



# Atlantic States Marine Fisheries Commission

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## Atlantic Menhaden Stock Assessment Subcommittee (SAS) and Ecological Reference Point Workgroup (ERP)

### Methods Workshop II Summary

*Arlington, Virginia*

*November 5 -8, 2024*

The Atlantic Menhaden Stock Assessment Subcommittee (SAS) and Ecological Reference Point Workgroup (ERP) met in Arlington, Virginia, and via webinar to discuss a re-analysis of the historic tagging data that resulted in a different estimate of natural mortality and model development of the single-species Beaufort Assessment Model (BAM) and suite of ERP models. The SAS met November 4-5, and the ERP met November 5-8.

**SAS Committee Members in Attendance:** A. Schueller (SAS Chair), M. Cieri (ERP Chair), C. Craig (TC Chair), S. Alhale, J. Brust, B. Lowman, J. McNamee, A. Sharov, J. Boucher, M. Celestino, D. Chagaris, S. Madsen, C. Swanson, A. Buchheister, M. Dean

**ASMFC Staff:** J. Boyle, K. Anstead, K. Drew

**Public:** J. Ault, S. Gehan, P. Himchak, J. Higgins, B. Chiles, A. Colden, J. Kaelin, A. Kornbluth

#### SAS Meeting Summary

##### **Natural Mortality**

Over the last few check-in calls, the SAS discussed a re-analysis by Jerry Ault of the historic tagging data that estimated a lower natural mortality ( $M$ ) than that of Liljestrand et al. (2019), which is currently used in the base run of BAM. While both analyses use historic (1966-1969) tagging data, Liljestrand et al. (2019) used Coston (1971) data and confidential spatial data for effort. In recent years, the data were re-digitized, although they were missing some batches of tags present in the data in the Coston report. Ault et al. (2024) used the re-digitized data and Liljestrand's model along with effort data provided by NMFS and reconstructed from public datasets to re-estimate  $M$ . Because of the importance of  $M$ , the SAS agreed to consider Ault et al. (2024) and Liljestrand et al. (2019) over the next few months and decide how  $M$  should be estimated for use in the base run of BAM. While the single-species assessment is an update, there is a term of reference in the ERP assessment that could provide an avenue to have  $M$  peer-reviewed.

At the workshop, the SAS enumerated the issues to be explored by a subgroup of the SAS and determined which workgroup members will be responsible for each task.

1. Characterize Coston (as used by Liljestrand) vs re-digitized dataset (as used by J. Ault) (J. Brust, B. Lowman, A. Sharov)
  - a) Evaluate the use of primary vs secondary magnets
2. Characterize the differences in effort datasets (S. Alhale)
3. Characterize plant efficiency estimates (K. Drew)
4. Evaluate the modeling choices and migration rate estimates (A. Schueller)
5. Update the literature search (C. Craig)

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The first task will be to characterize the differences between the data used by each analysis and evaluate how the use of primary magnets and both primary and secondary magnets may affect the results. The goal is to determine the most appropriate data filtering approach. Similarly, the differences in the confidential effort data used by Liljestrand et al. (2019) and the confidential and publicly sourced effort data used Ault et al. (2024) need to be characterized to determine if these data have a large or negligible effect on the  $M$  estimates. Not all SAS members will have access to the confidential data and the SAS will need to work with the Southeast Fishery Science Center to determine what can be publicly shared. At the time of the tagging study, several menhaden plants participated, and plant efficiency recapture rates were estimated and published in the literature. How these plant efficiency estimates were used in the model may affect the results. While the same code was used for both  $M$  analyses, it is possible that different choices were made for parameter estimation and a SAS member should compare choices made throughout the code.

The  $M$  workgroup will work over the next few months and make a recommendation to the SAS on what  $M$  should be used in the base run of BAM. Data and code will be requested from Ault and Liljestrand. BAM sensitivity runs would include the currently used  $M$  for continuity if another  $M$  is chosen. Work on  $M$  should be resolved by early 2025 (January is the goal, with March at the latest) to provide a base run and any applicable sensitivity runs to the ERP group for their model development. A working paper will be developed and provided to the Peer Review Panel later in 2025.

### **BAM Sensitivity Runs, Monte Carlo Bootstrap Uncertainty Analysis, Reference Points, Retrospective Pattern**

The SAS reviewed the two sensitivity runs for the BAM: including the MARMAP-EcoMon survey and including the 2020 southern bait age compositions. The results were similar to the stock assessment update in 2022 where BAM would not converge with the inclusion of the MARMAP-EcoMon survey, and the hessian would not invert. The SAS agreed to omit this index again in the base run. The 2020 commercial age compositions were censored from the base run during the 2022 stock assessment update due to a lack of sampling during the COVID pandemic and that decision was maintained for this base run. No other sensitivity runs were identified by the SAS other than those around natural mortality, which will be determined at a later date.

The SAS reviewed the MCB analysis and single-species reference points. The uncertainty analysis results were similar to past assessments. Using the single-species reference points, Atlantic menhaden are not overfished, and overfishing is not occurring, but the SAS debated the usefulness of including these reference points since stock status is now determined by ERPs, not the single-species reference points, and including both may lead to confusion. The SAS ultimately agreed that the single-species reference points graphs should be included in the appendix of the update report. These reference points may have value to the ERP group because there could be ecosystem overfishing but not single-species overfishing, for example, and knowing the single-species stock status may provide context.

During the last assessment, there were some retrospective concerns, and the SAS asked the Assessment Science Committee (ASC) to develop a rubric to provide guidance for when a retrospective adjustment should be made. Like the 2022 update, this update shows a retrospective pattern of fecundity being overestimated and fishing mortality being underestimated. The SAS walked through the ASC flowchart for deciding when to make an adjustment and the results were similar to last time with some support

for and against. The SAS agreed to reevaluate the retrospective pattern if and when  $M$  is revised and once the ERP models are more fully developed.

