown what instigated these recent toxic events in NB: whether a changing environmental factor altered the physiology of *Pseudo-nitzschia* strains present or new DA-producing strain(s) were introduced to the NB ecosystem.

In order to investigate, we conducted year-long sampling of NB from Sept. 2017 - 2018 at several sites, including the NB mouths and inner regions. DNA from biomass collected on filters (> 5.0 um) was extracted and amplified using diatom-specific primers in order to track community composition. Cell-associated DA was quantified, with accompanying environmental metadata (e.g. nutrients, temperature, and salinity). Low DA concentrations were detected throughout, with the highest peaks in Sept. and Jun. at NB mouths. There is one *Pseudo-nitzschia* sequence dominant in the winter, and a higher diversity of sequences in the summer months.

This analysis will assist in identifying strains responsible for DA production in NB and help identify ecological factors that may correlate with elevated DA.

Oysters and Microbes and Narragansett Bay, Oh My!

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Oysters are keystone species in the coastal environment and play a crucial role in nutrient cycling and improving water quality for other marine organisms and humans. As estuarine organisms, they are subject to fluctuating environmental conditions, including nutrient loading, runoff, pollution, and anoxia, that impact their health and function. A potential mechanism of acclimation in oysters is the recruitment of diverse microbial communities.

Our research seeks to characterize adult oyster microbiomes and health at 7 sites along an estuarine nutrient gradient in Narragansett Bay using histology, qPCR detection of specific pathogens, and 16S rRNA amplicon sequencing. Adult oysters were collected from ambient conditions at all 7 sites, along with oysters treated with additional fertilizer (to simulate nutrient loading) at 2 of the sites located in Point Judith Pond. Tissues (gut, inner and outer shell biofilms) were processed and DNA was extracted for disease analysis and microbiome sequencing. As expected, a strong North to South estuarine gradient was observed in the Bay, with increasing salinity, pH, and dissolved oxygen, and decreasing nitrate, nitrite, and phosphate concentrations. Differences in several oyster health parameters, including prevalence of the parasite *Perkinsus marinus,* were detected between sites, and the highest disease levels were seen at the site with the highest ammonium concentration and salinity. Within the Point Judith sites, oysters exposed to a high nutrient load showed a significant change in their ability to denitrify, as well as changes in the microbial composition in oyster gut, suggesting that this change in denitrification is mediated by the gut microbiome.

Further analysis is focused on determining: a) how the oyster host and its microbiome interact to respond to estuarine conditions; b) how microbial composition and function differ within different tissues of an oyster using metatranscriptomics; and c) changes in expression of microbial genes associated with nitrogen cycling processes.

Dynamic Temperature Affects the Response of Phytoplankton Growth and Production to Temperature

Jacob P. Strock & Susanne Menden-Deuer

Graduate School of Oceanography, University of Rhode Island, Narragansett, RI

Temperature is a major predictor of growth and physiology of phytoplankton, but despite decades of thermal study, the growth and production of marine phytoplankton under changing temperature has not been described. To address this major knowledge gap, we treated a coastal phytoplankton model, *Heterosigma akashiwo*, with ecologically relevant temperature shifts (2- 4°C), across the reaction norm.

With a symmetric design, we were able to test potential importance of both the direction and total magnitude of temperature change. The smallest temperature shifts and most extreme resulted in immediate specific growth and production consistently lower than acclimated. Temperature changes cumulatively totaling 5-13°C resulted in immediate growth rates which were higher than acclimated. Temperature-size differentiation disproportionately affected production relative to specific growth. Beyond the mean response, with more thermal shifts, the intraspecific variability in growth increased exponentially.

Together, these results, contextualized with *in situ* data from Narragansett Bay, demonstrated how actual production rates could differ from current model assumptions of acclimated rates by -100 to +50 percent.

Addressing Predictive Modeling Knowledge Gaps to Improve Information Used in Decision-Making

Coleen C. Suckling

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Rapid changes in the climate threaten the future of marine coastal ecosystems as warming temperatures and ocean acidification strongly influence marine communities. However, much of our understanding of how communities respond to change have been extrapolated from predictive computer models built primarily upon data available from published literature. Such an approach is risky, particularly when attempting to enhance decision-making at the regional, community or species level. Models are only as good as the quality of the data that is being entered and when parameterizing models, there is a need to ensure that the best available data, which considers key species, particularly those from the regional species pool.

The goal of this seed grant is to address these gaps by contributing new information that will enhance models developed to predict changes in New England's coastal ecosystem. There is strong evidence to show that coastal shellfish (e.g. mussels) are vulnerable to the effects of climate change, but there is little consideration on how their predator's feeding behavior and physiology will be impacted since this will influence shellfish communities. The few studies that do take this focus fail to address the metabolic status of the predator and whether food intake can satisfy their energetic requirements. In this context, it is not known whether predators select larger and higher value prey with greater return for effort or opt for smaller and lower value prey with less return for effort. Any changes in predatory metabolic status under a future climate will strongly influence their predatory pressure on shellfish coastal communities, how they are structured and decision-making processes associated with their management.

