Virtual Assessment for the Description of Ecosystem Responses (VADER) Multispecies Statistical Catch-at-Age Model Description and Output

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SEDAR 102 WP-08: Virtual Assessment for the Description of Ecosystem Responses (VADER) Multispecies Statistical Catch-at-Age Model Description and Output

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1 VADER DESCRIPTION AND CONFIGURATION

1.1 Treatment of Indices & Input Data

The multispecies statistical catch-at-age model (hereafter referred to as Virtual Assessment for the Description of Ecosystem Responses, or VADER) used for this study is constructed around the six key ERP species: Atlantic menhaden, striped bass, bluefish, weakfish, Atlantic herring, and spiny dogfish. Some of the earliest multispecies work done was to connect virtual population analysis models together with predation functions (Helgason and Gislason 1979; Gislason and Helgason 1985; Sparre 1991; Livingston and Jurado-Molina 2000). This modeling approach can be helpful in a complex fisheries modeling environment because the strong assumptions on certain parameters aid in the estimation of the remaining parameters. From this more deterministic modeling technique, statistical approaches were then developed using either age-based, or length-based statistical models. These statistical approaches are more comparable to some of the single-species assessment methods that are now used and have the added benefit of allowing the estimation of uncertainty around the estimated population parameters (Lewy and Vinther 2004; Van Kirk et al. 2010; Curti et al. 2013). The goal of these multispecies approaches is to create more realistic information on which to base fisheries management practices (Gislason 1999; Moustahfid et al. 2009). The VADER model adopts the more progressive statistical approach for its modeling methodology and works from the strong foundational work of Curti et al. (2013).

The species were selected based on a review of important predator diet information, the availability of age-structured data for the species, and knowledge of the migratory patterns of the species. The migratory pattern aspect allows the confounding factor of temporal and spatial overlap to be mitigated to some degree in that the species selected all have similar seasonal migratory patterns. Atlantic herring and spiny dogfish do not overlap as significantly as the other species though, an important consideration when interpreting the output from this assessment model that does not explicitly account for spatio-temporal overlap in predators and their prey.

In the model, striped bass, bluefish, and spiny dogfish are top predators of both Atlantic menhaden and Atlantic herring, and both Atlantic menhaden and Atlantic herring are strictly forage species. Weakfish serves as both a predator of Atlantic menhaden and Atlantic herring, as well as a prey species for striped bass, bluefish, and spiny dogfish. Cannibalism by any species is not accounted for in the model. All symbols and likelihood components for the multispecies model are indicated in Table 1.

As in Curti et al. (2013), there are six types of input data needed for each species in the model: total fishing catch in weight, fishery-independent cpue indices, age proportions for both fishery and fishery-independent survey catches, average weight-at-age by year, and age-specific predator diet information. All six species examined in this research currently have single-species statistical catch-at-age models that are used for management. Unless otherwise noted, all data inputs used were taken directly from recent stock assessment documents and from direct communication with the stock assessment researchers that work on these species. Of note, the modeling structure is intentionally simplified relative to the existing single species models. The simplifications are noted in the narrative below.

For all species, total fishery catches represent landings plus dead discards from both the commercial and recreational fisheries in weight (thousands of metric tons). Assumptions about discard mortality for this study were consistent with assumptions from the reviewed assessments for each species. This model uses a single fleet for each species for removals.

Annual catch-at-age in millions of fish for the entire time series were used to calculate age proportions from the catch. The information used to construct age-specific catch from the recreational fishery is generally believed to be more reliable in numbers than it is in weight. Again, for all species used in this study, this time series of information was obtained from the most recent stock assessment. In contrast to the single-species assessments for these species, which usually model recreational and commercial catches as separate fleets with separately estimated selectivities, all removals were modeled as a single fleet for each species with one selectivity pattern for each fleet. This is not a poor assumption for the species selected for this project as each species has one predominant fishery and gear type that prosecutes the fishery (i.e. striped bass is predominately a rod and reel fishery when considering both the commercial and recreational fishery, while menhaden is predominately a commercial purse seine fishery). Therefore, there is most likely one predominant selectivity that governs the age structure of the removals.