### **Future Work**

The SAS had a lengthy discussion about how uncertainty is estimated. It was suggested that during the next benchmark, the SAS might want to reconsider the MCB and the MCMC analysis and which to use. A suggestion was made to explore the gradients or convergence on the MCB runs, how many parameters were near their bounds, or other metrics to separate out the MCB runs.

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**ERP Work Group Members in Attendance:** D. Chagaris, M. Cieri, S. Madsen, J. McNamee, A. Schueller, M. Celestino, A. Sharov, A. Buchheister, G. Nesslage, M. Dean, J. Boucher

**Staff:** K. Drew, K. Anstead, J. Patel, J. Boyle

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### Ecological Reference Point Work Group Meeting Summary

#### **Menhaden Single-species Update**

The update covered the discussion had by the SAS during the first 1.5 days of the workshop. The SAS discussed the pros and cons of the Monte-Carlo Bootstrap Ensemble (MCB/MCBE analysis) versus the MCMC analysis for uncertainty. MCMC underestimates uncertainty but MCBE probably overestimates it; they are characterizing different sources of uncertainty. The SAS decided that they will not update the MCMC analysis, which was the same decision as the previous assessment. The SAS also covered whether they could correct for correlations between  $M$  and fecundity, but ultimately decided that probably not for this update because there are little to no data to inform that decision. Single-species reference points and terminal year estimates are bimodal for MCBE analysis, which is the same as the benchmark. There is the possibility of 2 states of nature or 2 solutions depending on  $M$ -fecundity combinations, and it was proposed that the combinations are explored in the next benchmark.

The SAS also covered retrospective adjustments. The  $\rho$  is within ASMFC guidance bounds, but adjusted values fall outside the 90% confidence intervals of the terminal year for  $F$ , and just barely for SSB/fecundity (mainly because CIs are asymmetrical – adjustment results in higher  $F$  and lower SSB, but CIs are slanted towards lower  $F$  and higher SSB). The group explored how to evaluate stock status questions in the flowchart by using ERPs, and not a single-species threshold. Ultimately, the decision on retrospective adjustments was postponed until a recommended ERP target and threshold was determined.

**Next steps:** SAS to use ERP target and threshold for stock status for menhaden update; update single-species targets and thresholds for ERP context/discussion but do not present in single-species update report.

#### **ERP Species Data Updates**

##### *Assessment Updates*

The menhaden, striped bass, and Atlantic herring assessments were all completed with a terminal year of 2023, while the Spiny dogfish and bluefish assessments had a 2022 terminal year. The weakfish

assessment is currently in progress with a terminal year of 2023 and is behind schedule but has an anticipated completion by the end of 2024.

Looking at status changes from the 2019 ERP assessment (terminal year 2017), in the 2019 assessment, Atlantic herring was not overfished (but just barely above threshold) and no overfishing was occurring. In 2023, Atlantic herring was overfished and overfishing was occurring. In 2019, bluefish was overfished with no overfishing. In 2022, bluefish was overfished (but below target) and overfishing was not occurring. In 2019, spiny dogfish was not overfished (well above target) and no overfishing was occurring. In 2022, spiny dogfish was not overfished (just above target) and still not experiencing overfishing. In 2019, striped bass was overfished with overfishing occurring. In 2023, striped bass was overfished (just below threshold) with no overfishing occurring. In 2019, weakfish was depleted (below biomass threshold) and was being overfished (but above Z threshold). The 2023 assessment is still pending but there is likely to be little change.

Spiny dogfish and bluefish have had research track assessments since the last ERP benchmark, while menhaden, striped bass, herring, and weakfish have (or will have) assessment updates. Therefore, there are more significant changes to trajectory and status for spiny dogfish and bluefish than for other species. Spiny dogfish changed from a swept-area biomass approach to a SS3 model, and inputs and outputs are now more compatible with VADER and NWACS. Spiny dogfish uses spawning output (number of pups produced) instead of spawning stock biomass for the SSB reference points and the overfished status determination. Total biomass is more relevant to the EwE models and can be extracted from the SS3 output files and update report. The group will potentially need to modify “SSB” target and threshold values to be more directly comparable to total biomass for EwE models.

**Next steps:** K. Drew will investigate spiny dogfish reference points and verify if the assessment used a calibrated or an uncalibrated Bigelow index.

The group discussed the terminal year of the ERP species assessments for the NWCAS-MICE. The 2023 values are not available for spiny dogfish and bluefish from each assessment yet. It is possible to use the 2022 year as the terminal year for all assessments, but that would cut off the last year of data for striped bass, menhaden, herring, and weakfish. Another possibility is to use the projected or status quo value for 2023 for spiny dogfish and bluefish. NWACS-MICE uses the terminal year as the starting point for projections, not for stock status, so likely not a huge impact either way.

**Next steps:** Use terminal year of 2023 for all ERP species assessments. K. Drew will find 2023 values for F/catch and biomass from the spiny dogfish and bluefish assessment projections.

#### *Bluefin Tuna Update*

Seasonal density estimates were developed for bluefin tuna based on satellite tagging data. It was estimated that 13%-58% of the bluefin tuna population overlapped with the NWACS model domain, depending on the season. Back-of-the-envelope calculations of potential menhaden consumption using q/B value from the NWACS-Full model for the highly migratory species group (6.794, taken from EMAX) were conducted. From there, the biomass of bluefin tuna in the NWACS domain and an average percent menhaden from diet studies were estimated. It can be assumed that 12,000 MT (13%) to 56,000 MT (58%) of menhaden are consumed by tuna populations. NWACS-MICE estimated menhaden consumption by striped bass at 30,000 MT.

