Project Narrative

Project Title: Defining foraging hotspots of finfish and sharks in the New York Bight: linking trophic dynamics with spatiotemporal trends in species distributions

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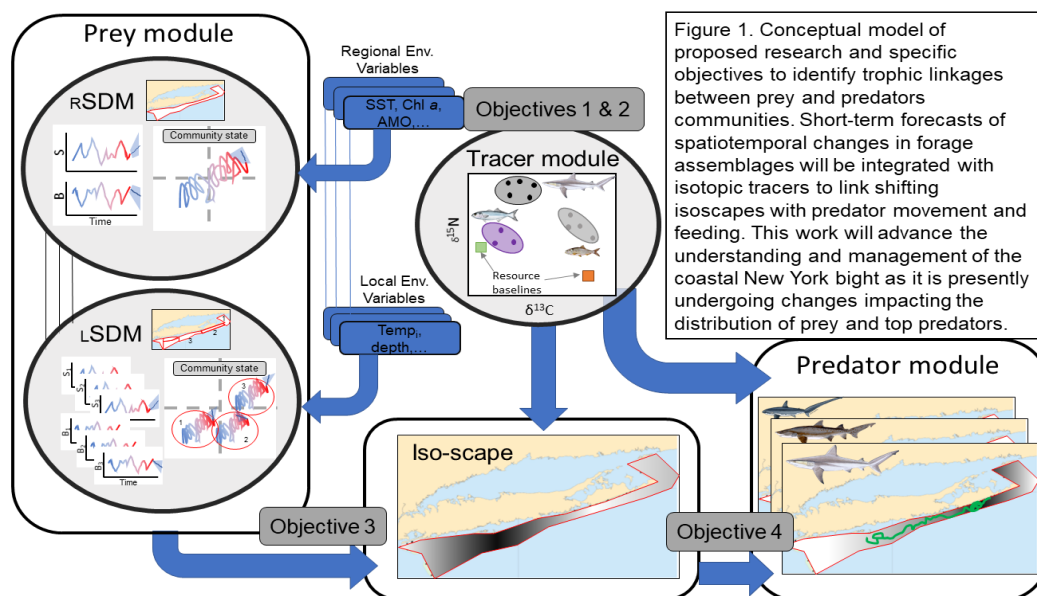Co-I: Cerrato, Robert M., School of Marine & Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11790; 631-632-8666; robert.cerrato@stonybrook.edu
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Project Objectives: We propose to quantify the *spatiotemporal distributional patterns* of forage species and the subsequent biomass *transfer of these dietary resource pools* to ecologically, recreationally and commercially important shark and finfish species in the coastal waters of New York, to enable predictions of foraging hot spots. As outlined in Fig. 1, we will (1) estimate the contribution of specific energy pathways and forage species production to sharks and finfish biomass; (2) quantify key trophic linkages and determine the functional roles of forage species and predators; (3) evaluate temporal trends and forecasts how, for example, climate (i.e., temperature increase) and demography (i.e., body-size, age structure driven migratory patterns) change prey distributions; and (4) develop spatiotemporal isoscapes to model overlap in predator-prey distribution and foraging hotspots of predators. We will assess three functional groups inhabiting coastal waters of New York: forage (i.e., menhaden, scup, squid), commercial and recreational finfish (i.e., bluefish, black sea bass, tautog) and highly migratory sharks (i.e., sandbar, sand tiger, common thresher, dusky).

Figure 1. Conceptual model of proposed research and specific objectives to identify trophic linkages between prey and predators communities. Short-term forecasts of spatiotemporal changes in forage assemblages will be integrated with isotopic tracers to link shifting isoscapes with predator movement and feeding. This work will advance the understanding and management of the coastal New York bight as it is presently undergoing changes impacting the distribution of prey and top predators.

This approach will contribute to our understanding of the linkages between prey and predators, advancing our understanding of species interactions in coastal food-webs. The proposed research will advance systems ecology by combining disparate data sources and innovative modeling approaches to address spatial and temporal patterns in coastal systems, which is important for both the understanding and management of the New York Bight (NYB); a region presently undergoing change that is impacting the distribution of prey and top predators.

Objective 1: Estimate the contribution of specific energy pathways and forage species to shark and finfish biomass (Years 1, 2; Priority: 1 NY-OAP). *The application of stable isotope analysis in this proposal provides the mechanism by which we will distinguish the range of energy channels available to consumers and trace biomass flow between subsequent trophic levels.* To accomplish this objective, we will use bulk stable isotopes of carbon ($\delta^{13}C$), nitrogen ($\delta^{15}N$) and sulfur ($\delta^{34}S$) to evaluate the reliance of forage species on specific primary productivity regimes (herein: energy channels); defined as estuarine, coastal benthic, and coastal pelagic. This information will determine the diversity of productivity regimes supporting biomass at lower portions of the food-web, which is a critical step for establishing energy and biomass transfer to predators (e.g., sharks and finfish).