Although we do not have the data from this project yet, we will present some information about how we are simulating climate change conditions in the laboratory and how we collect information to address this information gap. Additionally, we will provide information about how the seed grant has provided some opportunities for students to develop their skill sets and experience.

Diatom Community Composition: Comparison Study Between Fox Island and Graduate School of Oceanography Dock

Erin M. Tully[1], Alexa R. Sterling[2], Samantha B. Vaverka[3], Riley D. Kirk[4], Matthew J. Bertin[4] & Bethany D. Jenkins[2,5]

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C-AIM is developing a Narragansett Bay (NB) Observatory site at the URI Graduate School of Oceanography (GSO) long-term plankton time series location at Fox Island. Other C-AIM investigators have autonomous sampling capability at the GSO dock, which has shore power. Our goal was to compare the composition of planktonic communities over time at these two sites. Our comparison focuses on diatom communities.

Diatoms are microscopic algae that are nutrient cyclers and are an important food source for zooplankton and shellfish in NB. Important diatom community composition has been documented for over the last 50 years at the Fox Island site using microscopic methods. We used DNA based barcoding methods to compare weekly diatom community composition at the Fox Island and GSO dock sites over the summer of 2018. In weekly sampling, water was collected at these two sites on the same day and filtered for phytoplankton biomass (> 5.0 μm). DNA was extracted from the collected cells and diatom community composition was determined using diatom specific PCR primers that target the highly variable V4 region of the conserved eukaryotic 18s rRNA gene and high throughput sequencing on the Illumina MiSeq platform. Community composition was determined using the DADA2 pipeline. Comparisons of sequence similarity by site was conducted with Bray-Curtis analysis with NMDS scaling.

Preliminary analysis shows that sampling month is a more important driver of diatom community composition than sampling location. Detailed comparisons of diatom communities between paired sampling sites are ongoing. This information will be helpful for aiding the C-AIM community to understand the relationship between diatom communities at Fox Island and GSO dock.

Progress on OSOM-CoSiNE for Coupled Simulations of Narragansett Bay Hydrodynamics and Ecology

David Ullman

Graduate School of Oceanography, University of Rhode Island, Kingston, RI

An implementation of the Regional Ocean Modeling System (ROMS), the Ocean State Ocean Model (OSOM), has recently been coupled with the Carbon, Silicate, Nitrogen Ecosystem (CoSiNE) model in order to provide realistic simulations of the hydrography, circulation and lower trophic level ecology in the Narragansett Bay (NB) region.

The CoSiNE model is a complex lower trophic level (phytoplankton and zooplankton) ecosystem model with 15 state variables, including 4 nutrients. Using all available nutrient observations, the initial focus was the development of time series of nutrient concentrations in the rivers and wastewater treatment plants that discharge into NB. With forcing from these time series, the coupled OSOM/CoSiNE model has been run for a full year (2006). This simulation is presently being compared with historical observations of chlorophyll and dissolved oxygen from the Narragansett Bay Fixed Site Monitoring Network (NBFSMN) and with nutrient data from the GSO Plankton Time Series station with the objective of optimizing the various biological rate parameters in CoSiNE.

The simulations from OSOM-CoSiNE will ultimately be used to address a number of questions related to the ecology of NB, such as the effects of intrusions of nutrient enriched deep coastal water into NB and the influence of managed reductions in anthropogenic nutrient inputs on summertime hypoxia in the Bay.

AGENDA

8:00 am – Poster Setup *(Atrium I & II)* and Continental Breakfast *(Ballroom)*

9:00 am – Welcoming Remarks *(Ballroom)*

Dr. Geoffrey Bothun, Principal Investigator & Project Director

The Honorable Jack Reed, U.S. Senator, Rhode Island

9:30 am – RI NSF EPSCoR: 15 years of enhancing state capacity in research and economic development

Dr. Geoffrey Bothun, Principal Investigator & Project Director

10:00 am – Invited Graduate Student Presentation *(Ballroom)*

"Advances in seawater nutrient detection: new devices for nitrite and phosphate detection, cell phone-based detection strategies, and citizen science in undergraduate laboratories"

Teresa Mako, *Graduate Research Assistant, Dr. Mindy Levine Lab Department of Chemistry, University of Rhode Island, Introduction by Dr. Jason Dwyer, Research Thrust 3 Lead*

10:30 am – Poster Reception and Networking *(Atrium I & II)*

12:30 pm – Lunch *(Ballroom)*

1:00 pm – Keynote Address *(Ballroom)*

"Coastal Disasters: Lessons and opportunities for research and policy"

Dr. Kim Waddell, *University of the Virgin Islands, Director VI-EPSCoR Introduction by Dr. Geoffrey Bothun, Principal Investigator & Project Director*

2:00 pm – Coffee and Desert Break *(Ballroom)*

2:30 pm – Invited Postdoctoral Fellow Presentation *(Ballroom)*

"Rethinking model-driven, realistic storm-surge graphics"

Dr. Peter Stempel, *Architect, Provost's Fellow, Rhode Island School of Design, Introduction by Neal Overstrom, Co-Principal Investigator*

3:00 pm – Closing Remarks & Adjournment

University of Rhode Island | Brown University | Bryant University | Providence College | Rhode Island College | Rhode Island School of Design | Roger Williams University | Salve Regina University

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