The group discussed if bluefin tuna should be added as a predator species since it appears to be a predator on the same scale as striped bass. A large part of the population is outside the NWACS domain, but this is not necessarily a problem for understanding the impact of bluefin tuna on menhaden, if the group can split the biomass and catch correctly. There is more of an issue in understanding the impacts of menhaden fishing on bluefin tuna (a major objective of this model) as the overall biomass trends for bluefin tuna could be affected by dynamics outside the model domain. Adding any one specific predator is not likely to have a large impact on eco-trophic efficiency or the unexplained mortality component of EwE, given how high menhaden  $M$  is and how widely preyed-upon menhaden are. Bluefin tuna is a species that has the potential to switch from Atlantic herring to menhaden as Atlantic herring biomass declines and it could be worth capturing this dynamic. Assessment biomass trends show a slow increase over NWACS temporal domain, so the model will not have to chase significant changes, but it is unclear how much additional information this will provide. Bluefin tuna-menhaden interactions can be more intense and localized than spatial density estimates, but this is true for multiple predators. There is stakeholder interest in bluefin tuna diet and abundance, so it's worthwhile to incorporate them now and be prepared to do more with them in a more spatial model.

**Next steps:** Replace the highly migratory functional group within NWACS-Full with bluefin tuna and do not include in NWACS-MICE or VADER models.

To use bluefin tuna in the NWACS-Full model, biomass is needed from spatial density and ICCAT bluefin tuna assessments. Diet composition is available from several studies, including recent ME DMR data, but it needs to be compiled into a matrix that matches the NWACS-full functional groups and summarized and weighted appropriately. Size preference data are probably limited so assume 0 YOY, 100% age-1+ menhaden.

**Next steps:** M. Dean will work with A. Buccheister, J. Patel, and Diet Data WG to pull these data together.

#### *Anchovy Updates*

Raw survey data from NEFSC and SEAMAP (Coastal Trawl and P195 Pamlico Sound Trawl), NEAMAP, NJ DE Bay Trawl, and ChesMMAP (working on getting data for CT LISTS) was compiled to try to develop a time-series of anchovy biomass and abundance. The swept-area biomass estimates for all the surveys were calculated. NEFSC developed an estimate of  $q$  to calculate a total/absolute biomass estimate, but there are no  $q$  estimates for the other surveys. With the  $q$  adjustment, the NEFSC estimates dominate the time-series; without the  $q$  adjustment, the other surveys dominate. NEFSC time-series drops precipitously in 2009 with the switch to the Bigelow and the associated loss of sampling the inshore strata. The question remains as to whether the  $q$  was developed based on Albatross data and if it can be applied to the Bigelow years. Additionally, the group was wondering if the calibration factor for anchovy is reliable and applicable (i.e., can side-by-side tows account for the loss of the inshore strata where abundance is higher, since the paired tows didn't occur in those areas?). There is no significant trend in anchovy biomass from any of the composite methods but several consistent spikes in abundance across surveys. It is unclear if the time-series of biomass will provide more information than the current constant biomass approach, but the NWACS-MICE model could potentially capture those spikes with the primary productivity drivers.

Ed Houde produced estimates of bay anchovy biomass in Chesapeake Bay in the 1990s that may overlap temporally with ChesMMAP and help estimate a  $q$  for that survey. NEFSC overlaps also spatially and temporally with the NEAMAP survey for a couple of years.

**Next steps:** Use a spatial density modeling approach to explore combining the various surveys. This work could form a template for spatial distribution maps for other species.

Something like VAST or sdmTMB can estimate a vessel effect within a GLMM framework and use the NEFSC estimate of  $q$  to scale the other surveys appropriately. This would also allow estimation of total biomass for years where only the NEFSC survey was operating (incorporating estimates of biomass from inshore areas/bays/sounds where the NEFSC did not sample).

**Next steps:** M. Dean will work with M. Celestino to get the data and explore this approach. SEAMAP coastal trawl data will be excluded from this analysis since most of the survey is outside the NWACS-MICE spatial domain. In parallel to this analysis, M Celestino will assemble a point estimate of anchovy biomass for 1985, and then one (or more) relative time series beyond that. Will circle back to considerations related to EcoSpace (e.g., different trends in different regions) at some point.

### *Zooplankton*

The Northeast Fisheries Science Center maintains an index of abundance for zooplankton and pteropods, but their indices didn't include estimates of uncertainty. Uncertainty can be used to weigh the time series if it's available. The NEFSC also breaks up their indices into 4 seasons, so the group advised stitching the seasons together.

The NMFS list of zooplankton were binned into NWACS groups and abundances were organized by season and EPU. There were 3 possible approaches to estimating biomass with these data: 1) use EMAX approach with little deviations from that approach, 2) tune the EMAX approach using biological parameters (e.g., avg weight) that approximate results from NWACS ASMFC (2008) outputs, and 3) use approach 2 but include pteropods. Approach 1 showed a zooplankton population dominated by gelatinous zooplankton which is inconsistent with our understanding of oceanic zooplankton population structure. Approach 2 showed a zooplankton community dominated by copepods which is what we empirically expect, and Approach 3 demonstrated that pteropods were not a trivial amount of biomass.

It was noted that many species of micronekton were krill species.

**Next Steps:** M. Celestino to try to obtain estimates of uncertainty of zooplankton, develop both annual and seasonal estimates of zooplankton biomass, try to get biovolumes by Ecological Production Units and for the coast, include Scotian Shelf in estimates, develop an estimate of microzooplankton to incorporate into the zooplankton group.