Objective 2: Quantify key trophic linkages and determine the functional roles of forage species and predators (Years 1, 2; Priority: 1 NY-OAP). We will use isotopic data derived from ***Obj. 1***, to determine key trophic linkages between forage species, finfish and sharks. To understand energy and biomass distribution we will group forage species based on their use of available energy channels. Next, we will quantify the proportional reliance of shark and finfish on these forage species. This information will be used to determine the strength of predator-prey interactions (assuming greater reliance on a specific prey group reflects the strength of the interaction), while revealing how energy is distributed by prey groups throughout upper portions of the food-web. Next, we will determine trophic position and isotopic niche width; key parameters for understanding a species' functional role and trophic diversity within the food-web. Finally, we will combine estimates of trophic position, isotopic niche width, and the proportional reliance of each species on available energy channels, with hierarchical clustering algorithms. This approach will group species based on several key parameters related to their functional role. This approach has rarely been applied to determine functional diversity in marine species, but has recently illustrated how distinct functional groups of elasmobranchs can connect discrete regions of marine seascapes[1].

Objective 3: Evaluate temporal trends and forecasts how, for example, climate (i.e., temperature increase) and demography (i.e., body-size, age structure driven migratory patterns) change prey distributions (Years 2; Priorities: 1, 2 NY-OAP). We will leverage data from the Nearshore Trawl Survey to develop spatiotemporal models and forecasts of forage species distributions. Specifically, we propose to establish: 1) a flexible, automated workflow for data assimilation and multi-model generation, and 2) iterative, probabilistic forecasts of forage communities in space and time. A core set of 'best practices' have been proposed to maximize the utility of ecological forecasts for science, management, and society[2-4]. The workflow and product proposed here builds on the existing framing set by these best practices, focusing on a number of principles, including; 1) openness and reproducibility, 2) automation, 3) quantifying uncertainty, and 4) flexible and varied modeling frameworks. These practices lay the foundation on which we propose to build our framework.

Objective 4: Develop spatiotemporal isoscapes to model overlap in predator-prey distributions and foraging hotspots for predators (Year 2; Priority: 1 NY-OAP). We will incorporate stable isotope derived metrics from ***Obj. 1 & 2*** and distributional changes from ***Obj. 3*** to enable forecasting of biomass change and predator-prey dynamics under different projected local and regional environmental scenarios, relating trophic interactions, abundance, and distribution of species. Spatial variation in forage species isotope values (***Obj. 1 & 2***) can be combined with spatial variation in forage species abundances (***Obj. 3***) to reveal local variation in oceanographic regimes, these are typically referred to as prey-based isoscapes; this variation has been illustrated in winter and little skates[5]. As this variation is reflected in the isotopic composition of predator tissues, assignment models can be used that assign individuals to probable areas of the seascape in which a high proportion of trophic interactions occur[6,7]. We will combine predator isotope values with prey-based isoscapes (i.e., spatial interpolations of prey isotope values) to assign probable foraging grounds and areas of high predator-prey interactions occurring within the study area. Our assignment models will integrate prior information on predator habitat use through existing and newly collected passive acoustic telemetry data.

Introduction / Issue / Justification: The regulation of food web structure by production resources (i.e., primary and secondary) is fundamental for understanding food web responses to environmental, ecological, and anthropogenic change[8-10]. Ecological communities are continuously experiencing both biotic and abiotic disturbances and the ability of food webs to respond to these changes is crucial for ecosystem stability[11-12]. In marine food webs, physical ocean conditions can affect primary production, constraining energy availability and thus biomass, at higher trophic levels[13-15]. Large-scale changes in nutrient availability, primary and secondary productivity, and top predator abundance often occur simultaneously but may take years to propagate through a food web[14,16-18].

The NYB has seen historical declines in predator species, such as sharks, which has been linked to long-term reductions in ecosystem maturity[19]. Though spatial distributions and interactions of prey and predators dictate the structure and function of marine ecosystems[20-21], current management approaches are challenged by knowledge gaps in these dynamics and the movement of energy and biomass through marine food webs. Increases in local abundances of key forage and predator species have been reported in coastal areas of NYB. For example, the frequency of human-shark interactions and incidences of nearshore schools of forage fish has increased in recent years. Even in the absence of scientific data it has been widely reported in the media that Atlantic menhaden, sharks and whales have increased in abundance. However, these observations could be explained by a temporal and/or spatial change in environmental conditions that have shifted forage species, and as a result, higher level consumers closer to shore, leading to the perception of increased abundance. This may be due to shifts in local productivity, creating favorable conditions that support foraging hotspots in nearshore waters and/or climate-induced shifts in temperature regimes that result in species distributional changes[22-23]. Limited information exists on the spatial and temporal distribution of forage species, the predators they support, and how prey biomass is transferred to higher levels of the food web.