In contrast to the work done by Curti et al. (2013), the species used in this study have a diverse series of surveys used to estimate stock abundance through time with differing time-series and consisting of different gear types. To accommodate the multiple surveys while keeping the model structure as simple and computationally efficient as possible, only a subset of the various surveys for each species was used. This subset was determined by the ASMFC Stock Assessment Subcommittee's for these species, as the most appropriate indices of abundance. The survey selection is consistent with the previous peer reviewed version of this model. Data for these indices included the number per tow in each year, uncertainty around the index values, and age composition data, all taken from the stock assessment documents and most recent assessment information. For each species, one young-of-the-year survey was selected along with two adult indices when available. The case of Atlantic menhaden used all the same indices as used in the benchmark assessment as this is a species with high focus for this work, and Atlantic herring and spiny dogfish only used two and one index respectively, with no young-of-the-year surveys. The surveys used by species are listed in Table 2.

Average individual weight-at-age is needed in the model to convert from numbers to biomass units. The weight-at-age information is introduced in the model as a matrix, so the information varies not only by age, but by time as well. This is an important consideration as several of the species used in the model have significant shifts in weight-at-age through time.

For the trophic interactions of the multispecies runs, data are needed on species food habits, consumption estimates, and information on biomass throughout the ecosystem. These data include consumption-to-biomass estimates for each species (consumption:biomass or C/B), an estimate of the biomass of "other food" in the ecosystem, and average predator diet information.

Age-specific C/B ratios were obtained by the methodology from Garrison et al. (2010) as developed for the Multispecies Virtual Population Analysis (MSVPA) model developed for a similar suite of species. Food consumption rates in fish can vary strongly, particularly between seasons as a function of changing temperatures and metabolic demands. To account for these processes, a modified consumption model was implemented using the Elliot & Persson (1978) evacuation rate approach. These data were updated through 2025 as these species-specific data were available. As noted above, the C/B ratios were developed for the MSVPA with more resolution (i.e. daily C/B ratios by season), but these were aggregated across the whole year in this case to create a matrix of age-specific C/B ratios by species.

As assumed in Curti et al. (2013) and based on previous work (Sparre 1980; Tsou and Collie 2001), a constant, time-invariant total ecosystem biomass was assumed, permitting the biomass of available other food to vary annually, in other words, the total ecosystem biomass is time-invariant, but the biomass of the modeled components of the ecosystem (i.e. the six species selected for the model) can vary annually. Prior studies have confirmed that the total biomass in large marine ecosystems can remain relatively stationary through time (Link et al. 2008; Auster and Link 2009; Byron and Link 2010). There were no direct measurements found to develop what this overall biomass estimate should be, so as a starting point, a total biomass estimate from the MSVPA was used. To supplement and support the MSVPA derived total ecosystem biomass value, information derived from an Atlantic Coast Ecopath model was also investigated (Buchheister et al. 2017). Both values were close in magnitude. Testing with the multispecies assessment model indicated that performance was best for the value derived from the Ecopath model (94,800,000 mt) and therefore this value was the one selected for the base case run of the model.