### **NWACS-MICE Model Updates**

#### *Ecopath*

NWACS has updated its version from the previous assessment. It now operates on version 3.0 instead of 2.1.6, and EwE operates on version 6.7 (released in May of 2024). The biomass inputs are obtained from stock assessment or density data. The previous version of NWACS had biomass inputs in units of million mt. This was converted to mt/km<sup>2</sup> in the new version because of plans to translate the measurements into Ecospace. This can be done by dividing model area by 441,000 km<sup>2</sup> or converting density estimates directly. The total mortality rate (Z) and production ratio (P/B) estimates were changed slightly based on M, F, and N in the assessment. Values were not changed for non-assessed species and primary production. Catch and landing (C) inputs were obtained from stock assessment files and input as total dead biomass in the same units. No landings inputs were included for non-assessed species (anchovies,

invertebrates, etc.). The consumption rates have been changed from the 2019 version and the diet matrix still needs to be updated.

R scripts were written to read output files from stock assessments and extract inputs and time series for the MICE model. Changes to this version of the model include the use of mid-year abundance or biomass, the F timeseries calculated as  $C_y/B_y$  where C and B are total for each MICE species and age stanza, and M for each stanza is weighted based on  $N_a$ . The new script also determines  $W_{mat}/W_{inf}$  from growth and maturity vectors. The new script also extracts predicted time series and all indices of abundance to an excel file. The six main species in the MICE model have R scripts written for them and the Full model's functional groups that have stock assessment are also mostly processed based on these R scripts.

For the striped bass inputs for the MICE model, the "leading" stanzas were changed from age 6+ to age 2-5. This brings the last 2 stanzas in line with the stock assessment biomass. There was also a big change in the initial F for age 6+ and mismatch with the stock assessment. The input landings for striped bass may need to be revisited since it has missing F-at-age and catch biomass-at-age matrices.

The 1985 biomass was slightly higher from the 2022 BAM than the 2019 BAM for menhaden. The M for age 1+ stanza (adult) is the average  $M_a$  over ages 1-6, weighted by  $N_a$ . Ecotrophic efficiency is the same in the old and new versions of NWACS.

For spiny dogfish, there is no age structure in this model. In the last version, the swept area biomass was used and, in this version, mid-year biomass from SS3 was summed over all ages. The differences in Ecopath inputs result from changes in assessment methods.

For bluefish, adult biomass was estimated to be lower in the 2022 ASAP model while the juvenile biomass is higher. This is possibly due to different weight-at-age matrices in the previous assessment. There was some discrepancy in the juvenile stanza (age 0) biomass between EwE and ASAP. The first year of assessment is 1985 but that has a negative  $B_a$ . Juvenile Z and M are lower in the new version.

For weakfish, the same 2019 ASAP assessment is currently being used in the new version. Revised methods for processing ASAP outputs led to different model input values. Time varying M was used in the assessment and 1985 was a low year, so this doesn't balance well. When balancing version 2.1.6, M was assumed to be higher.

For Atlantic herring, the biomass inputs have changed very little. Z is lower in the new version, especially for juveniles, leading to a lower M. Juvenile F is closer to assessment than in the previous version.

Anchovies have no changes yet as M. Celestino is still working on a revised area swept biomass estimates. Benthic invertebrates also have no changes yet. Numerical density data have been obtained but weights are still needed to convert from N to B. For zooplankton, numerical densities are being used from NEFSC data with assumed body weights for taxonomic groups. The estimates are higher than in the previous version. Revised biovolume data should be used for this species. Phytoplankton production is being estimated from the GLORYS database, and carbon measurements need to be converted to biomass. Detrital inputs remain the same as the last model.

Spiny dogfish and bluefish have the highest biomass of the predators in 1985. Menhaden is the forage fish with the largest biomass in the model. Except with spiny dogfish, biomass didn't change much from version 2.1.6 to version 3.0.

Of the available diet data, there were >59,000 individual stomachs obtained from 4 data sources. NEFSC data are aggregated by region and decade. The most important step right now is to find a procedure to combine these data and estimate the diet matrix with uncertainty.

There are currently 5 model configurations: 1) continuity, 2) primary production forcing, 3) monthly egg production forcing, 4) predator-prey vulnerabilities, and 5) all seasonal dynamics.

In the first configuration there is a serious drop in all biomass when the NEFSC survey changes from the Albatross to the Bigelow and a smaller change in all zooplankton biomass. In the second, which has a timeseries multiplier on the primary production rate derived from GLORYS, the mean monthly primary production forcing is derived from the chl-a product (1993-2023) and is vertically integrated based on monthly averages. In the third configuration, a vector representing monthly spawning activity for each multi-stanza species is used based on the literature. In the fourth, which has the aim of achieving a more realistic prediction for predators that overlap seasonally with their prey, seasonal predator-prey overlap were determined as part of the 2014 MSVPA update for predators in the model by age. Spatial overlap is a function of predator/prey abundance in the different regions. Spatial overlap were averaged across ages within the MICE stanza then smoothed across months using a spline function (indexed to middle of season from February to November). The vector was then scaled to mean, and the amplitude reflects the strength of seasonality, showing that the model will predict higher intra-annual variability in diet. For the fifth configuration, the overall approach is to apportion annual F estimates to month using monthly information on effort or catch. Of these, striped bass, blue fish, spiny dogfish, and weakfish estimates can be found in MRIP. Menhaden estimates can be found from CDFR data and herring can be found from landings from 2015-17.