Identifying how animals use available prey resources and the environmental and ecological drivers of resource use are fundamental for effective species and ecosystem management, as well as, to protect important foraging grounds and prey resources supporting species productivity[24-26]. Optimal foraging theory dictates that animals should use available resources to optimize energy intake while minimizing energy expenditure[27]; however, for mobile predators that feed on

mobile prey, animal movement provides additional complexity. Energetic or resource landscapes (E-scapes) have been used to link species distributional patterns with their resource use[28-29]. Accurate representation of the resources available to a particular predator species is crucial, yet complicated, because predator-prey interactions are controlled by myriad factors from individual (e.g., physiology, morphology) to seascape (e.g., temperature regimes) scales. In addition, when predators consume multiple prey that are distributed variably in space and time, information on prey use and selectivity is necessary. Here, molecular biomarkers (i.e., stable isotopes) are effective for estimating broad-scale resource use among consumers and can act as molecular clocks for measuring resource use on varying timescales[30-31].

Stable isotope analysis provides ecological insights scaling from individuals to ecosystems through temporally-integrating consumer diets and reflecting the dominant energy pathway upon which species rely[32]. Carbon isotopes ($\delta^{13}C$) reflect primary production pathways[33], for example, the $\delta^{13}C$ values of marine organic matter (-18 to -22‰) differ from C_3 plants (-23 to -30‰[34]). Sulfur stable isotopes ($\delta^{34}S$) provide added resolution to distinguish marine from nearshore and estuarine[35] and can resolve benthic, pelagic and detrital sources supporting consumers[36]. Nitrogen isotopes ($\delta^{15}N$) reflect trophic position[37]. Together, these tracers have been used to differentiate resource use among estuarine, nearshore and offshore habitats and to determine the degree of residency of estuarine fishes[38-39]. Therefore, the combination of $\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$ will provide an understanding of spatiotemporal resource use by finfish and sharks while identifying key energetic pathways supporting these taxa.

To address these data gaps and clear management needs, the project will leverage PI Frisk's ongoing Nearshore Trawl Survey (2017-present; quarterly) and Acoustic Tagging Programs to (1) collect muscle and blood plasma samples from focal species (see below) and the greater nearshore community for stable isotope analysis, and (2) define temporal distributions of forage species (e.g., menhaden, scup, squid) and key predators (i.e., bluefish, black sea bass, striped bass, tautog, sharks) in NY's nearshore waters. This Nearshore Trawl Survey has operated for over five years and is funded for another five years by the NYSDEC. It will serve as the data source for modeling forage and finfish species distributions with the exception of large sharks which will be modeled using acoustic telemetry data. Ecological forecasting is emerging as a useful tool that benefits management, conservation, and the validation and development of ecological theory[40-41]. Here, we are proposing to combine survey, movement, and environmental data with stable isotope data to develop an innovative ensemble modeling framework that involves creating a diverse set of models and algorithms to analyze drivers, and forecast spatial and temporal trends in the NYB coastal food-web. The effort will produce a product directly usable by management agencies tasked with developing policies for the NYB.

The proposed project directly addresses two of the **Priorities** outlined in the OAP RFP, **(1)** *Examine predator-prey dynamics within foraging hotspots located in NYB, and* **(2)** *Identify likely species regime shifts of marine life occurring in the NYB with an increase in regional temperatures.* The proposed project is also responsive to **Actions 33** (Develop an ocean indicators system for the NYB), **22** (Monitor distribution and relative abundance of finfish, large pelagic, and endangered and threatened marine species inshore, offshore and in estuaries) and **4** (Strengthen criteria for designation of significant coastal fish and wildlife habitats) of the NY-OAP, as we will explicitly link prey distributions with resource use of important ecological, commercial and recreational species to identify foraging hotspots that directly inform criteria for designation of significant coastal fish habitats, and by identifying overlap in distribution patterns between predator and prey species, areas of finfish biomass production.

Approach: To address these data gaps and clear management needs, we propose to leverage PI Frisk's ongoing Nearshore Trawl Survey (2017-2027; quarterly–spring, summer, fall, winter), and Acoustic Tagging Programs (2020-2024). Collectively these programs provide the opportunity to quantify community compositional and trophic changes, and their response to environmental variability in coastal waters of NY. For the proposed work, sampling will be conducted using the School of Marine and Atmospheric Science's vessels *R/V* Privateer, *R/V* Pritchard and *R/V* Seawolf and through recreational anglers' personal vessels. All expenses related to collection of samples is provided by these NYSDEC supported programs.