### *Ecosim*

Accounting for seasonal processes in Ecosim, the preliminary results indicate improved fits when including trends in primary production and seasonal predator-prey dynamics. Incorporating primary production resulted in lower  $v_{ij}$  (vulnerability) estimates for all SB-AM interactions except one. Differences could be translated into alternative tradeoff relationships and ERPs. Last time, a "repeated search" approach was used, and N was estimated using the most sensitive vulnerability parameters. This was repeated until no further improvements were detected via SS and AIC. However, there are other ways to estimate  $v_{ij}$  and best practices for these can be found in Bentley et al. 2024. For Ecosim calibrations, vulnerabilities are conditioned on Ecopath inputs and other foraging area parameters that can be fixed during estimation. Essentially, Ecostat allows us to estimate the initial conditions (Ecopath) and other parameters that are aren't estimable within the software.

### *Ecospace*

By expanding NWACS-MICE into Ecospace, we can explicitly account for seasonal pred-prey overlap in ERPs and investigate abundance of menhaden. This would involve using the EwE spatial-temporal framework (Steenbeek et al. 2013) to drive phytoplankton, temperature, and salinity fields, defining environmental preferences, parameterizing the Ecospace habitat capacity model, incorporate migration patterns, and model spatial distribution of fishing effort. Most importantly, we would need a very data-rich system that could provide regional time series and spatial data to check against. For the MICE model, the base map for Ecospace would have depth and distance to shore as static layers, surface



temperature, salinity, and chl-a as the environmental drivers, and dynamic habitat layers used to constrain species distributions for menhaden, herring, and striped bass.

Ecospace regions are only used to summarize the output of the 5 geo-regions and 2 depth strata. This would be necessary for extracting diet and age composition for spatial regions. For calibration, we can extract predictions from the survey domain to make comparisons. Each species is assigned a preference function for each environmental driver with 52 total response functions. Preference functions determine 'foraging capacity',  $C$ , in each grid cell and includes habitat affinity input, which affects consumption and movement to and from a cell. Since temperature effects alone don't produce migration patterns very well, we can potentially contain seasonal distribution using input habitat layers. Tagging data could also be incorporated to determine dispersal.

Using the Ecospace habitat foraging capacity model, we can represent seasonal north-south and inshore-offshore migrations and expand the MICE model to Ecospace. Initial simulations demonstrate model stability and ability to account for seasonal and spatial dynamics in primary production, spawning, predator-prey overlap and fishing effort.

The goal is eventually to develop a new calibration procedure for Ecospace models to increase their reliability for providing routine management advice and advancing ecosystem-based fisheries management.

#### **NWACS-Full Updates**

The NWACS-Full model has 61 groups total with an emphasis on menhaden, their predators, and alternative prey.

Currently, there are biomass data requests out to NEAMAP and ChesMMAP. Values have been obtained from NEFSC and there are minor updates (number of positive tows, total tows, uncertainty), which are different from the 2014 data request.

There is some discrepancy in region-specific areas from 2014 to 2024 potentially due to a different set of strata, a different projection, or a different shapefile. Given the mostly consistent percent difference, this wouldn't affect calculations much. The MICE model and the Full model should double-check the size of the model area since there seems to be some discrepancies.

Most groups in the model have generally similar overall trends and magnitude by season, but the Full model will most likely use outputs from the stock assessments.

The main data needs for each group in the Full model are biomass time series, catch time series, and P/B (or Z). For multi-stanza groups, Von Bertalanffy  $K$ , and weight at maturity relative to the maximum weight is also needed. The assessment model output files for the functional groups in the model were requested and R scripts were modified to process files to extract the needed data. All requested data files have now been received.

For commercial and recreational landings from the NOAA Landings database, the spatial area stretches from Maine to North Carolina and most of the species were already classified into EwE groups. Unknown fish and confidential data, which were already small parts of the landings, were excluded. For fishing fleets, the gear information is no longer available, and fleets are species-specific or just labeled "commercial" and "recreational". Menhaden, bluefish, striped bass, and weakfish were comparable

between the Landings database and stock assessment reports, which suggests that MRIP data are adequately reported. The assessment report landings are higher than NOAA's for Atlantic herring and spiny dogfish. For the assessed species, the model will use the stock assessment values and for non-assessed, the model will use the landings database.

For diet data, some requests are still pending from VIMS, but diet data for key species groups are not expected to change much. Squid is one group that may need to be reevaluated. The group discussed the method of assessing menhaden as part of a squid's diet given that squid take bites out of their prey. Genetics is one avenue where one could look at the portion of the unknown fish in a squid stomach based on the relative biomass of the fish group and scale by frequency of occurrence.

For birds, the plan is currently to include 3 bird groups (osprey, nearshore birds without osprey, and seabirds). Osprey is separated out because it has the most data. It currently has an estimated time series based on the Breeding Bird Survey index and Partners in Flight population estimates. The latter is regionally weighted average by route over 10 years that is centered on 2011. This number was then extrapolated out based on the index. Then, it was multiplied by a biomass of 1.68 kg to get a biomass time series. Osprey diet data for this model currently relies on 12 papers that are in or around the model region and uses nest number as sample size for weight.

After some discussion, the group agreed that for diet data, percent biomass was the best to report prey numbers, but if that's not available, studies that have percent number can be used, just weighted less than the percent by biomass.

Mammals were also explored for the full model. All mammal data are based on Kenney et al. 1997 and Smith et al. 2015 (except for Pinniped abundances which were derived from two other papers). Kenney et al. 1997 has seasonal abundances by region for the model area and estimated total biomass by region. Smith et al. 2015 has individual biomass estimates. For diet, the Smith paper is a meta-analysis of mammal diets based on genetics, stomach content analyses, and other literature that is all used to derive the average consumption of different mammalian groups. Based on these two papers, for each prey species, a single weighted average by biomass for percent consumed was derived for Odontocetes, Mysticetes, and Pinniped functional groups. The group also agreed that for the groups in the Smith et al. 2015 paper that combined several of the model functional groups, a single percent should still be derived and then the percentages should be apportioned based on the relative abundance of NWACS-Full species/functional groups.