Field Sampling: The Nearshore Trawl Survey conducts four seasonal surveys that includes 30 stations randomly selected by region and depth strata (Fig. 2). The survey uses an 80' otter trawl towed for 20 minutes at each station. All trawled species are enumerated, measured for total length (TL; mm) in fishes and carapace/disk width (CW/DW; mm) in crabs, skates and rays. Muscle tissue samples are collected and stored frozen. In 2021, a total of 639 muscle samples, for example, were collected and archived from forage species (i.e., menhaden, scup, squid) and finfish (i.e., bluefish, black sea bass, tautog, summer flounder). Temperature (°C), salinity (psu) and dissolved oxygen (mg L^{-1}) profiles are measured with a CTD providing a whole water column

Figure 2. Trawl sampling stations conducted along the south shore of Long Island, New York waters from New York Harbor to Block Island Sound conducted as part of PI Frisk's Nearshore Trawl

profile at each station. This sampling approach will be used to collect data on prey distributions and tissue samples required to generate prey-based isoscapes.

The Acoustic Tagging Program conducts ~30 independent rod and reel angling trips annually for highly migratory sharks from June to November. When captured, sharks are secured alongside the vessel and length measurements including pre-caudal length (PCL), fork length (FL), and total length (TL), and girth measurements (frontal span [FS], lateral span [LS], proximal span [PS], and caudal keel circumference [CKC]) are taken from each animal, and 1-2g of muscle tissue is excised from the dorsal musculature and 2 mL of blood is collected via caudal vein puncture and stored in a heparin-lined vacutainer. All tissue samples are stored frozen. In 2022, a total of 40 blood plasma and muscle samples, for example, were collected and archived from sharks including sandbar, sand tiger, common thresher and dusky. Location, temperature (°C), salinity (psu), and dissolved oxygen (mg L^{-1}) is recorded during each fishing event with a handheld YSI Professional Plus meter. Data derived from these samples will be used to support the spatial assignment of predators using isotope-based approaches.

To quantify the isotopic composition of estuarine, coastal benthic, and coastal pelagic energy channels, plankton samples of primary producers will be obtained by plankton tows. Plankton tows will be obtained by obliquely covering the water column from 0.5 m off the bottom using a 0.5 m diameter, 64 μm mesh net equipped with a flow meter. Benthic samples for macrophytes,

microphytobenthos and macrofauna will be obtained using a 0.04 m^2 modified van Veen grab. Pelagic and benthic samples will be collected concomitant with the trawl survey (***Obj. 1***).

Objective 1: Estimate the contribution of specific energy pathways and forage species to shark and finfish biomass. Understanding the energy sources supporting food-web biomass is integral for evaluating complexity and stability, and ultimately, ensuring relative protections of habitats supporting broader ecosystem services. This objective will quantify the pathways of energy transfer between dominant primary productivity regimes and lower portions of the NYB food-web. Specifically, we will use carbon, nitrogen, and sulfur isotope values to evaluate the reliance of key forage species on estuarine, coastal-benthic, and coastal-pelagic productivity.

We will measure the isotopic composition of baseline organisms (herein: isotopic baselines) that categorize each primary productivity regime. This is a common approach that typically leverages the stable isotope values of organisms with low mobility[42]. Based on first principles, we assume that benthic productivity regimes will be isotopically distinct from that of pelagic productivity due to the influence of the microbial loop, which drives higher δ^{13}C values of benthic isotopic baselines (-15‰) due to the recycling of organic matter[33]. Sulfur isotope values associated with benthic food-webs are typically much lower relative to that of pelagic, due to activity of sediment bacteria that reduce pelagic sulfates to sulfides (-25‰ to -20‰[43]). Estuarine baseline values are inherently different to both benthic and pelagic, owing to the greater influence of fluvial productivity, and nutrient run off, which drives particularly low δ^{13}C values and high δ^{15}N values, respectively[38]. Thus, the combination of these stable isotope values offers a powerful tool for distinguishing productivity regimes associated with these three habitats. Baseline organisms will be collected during seasonal trawl surveys as outlined and opportunistic sampling in nearby estuarine systems.

Consideration of appropriate tissues for stable isotope analysis is crucial when assessing trophic interactions of species, particularly those that migrate between different habitats such as inshore or offshore, as species use dietary resources with stable isotope values that vary over time and space. Tissue isotopic turnover is mediated by two general processes; growth and metabolism[44]. Consequently, tissues that are more metabolically active or have faster rates of protein turnover tend to respond more quickly to dietary changes, whereas tissues that are less metabolically active or have slower rates of protein turnover require longer time frames to equilibrate with diet[45-46]. For example, turnover rates of δ^{13}C and δ^{15}N in summer flounder blood and muscle tissue range from 22–44 days and 49–107 days, respectively[47], suggesting blood as a more useful shorter-term dietary indicator relative to muscle. For less mobile species such as forage fishes, tissues with slower turnover rates, such as muscle, represent longer-term conditions of resource use. As such, we propose to sample muscle tissue from all species outlined in ***Obj. 1***.

Prior to analysis, all tissues will be freeze-dried and ground to a powder. Shark tissues will be triple rinsed with DI water to remove ^{15}N-depleted nitrogenous compounds, which are known to affect δ^{15}N values[48-49]. Relative abundances of nitrogen (^{15}N/^{14}N), carbon (^{13}C/^{12}C) and sulfur (^{34}S/^{32}S) will be determined from ~1.5 mg sub-samples sealed in tin capsules combusted on a mass-spectrometer coupled with an elemental analyzer in the Laboratory for Environmental Analysis of Forests Microanalytical Facility, Michigan Tech and performed by the PhD student. In cases where blood plasma and muscle tissues exhibit a C:N > 3.4, a taxa-specific lipid correction will be applied to δ^{13}C values[48,50-51].

To ensure isotopic baselines have been categorized appropriately we will use simulated prey mixing polygons[52] to ensure all consumers have a high probability of falling within the mixing space. Individuals with >95% probability of falling outside the mixing space will be removed from further analyses[52]. We will use Bayesian isotope mixing models implemented in the R package MixSIAR[53] to estimate the relative probabilistic contribution of the three energy channels to forage fish biomass. We will include 'individual' as a random effect in each model to evaluate intraspecific variation in the use of distinct energy channels. Models will be run for 100,000 iterations with a burn-in of 50,000 and thinning interval of 100. Model convergence will be evaluated using Gelman-Rubin diagnostics and Geweke statistics[53]. Trophic discrimination (i.e., the isotopic change between prey and predator) will be assigned based on literature compilations of all published fish discrimination factors[54-55]. An appropriate value will be selected for each isotope based on tissue type, phylogeny, and dominant temperature regime.

Objective 2: Quantify key trophic linkages and determine the functional roles of forage species and predators. To provide estimates of trophic connectivity between forage species and higher predators (finfishes and sharks) we will group forage species based on their relative use of dominant energy channels. These groupings will form the isotopic endmembers used to derive estimates of prey preference by larger predators. We will use Bayesian mixing models described in ***Obj. 1*** to establish proportional reliance of predator species on each forage group. Due to the slower growth rates of sharks and finfishes, and thus slower isotopic incorporation rate, we will generate isotope values from blood plasma, i.e., a tissue associated with higher rates of metabolism[31]. We will then use stable isotope values to calculate several metrics that, in part, define functional diversity between predators, including: trophic position (TP) and isotopic niche width (a proxy for trophic niche). Trophic position estimates will be calculated using a Bayesian framework in the R package 'tRophicPosition', which can scale TP estimates when the predator is reliant upon multiple isotopic baselines. Finally, we will derive three-dimensional estimates of trophic niche width using kernel density methods implemented in the package 'hypervolume'[56]. We will also evaluate changes to these metrics across sampling years to account for interannual variation in food-web dynamics.

Hierarchical clustering algorithms can be used to group species based on multivariate ecological data, and thus, can provide holistic estimates of functional diversity and redundancy within food-webs[57]. Recent work has used measures of proportional food-web reliance (e.g., seagrass vs. coral reef vs. oceanic forage) to create unique functional groupings of elasmobranch fishes, and used to determine their role in connecting discrete regions of marine seascapes[1]. The proposed work will build off this approach, through hierarchical clustering of isotopically-derived metrics including trophic position, isotopic niche width, and energy pool reliance to create novel functional groupings of predators and prey. Trophic metrics will be standardized and converted into Euclidean distances prior to *k*-means and hierarchical clustering implemented in the R package 'NbClust'[58]. The most appropriate number of clusters will be inferred using pre-processing algorithms such as Calinski-Harabasz Index.[58] This information will provide the first assessments of functional uniqueness and diversity across prey and predator guilds and highlight the degree of overall food-web structure and connectivity.

Objective 3: Evaluate temporal trends and forecasts how, for example, climate (i.e., temperature increase) and demography (i.e., body-size, age structure driven migratory patterns) change prey distributions.

3.1: Developing an automated workflow for data assimilation and multi-model generation

Ecological forecasts are becoming more common, yet, many forecasts are one-off endeavors, often limited to, and ending with, the publication of a paper or report. This approach to ecological forecasting has shortcomings[2]. First, forecasts are often not reassessed or updated with new observations. Without reassessment, a forecast's ability to predict new conditions is unknown, thereby limiting its utility to managers and researchers. Similarly, the accuracy of forecasts decreases with time and therefore forecasts have a limited window for which they are useful[59]. To counter this, we propose developing a workflow of data assimilation and multi-model generation that automates the updating process and reduces the barrier to continuous use and reassessment. In this sense, we treat the data workflow as a distinct output in itself, meant to be of use beyond the project team and funding timeframe and in doing so focus on a product that is open, reproducible, and automated.