### **VADER Updates**

The VADER model is now functional with updates from the last assessment process. This now includes multiple surveys, Dirichlet, and updated lognormal functions as well as built-in ADMB. Six input data series are required for each species – total fishery catch, and survey catch, age proportions for both fishery and survey, average individual weight-at-age, and age-specific predator diet. Additionally, data requirements include consumption/biomass estimates and biomass of "other food" in ecosystem.

The current focus is to explore bottom-up feedback explorations. The first step in this is to investigate the information available to inform the model of the effects in our system. To work in VADER, there needs to be estimable relationship between prey biomass and predator growth and/or mortality that can be quantified with the available data.

Initial investigations were conducted by J. Collie, J. McNamee, G. Nessler, and M. Wilberg. They explored the relationship between WAA of striped bass from the assessment and estimated biomass of menhaden from the assessment to attempt to identify density dependent growth and prey dependent growth. For WAA deviations over the years since 1985, there seems to be a temporal trend through time with higher variances earlier in the time series. A nonlinear function was used to identify density dependent growth evident in WAA for striped bass and this showed evidence of very weak density dependence. There was no evidence of prey-dependent growth in the analysis of striped bass WAA as a function of prey biomass. A second approach was used based on Rindorf et al. 2022. The differences are a simple calculation meant to reflect consumption is used, the analysis is broken into different age groups (2-4 and 5-15), and the weight deviations were analyzed relative to consumption. There was still no evidence of prey-dependent growth.

The same analysis was conducted using length-at-age (LAA) derived from an otolith dataset. Again, a nonlinear function was used to test for density dependence in LAA and this time, some evidence of density dependence was present. This trend was similar when menhaden biomass was the predictor variable. Per the Rindorf et al. method, the conclusion is that there is no evidence of prey-dependent growth. It is possible that more data is needed for both this and WAA analyses, although when more data is added to WAA, the younger age classes start to become obscured.

The possibility that more than just menhaden matters in determining prey-dependent growth (WAA) was explored too using all prey biomass used in the VADER model aggregated (menhaden, weakfish, and herring) as a predictor of striped bass WAA but there was still no evidence of prey dependent growth. Both methods of testing (Rindorf et al. and nls) showed the same result.

Two other bodies of work were investigated the deal with M impacts rather than growth: 1) Szalai (based on salmon and prey interactions), and Schiano (weight threshold below which M increases). After some discussion, the work group decided to move forward with the Schiano method, although the Schiano is seasonal, and this model won't be.

The group also discussed looping VADER into the diet data matrix for NWACS to more easily obtain diet data for this model.

**Next steps:** Move forward with the Schiano method.

### **WASPP Updates**

For the WASPP, there have been three main foci: 1) updating the model with the most recent assessment for striped bass and menhaden so the inputs are up to date and the consumption function and initial M can be tuned, and 2) running a 1985 forward simulation, and 3) consider using the model to generate test datasets for VADER. For the second objective, striped bass information is now available and there is a base run for menhaden. For the second objective, were waiting until the assessment is complete, but code has been written to compare assessment results with simulation.

**Next steps:** A. Schueller and K. Drew shared striped bass model outputs with G. Nessler. G. Nessler will update model with new assessments and run 1985+ simulation as well as model comparison forecasts described below. Will also generate test datasets for VADER, if desired and time allows for testing.

**Next steps:** J. McNamee and G. Nessler meet to discuss simulated data sets.

### **Model Comparison Criteria, Projections, and Reference Point Scenarios**

The selected model should have the ability to address management objectives. For each model, it may be worth comparing estimates of age-1+ biomass and exploitation rates with the BAM output (absolute estimates, relative scaled to each model's time series mean) and the current stock status (relative to the reference points). This may be possible for the VADER model, but the NWACS models are a bit more long-term reference points.

Models are compared based on whether they can inform management on the following metrics: the ability to sustain menhaden to provide for fisheries, the ability to sustain menhaden to provide for predators, the ability to provide stability for all types of fisheries, and the ability to minimize risk to sustainability due to changing environments.

The group discussed the merits of comparing models to past runs, and decided that Age1+, F, Z, and M2 outputs should be compared. Diagnostics for these comparison runs can go in their own report section and should be standardized by showing fits to certain indices. It should, however, be noted, that traditional diagnostics aren't comparable across these model types, so comparing them across models may be difficult for the NWACS models.

Estimates of biomass and exploitation rate from the ERP models are very similar to estimates from BAM in both scale and trend. They even have the same inputs (landings, indices, life history information), and in some cases output from BAM to parameterize ERP models. All the models generate MSY or MSY-proxy reference points. All the ERP models agreed with the BAM model that in 2017, overfishing was not occurring and (where BMSY was calculated) the stock was not overfished/ All reference points were calculated based on current ecosystem conditions (current productivity and/or predation mortality). VADER and NWACS are the only models that provide information on predator biomass and fishing mortality. Only NWACS models include "bottom-up" feedback to evaluate effects of menhaden biomass/F on predator population dynamics.

The group discussed which equilibrium scenarios to use. After some discussion the following were selected: 1) target biomass or F for predators/non-menhaden prey, 2) status quo biomass or F for non-menhaden prey, target biomass for predators, and 3) status quo biomass or F for predators /non-menhaden prey.

The group agreed that there is a need to do a workshop about spatial goals and objectives, but that that may not be possible for this assessment.

The projections for this assessment will be like the reference point scenarios, and the SAS will likely have to do projection. This group can't do short-term projections from the NWACS models and WASPP but maybe it could for the VADER. This may be important since this is what will be used for short-term management advice. The only wrinkle to using VADER for short-term projections is that a choice needs to be made for M.