   Much of the groundwork for developing such a framework has been undertaken and our proposed work will draw heavily from these efforts which have been made available as open source, free-to-use products (https://portal.weecology.org/project/forecasting/)[4]. To briefly summarize the higher-level structure of this workflow (see *Data Management Plan*), it will contain multiple 'modules', i.e., compartmentalized data pipelines, that each have distinct spatial and temporal extent and coverage. This compartmentalization allows different data types to be isolated to address specific research and management questions, when needed. Each module will follow the general pipeline of White et al.[4] (Fig. 1), where multiple interdependent stages–from data entry to model fitting–are conducted with the output of one step providing the input for the next. For each module, the data pipeline is rerun when new data is entered. The outputs from each module will be combined to build forecasts from integrated data streams.

3.2: Developing iterative ensemble forecasts of forage community

We propose to model and forecast temporal distributions of forage species in NY's coastal waters. For forage community composition modeling, we will use a hierarchical approach[60] that models and forecasts community composition and abundance/biomass at multiple spatial scales: 1) the 'regional', encompassing the entire sampling area (Fig. 2) and 2) 'local', developed from downscaled and spatially interpolated contour maps of the forage community (Fig. 3). This approach is advantageous as it allows model and forecast assessments across spatial scales, as it is expected that the variability, inherent predictability, and ecological drivers of species distributions will change

Figure 3. Spatially interpolated contour maps of Longfin Squid along the south shore of Long Island.

depending on the scale of prediction[61]. Second, given the scale-dependence of many drivers, this approach allows us to connect regional and local models to account for processes operating at different scales[62].

   The Nearshore Trawl Survey will provide the community data for developing forage species community models and forecasts. Initial survey data (2017-2024), will be integrated with other streams for environmental (e.g., sea surface temperature; SST) and climatic variables (e.g., North Atlantic Oscillation; NAO, Gulf Stream Index; GSI) to fit a varied suite of models from simple baselines to time series to ecological distribution models at the regional scale. We will then
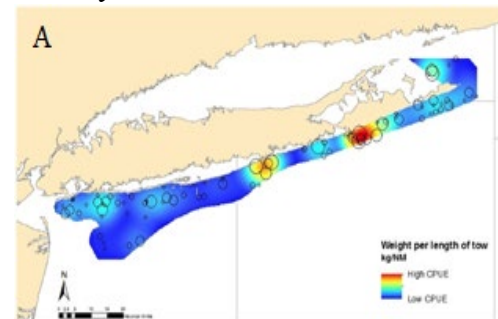
incorporate both static physical variables (e.g., depth, distance from shore, bathymetry) and localized environmental measures (e.g., spot measurements from routine sampling) to create local environmental offsets maps for model suites at the local scale.

Regional scale: Multi-model generation and ensemble development

(1) <u>Baseline models</u>: Since there are many sources of uncertainty (e.g., observation, process, stochastic) and near limitless model complexity, it is important to quantify how much information is gained by a model compared to simply assuming that the community is static[3]. We will include two baseline models to assess how well we can predict by assuming the system is static or governed by simple random error.

- *'Average' model*: This model assumes the variable of interest (e.g., regional abundance, Longfin Squid CPUE; Fig. 3) is static and the predictions are centered on the mean value of the training data and confidence intervals take constant width based on the standard deviation of measurements.
- *'Naive' model*: This baseline is a simple autoregressive model with a single sample of history, also known as an ARIMA (0,1,0) or random walk. Confidence intervals increase for predictions farther out as error accumulates, in contrast to the 'Average' model.

(2) <u>Time series models</u>

- *'Auto-Arima' models*: This group of models are similar to the 'Naive' model, but allow for many different autoregressive components and longer-term dependencies. In addition, they include moving average models and models with seasonal components incorporated. These models will be implemented in the *fable* package[63] in R, which automates the model selection process for time series models by using information criteria (e.g., AIC).

(3) <u>Environmental models</u>: The Baseline and Time Series models require no information beyond the trawl community data. Yet, it is widely known that environmental conditions can constrain species distributions. Building more complex models for forecasting is challenging, given the need for data sources with the spatial and temporal coverage to build training models. Further, to forecast future states of the system, environmental data must either be relatively static (e.g., depth, bathymetry) or forecasts of environmental data made available on timescales that allow predictions prior to sampling. Recent projects such as the subseasonal experiment (SubX) have showcased the utility of short-term forecasting for ecological phenomena[64-66].

For regional environmental models, subseasonal retrospective forecasts for SST will be acquired from the NOAA-GEFS AWS server (https://registry.opendata.aws/noaa-gefs/). As these forecasts are a global product, SST forecasts from individual model ensembles will be compared to measured SST from the study area during the training period to determine if specific models perform best[66] based on local SST vs. global estimates. In addition, we will include indices for important climatic cycles such as the NAO[67], and GSI[68]. Regional environmental data with available forecasts will be used to develop environmental models of species distributions.