### **ERP Stakeholder Exit Survey Discussion**

An ERP stakeholder exit survey was sent out to 100 people, which included members of the board, advisory panel, and other representatives from NGOs and citizen groups to gauge how well stakeholders understand ecosystem models. This survey was first sent out a year ago and there are plans to send it out again. Some of the questions included identification questions, questions about interest in fishery, length of

involvement, and ERP and Board meetings attended. The survey wraps up by asking how well you think the models can aid in the management of menhaden.

The initial survey had 21 responses, and most respondents were board members. The group would have liked to see more public “private citizens” respond to get a larger range of answers. Most of the people that this survey was sent to were identified based on their attendance at board and ERP meetings.

Overall, most of respondents seemed to have a generally accurate sense of what ERP models can do. One finding of note was that a few respondents thought that models can define a fishing season and spatial closures, which they can’t, so it may be worth trying to manage expectations there through outreach.

The group discussed potentially reaching out to SeaGrant or A. Scheld at VIMS to look at the survey and offer minor changes. The group also suggested sending this out after a major change to see if we are influencing their perception.

**Next steps:** Send out the same survey and identify another set of people that weren’t part of the first mailing list.

### **Report and Peer Review Framing Discussion**

The group discussed which parts to change from the last assessment. The consensus was to add EwE to BAM (sections 10 and 11 in the previous assessment) under assessment history, include ERP target and threshold reference points with recommendations, and modify the introduction to match what’s included in the models and update historical section. The models will also be written up in detail.

The group has yet to decide what will go in the main body of the report or appendix. The Commission does post the appendix with report.

The final report is due May 16<sup>th</sup>.

### **Review Next Steps & Timeline**

The ERP group will have an in-person meeting in March and monthly online meetings until then with a longer online meeting in January.

Tasking by model is as follows:

- **NWACS-Full**
  - Replace HMS group with bluefin tuna – **M. Dean & A. Buchheister**
    - Summarize diet data, provide biomass and catch time-series (apportion catch to NWACS-Full domain)
  - Add osprey as a new functional group – **J. Patel & A. Buchheister**
    - Subtract osprey from nearshore piscivorous birds
    - Add freshwater groups to diet import for osprey
    - Use average diet composition from studies focused on Atlantic coast
  - Keep existing marine mammal groups – **J. Patel & A. Buchheister**
    - Apportion published mammal diet composition groups based on relative abundance of NWACS-Full species/functional groups
  - Finalize other species assessment datasets

- Complete northern shrimp assessment update – **K. Drew**
    - Silver hake time-series – **J. Boucher**
    - Haddock & Yellowtail Flounder – **J. Patel**
- NWACS-Full & MICE
  - Update diet data matrices, update to match VADER format as well if time allows – **Diet Data WG (J. Patel)**
    - Incorporate individual studies and updated time-series data (including ME-NH and RI) into seasonal diet matrices
    - Weight by sample size and diet metrics (% diet in numbers gets a lower weight than % diet in weight)
- NWACS-MICE
  - Develop seasonal overlap parameters; explore MRIP data for predators (**D. Chagaris**) and monthly bait landings for menhaden (**K. Drew**)
    - Revise/calculate dispersion parameter calculations
      - Redo striped bass calculations to divide distance traveled by time-at-large for fish at large in 3-month or 6-month intervals – **D. Chagaris**
      - Find tagging information on bluefish, weakfish, and Atlantic herring – **K. Drew, M. Cieri**
  - Develop spatial biomass density estimates for anchovy from existing survey data (time permitting) – **M. Celestino, M. Dean**
  - Develop habitat preference functions from survey data using GAM – **M. Dean**
  - Update single-species reference points in terms of total biomass and percent change needed to reach target and threshold – **K. Drew**
- VADER
  - Conduct short-term projections using the same scenarios from the single-species update – **J. McNamee**
  - Use Schiano et al. method for bottom-up feedback – **J. McNamee**
- VADER/WASPP
  - Simulation datasets
    - Decide on scenarios for simulated datasets – **G. Nessler, J. McNamee**
    - Simulate data in WASPP and provide output compatible with VADER – **G. Nessler**
    - Run VADER with simulated dataset – **J. McNamee**
- NWACS-Full/MICE/VADER
  - Finalize ERP species inputs
    - Complete weakfish assessment update – **K. Drew**
    - Provide projected biomass and F for 2023 for bluefish and spiny dogfish – **K. Drew**
  - Conduct historical retrospective on final base run (compare output from 2025 benchmark to 2020 benchmark results for each model) – **D. Chagaris, A. Buchheister, J. McNamee**
  - Model comparisons
    - Provide fits to indices/time-series used and output time series of age-1+

biomass, exploitation (catch/biomass), Z (age-1+ biomass-weighted for age-structured models), and M2 for menhaden – **D. Chagaris, A. Buchheister, J. McNamee, A. Schueller**

- Plot and write-up comparisons – **K. Drew**
- All Models
  - Conduct long-term equilibrium projections under 3 scenarios and produce the corresponding rainbow plots – **D. Chagaris, A. Buchheister, J. McNamee, G. Nesslage**
    - Target biomass or F for predators/non-menhaden prey
    - Status quo biomass or F for non-menhaden prey, target biomass for predators
    - Status quo biomass or F for predators /non-menhaden prey
- Writing
  - Executive summary and TOR summary report – **M. Cieri, K. Drew, J. Patel**
  - Introduction (parts 1-8) – **S. Madsen** (with help for data sources)
  - Single species assessments and stock status – **K. Drew, S. Madsen**
  - Assessment update – **K. Drew, S. Madsen**
  - BAM update – **A. Schueller**
  - Model sections (don't have to follow exact outline from last time) - **D. Chagaris, A. Buchheister, J. McNamee, G. Nesslage**
  - Model comparisons – **K. Drew**
  - Discussion/synthesis of findings – **M. Cieri**
  - How Research and modeling recommendations from 2019 have been addressed – **M. Celestino**
  - Reference points (TBD after March meeting) – **M. Cieri, A. Schueller, K. Drew, J. Patel**