- *stacked SDMs*: Species distribution models (SDMs) predict species-level occurrences and abundances based on environmental variables. Models for individual species can be 'stacked' to estimate regional abundances and species composition. Species distributions models can be driven by a number of modeling techniques (e.g., generalized linear and additive models, random forest[69]), allowing flexibility to include complex, non-linear responses.
- *joint SDMs*: Joint SDMs (*jSDMs*) do not assume the independence of individual species, rather attempt to model the entire composition of a community[70]. There are diverse

approaches such as multi-step *jSDMs*[71] which estimate species abundances based on the environment followed by a separate step including species interactions.

(4) <u>Ensemble model</u>: Each modeling framework and individual model has biases and uncertainties, however, together these biases can offset each other. For this reason, combined "ensemble" models often perform better than any single model[72]. The ensemble model will integrate all other models as a weighted average based on model fit such as Akaike's Information Criterion (AIC), Akaike weights (AICw), and evidence ratios[73].

(5) <u>Future model opportunities</u>: Availability of forecasts and modeling approaches are rapidly evolving. Our flexible workflow will allow future iterations and advancements (e.g., state-space models) to be easily incorporated. As long as a model can run and provide a standardized output, it can be incorporated and integrated into the workflow and ensemble model above. This is especially relevant given that the Nearshore Trawl Survey will be conducted until 2027.

Local scale: Downscaling 'regional' to 'local' models: We will integrate spatially explicit local environmental data and static environmental variables (i.e., depth, distance from shore) to a local grid of the study area. Environmental data will be obtained from existing platforms located on coastal acoustic arrays, observational buoys, and SST provided by NOAA/OAR/ESRL (Boulder, CO, USA). As an example, local SST will be integrated and compared to regional re-forecasts of SST. Local SST offsets will be estimated for each grid cell and estimated SST (with full uncertainty) will be used for developing the local model suite in each grid cell. In addition to the regional model suite described above, we will develop null baselines for local communities by randomly sampling individuals from regional forecasts. Local forecasts will be smoothed through spatial interpolation to develop continuous estimates of community composition.

Objective 4: Develop spatiotemporal isoscapes to model overlap in predator-prey distributions and foraging hotspots for predators. Spatial distributions of forage species and derived isotope values will provide the basis for prey-based isoscapes. We will generate both benthic, pelagic and estuarine isoscapes based on forage species isotope values (derived from ***Obj. 1***) prior to predator (finfish, shark) assignment models. For each predator, we will use prey-based isoscape most closely aligned with the energy channel contributing predominately to their diet (derived from ***Obj. 2***). The extent of spatial variation in prey isotope values will inform the location of a series of gridded cells, which represent regions of distinct prey isotopic composition (***Obj. 3***) and will form the assignment regions for predators[74].

Prey-based isoscapes and predator assignments will follow well-established Bayesian methods[6]. Here, we will determine the relative probability that an individual predator originates from a series of gridded cells (see above) in the study area (Fig. 2), by comparing their measured isotope values to that of the prey-based isoscape. Predator tissues will be corrected for trophic discrimination using the same approach outlined in ***Obj. 2***. Assignment models will incorporate significant sources of variance, such as machine analytical precision, between-individual isotopic variation, and variation observed across the initial prey-based isoscape[75]. We will also use existing passive acoustic telemetry data as *a-priori* information in the final assignment model, which will provide additional accuracy based on known animal movements. These models will provide probable regions of predator-prey interactions and how this varies across different species and functional groups (see ***Obj. 2***). Spatial contour maps will be produced to graphically illustrate the predicted and interpolated distribution of stable isotope parameters to delineate and define geographically distinct foraging areas[76].

Roles and Responsibilities: PIs will have joint responsibility for the research and they bring complementary backgrounds to this project. Frisk is the project's PI and has a research background in movement and fisheries ecology. PI Frisk is responsible for overseeing all aspects of the research, including project administration and coordinating with agencies including NYSG and NYSDEC, in addition to writing reports and communicating findings to local, regional and national groups. Co-I Cerrato is a benthic ecologist, with expertise in benthic-pelagic coupling and multivariate statistics. Cerrato will assist with project oversight, data management and analysis, and report writing. Co-I Shipley is a community ecologist with expertise in food web ecology, molecular tracer techniques and animal movement. Shipley will assist with stable isotope data management, data analysis, dissemination of results and by mentoring graduate and undergraduate students in website and outreach material development. Co-I Junker is an ecosystem ecologist with expertise in food web ecology, statistical analysis, and data management. Junker will assist with model development, ensemble model data management and dissemination of results. Junker will mentor the graduate student in developing and implementing the modeling framework. Co-I Olin is a community ecologist with expertise in community assembly, food web ecology and molecular tracer techniques. Olin will be responsible for project administration, oversight of administrative duties and budget management for Michigan Tech resources. Olin will also contribute to data analysis, report writing and dissemination of results and serve as the primary mentor for the PhD student. A PhD student (TBD) will be responsible for sample acquisition and processing, data analysis and model development, publication preparation and presenting the results of our work to the public. Undergraduate students (TBD) will assist in sample processing and work with PIs to develop a website and outreach materials to communicate the results of our work to the public.

Facilities: *Stony Brook University*: PI Frisk and Co-I Cerrato operate and maintain well-equipped laboratories with analytical equipment necessary for completion of proposed projects. Frisk's laboratory for fisheries studies is equipped with field equipment including trawls, seines, plankton nets, longline gear, and YSI water quality instruments and access to desktop computers with internet access and software for data organization and analysis (Excel, R Studio, etc.). Facilities for dissection analyses include measurement tools, and storage containers, and for tissue processing prior to stable isotope analyses. Cerrato's lab is comparably equipped, and in addition includes several dissecting and compound microscopes, a drying oven, and an Ohaus Explorer EX125D microbalance. *Michigan Technological University*: Co-I Olin's laboratory for community and trophic ecology is comparably equipped to Frisk's and Cerrato's, with analytical instrumentation for deriving bulk stable isotope data. Lab equipment includes freezers (-80°C; -20°C), Labconco freeze dryer, drying ovens, Labfreez ball mill grinder and Mettler Toledo XP microbalance. Olin's and Junker's offices (and PhD student) are equipped with networking capabilities, desktop computers with Microsoft Office Suite, ArcGIS, R and RStudio for data analysis, computation and visualization with access a laptop for field/travel use. Analytical and computing facilities available to Olin/Junker includes the Laboratory for Environmental Analysis of Forests which specialize in isotopic analyses, offering hands-on training and sample analysis using a Thermo Scientific ConFlo IV Interfaced with a DeltaV Isotope Ratio Mass Spectrometer and *Superior*, MTU's shared high-performance computing infrastructure. *Superior* contains multiple nodes with 16-24 cores and 64-256 GB of memory for active computing and 3 nodes with 32 TB of usable storage capacity, offering researchers access to multi-core computing nodes with the processing, memory and storage capacity necessary for multi-model execution,

ensemble model creation, and summarization of model outputs. *Beneath The Waves*: Co-I Shipley's office is equipped with several laptops and a high-powered desktop computer. Shipley's computers are equipped with a RAID hard drive (60TB) to support long-term storage and provide backup of large data volumes. All computers also have Microsoft Office and Adobe Suite including Illustrator and Photoshop, R and RStudio.

Expected Products and Anticipated Outcomes/Impacts: Our proposed research will assess nearshore ecosystem health, identify characteristics increasing species vulnerability and strengthen the development of management strategies supporting ecological resilience. The proposed research will enhance ongoing management by providing needed information including: (1) important resource pools that support biomass of various life-stages and (2) hotspots of potential fisheries and human interactions. Our results will provide a baseline representation of NY's coastal food web that can be used to forecast foraging hotspots under expected climate regimes. This is of considerable value and interest to multiple stakeholders including state and federal agencies tasked with management of these species, as well as non-profits, such as the NY Aquarium, that provide community education and outreach related to fishes in NY waters. NYSDEC Marine Fisheries Bureau Chief and Supervisory Fishery Biologist support the proposed research (*see Support Letter*), stating, 'The results of this study…inform public safety efforts as they relate to minimizing negative interactions with beachgoers and sharks' and 'DEC has collaborated with the Frisk Lab…and we look forward to collaborating with them on this research.'

Motivation for the proposed research is derived both from a scientific inquiry and from a practical viewpoint of the need to develop innovative management approaches. We are leveraging existing projects that are supported by NYSDEC and address Action 22 of the OAP. The proposed research will enhance existing nearshore finfish and shark research efforts and provide data to NYSDEC and federal agencies responsible for the management of coastal species. PI Frisk is the Chair of NY's Marine Resources Advisory Council and results will be disseminated to members to inform local constituents. Due to current collaborative work between the PI's and NYSDEC the results from this work can be directly implemented into state-based management and communicated to regional management agencies such as the Atlantic States Marine Fisheries Commission. PI Frisk and Co-I Shipley are members of the NYSDEC coastal sharks working group, which consists of recreational fishers, state marine resource managers, NGO and academic researchers. Data collected from this study will be disseminated through this group to all relevant local, regional and national stakeholders.

We are invested in diversifying the field of aquatic sciences by creating inclusive research experiences for graduate and undergraduate students from u-STEM and fostering marine stewardship by training a more diverse generation of scientists. The proposed work will support a PhD student at Michigan Tech and undergraduate capstone research projects in the MCP Program at Stony Brook University. As part of their training, students will enhance their science communication skills by developing an outreach strategy with the PIs to include social media, presentations to NGOs, government agencies, and the public, in addition to publishing their findings in peer-reviewed journals and popular press. Travel funds have been included in the budget to allow reporting of results at professional meetings. We expect three peer-reviewed publications resulting from this work that will advance the current state of knowledge regarding predator-prey dynamics, ecosystem connectivity and food-web structures of New York's nearshore ocean environment.

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