Tasking by individual is as follows:

#### A. Buchheister

- Replace HMS group with bluefin tuna for Full model
- Add osprey as a new functional group (subtract osprey from nearshore piscivorous birds, add freshwater groups to diet import for osprey, use average diet composition from studies focused on Atlantic coast)
- Keep existing marine mammal groups and apportion published mammal diet composition groups based on relative abundance of NWACS-Full species/functional groups
- Conduct historical retrospective on final base run (compare output from 2025 benchmark to 2020 benchmark results for each model)
- Provide fits to indices/time-series used and output time series of age-1+ biomass, exploitation (catch/biomass), Z (age-1+ biomass-weighted for age-structured models), and M2 for menhaden for model comparison
- Conduct long-term equilibrium projections under 3 scenarios and produce the corresponding rainbow plots
- Write NWACS-Full section of report including research and modeling recommendations

#### D. Chagaris

- Develop seasonal overlap parameters for MICE model; explore MRIP data for predators
- Redo striped bass calculations to divide distance traveled by time-at-large for fish at large in 3-month or 6-month intervals
- Conduct historical retrospective on final base run (compare output from 2025 benchmark to 2020 benchmark results for each model)
- Provide fits to indices/time-series used and output time series of age-1+ biomass, exploitation (catch/biomass), Z (age-1+ biomass-weighted for age-structured models), and M2 for menhaden for model comparison
- Conduct long-term equilibrium projections under 3 scenarios and produce the corresponding rainbow plots
- Write NWACS-MICE section of report including research and modeling recommendations (including a separate section for spatial research needs)

#### J. McNamee

- Conduct short-term projections using the same scenarios from the single-species update
- Use Schiano et al. method for bottom-up feedback
- Decide on scenarios for simulated datasets with G. Nessler
- Run VADER with simulated dataset
- Conduct historical retrospective on final base run (compare output from 2025 benchmark to 2020 benchmark results for each model)
- Provide fits to indices/time-series used and output time series of age-1+ biomass, exploitation (catch/biomass), Z (age-1+ biomass-weighted for age-structured models), and M2 for menhaden for model comparison
- Conduct long-term equilibrium projections under 3 scenarios and produce the corresponding rainbow plots
- Write VADER section of report including research and modeling recommendations

#### G. Nessler

- Decide on scenarios for simulated datasets with J. McNamee
- Conduct long-term equilibrium projections under 3 scenarios and produce the corresponding rainbow plots
- Write WASPP section of report

#### J. Boucher

- Finalize silver hake assessment time series

#### M. Dean

- Replace HMS group with bluefin tuna for NWACS-Full model (Summarize diet data, provide biomass and catch time-series; apportion catch to NWACS-Full domain)
- Develop spatial biomass density estimates for anchovy from existing survey data with M. Celestino for NWACS-MICE (time permitting)
- Develop habitat preference functions from survey data using GAM for NWACS-MICE



#### M. Celestino

- Develop spatial biomass density estimates for anchovy from existing survey data for NWACS-MICE (time permitting)
- Follow ups as listed in Zooplankton and Anchovy sections above.
- Write what the group has done to date to address research recommendations from previous assessment

#### A. Schueller

- Provide fits to indices/time-series used and output time series of age-1+ biomass, exploitation (catch/biomass), Z (age-1+ biomass-weighted for age-structured models), and M2 for menhaden for BAM model
- Write BAM update for report
- Write reference points part of report with staff (after March)

#### M. Cieri

- Find tagging information on bluefish, weakfish, and Atlantic herring for dispersion parameter calculations for the NWACS-MICE model
- Write executive summary and TOR summary report with staff
- Write discussion/synthesis of findings for report
- Write reference points part of report with staff (after March)

#### S. Madsen

- Write introduction (parts 1-8) for report
- Write assessment update section of report with K. Drew
- Write single species assessments and stock status section of report with K. Drew

#### K. Drew

- Complete northern shrimp assessment update for NWACS-Full model
- Develop seasonal overlap parameters for monthly bait landings for menhaden for the NWACS-MICE model
- Find tagging information on bluefish, weakfish, and Atlantic herring for dispersion parameter calculations for the NWACS-MICE model
- Update single-species reference points in terms of total biomass and percent change needed to reach target and threshold for the NWACS-MICE model
- Complete weakfish assessment update for the NWACS models and VADER
- Provide projected biomass and F for 2023 for bluefish and spiny dogfish for the NWACS models and VADER
- Plot model comparisons
- Write executive summary and TOR summary report with M. Cieri and J. Patel
- Write single species assessments and stock status section of report with S. Madsen

- Write assessment update section of report with S. Madsen
- Write model comparisons section of report
- Write reference points part of report with M. Cieri, A. Schueller, and J. Patel (after March)

#### J. Patel

- Add osprey as a new functional group (subtract osprey from nearshore piscivorous birds, add freshwater groups to diet import for osprey, use average diet composition from studies focused on Atlantic coast) for NWACS-Full model
- Keep existing marine mammal groups and apportion published mammal diet composition groups based on relative abundance of NWACS-Full species/functional groups
- Process haddock and yellowtail stock assessment output files for NWACS-Full model
- Update diet data matrices, update to match VADER format as well if time allows
- Write executive summary and TOR summary report with M. Cieri and K. Drew
- Write reference points part of report with M. Cieri, A. Schueller, and K. Drew (after March)