Stomach-content data were obtained from two main sources. The NEFSC Food Web Dynamics Program, which has systematically sampled predator food habits since 1973 (Link and Almeida 2000), was one source. These food-habits data are structured by predator species and length, because prey lengths and ages are not routinely measured. A subset of the database is structured by both predator and prey lengths, which was used for part of the following analyses. In addition to the NEFSC Food Web Dynamics Program data, the North East Area Monitoring and Assessment Program (NEAMAP) and Chesapeake Bay Multispecies Monitoring and Assessment Program (CHESMAP) also collect stomach-content data under similar protocols to the NEFSC program. These data were used to supplement the stomach-content data and have an added benefit of increasing the coastal area covered for this dataset (NEAMAP and CHESMAP sample areas further inshore than the NEFSC sampling program). Both datasets have attributes (e.g. the NEFSC data has a long time-series and the NEAMAP data is more inshore so is better able to acquire many of the species used in this study) and drawbacks (e.g. the NEFSC data are from further offshore and the NEAMAP data timeseries is shorter than the NEFSC dataset) but taken together they offer a fairly comprehensive account of diet compositions for the modeled speciesfeeding habits of. These length-based data for predator and prey from stomach-content information are converted to weight through the use of length-weight relationships as collected in Wigley et al. (2003). For this update, additional diet data sources were aggregated into a comprehensive diet database. This is described in the main assessment report and was used to update the diet data for VADER. Age-specific predator diet habits, input to the model as proportion by weight for each age class, were averaged over 4-year periods to reduce the inherent variability in the dataset as well as to reduce the amount of missing data and increase the sample size being used for any year (Van Kirk et al. 2010), while still capturing the temporal trends. There were cases where data did not exist for a specific species, age class, year bin combination, and in those cases, additional aggregation was done so that some empirical information was used in the diet data for VADER.

Parameterization

The model used in this study follows a traditional statistical catch-at-age structure as used for many single-species stock assessments. These traditional catch-at-age equations are then linked and interact through a set of trophic interactions. All model equations will not be presented in this document as they follow the equations as developed in Quinn and Deriso (1999), but some of the main equations used will be described for the catch-at-age portions of the model, and the trophic calculations will be presented in detail.

Progression of year class abundance is implemented by the equation:

$$N_{i,a+1,t+1} = N_{i,a,t}e^{-Z_{i,a,t}} \tag{1}$$

where N = species abundance in millions of fish, Z = total mortality, i = species, a = age class, and t = year. As there are plus groups for each species used in this project, the final age class modeled (i.e. when a = amax) needed to be adjusted using the equation:

$$N_{i,a,t+1} = N_{i,a-1,t}e^{-Z_{i,a-1,t}} + N_{i,a,t}e^{-Z_{i,a,t}} \tag{2}$$

Fishery catch-at-age is calculated using Baranov's catch equation:

$$C_{i,a,t} = \frac{F_{i,a,t}}{Z_{i,a,t}}N_{i,a,t}(1 - e^{-Z_{i,a,t}}) \tag{3}$$

where C = fishery catch (recreational, commercial, and dead discards for each) and F = fishing mortality. Fishing mortality-at-age (assuming separable fishing mortality) follows the equation:

$$F_{i,a,t} = s_{i,a}F_{i,t} \tag{4}$$

where s = fishery selectivity. Fishery-independent survey catch ($FIC_{i,t}$) was related to species-specific abundances through the following equation:

$$FIC_{i,t} = q_i r_{i,a} N_{i,t} e^{-\frac{m}{12}Z_{i,t}} \tag{5}$$

This mathematical configuration assumes an age and time-invariant catchability (q_i), age-specific survey selectivity coefficients ($r_{i,a}$), and also accounts for the time of year during which the survey was conducted (m) so total mortality can be applied to the index appropriately. Species-specific catchabilities (q_i) were calculated from the entire time series deviations between the model predicted absolute abundance and model predicted relative abundance (Walters and Ludwig 1994).

Finally, age-specific fishery and survey selectivity coefficients were estimated for each species for all age classes through the choice of either a logistic or double logistic selectivity function, depending on the choices made by the single-species stock assessment teams. Young-of-the-year surveys assumed age specific selectivity, with selection being 1 for the first age class and 0 for all other age classes. This formulation departs from previous work (Curti et al. 2013) and was reconfigured to better simulate what is believed to be the selectivities for the species examined in this study by allowing doming in the selectivity-at-age where appropriate, and is also consistent with the selectivity shape used in the approved single-species assessments for these species. The four-parameter double logistic equation used for both the fishery selectivity and the fishery-independent survey selectivity was:

$$Sel_{x,i,a} = \left(\frac{1}{1 + e^{-(a-\alpha_1)/\beta_1}}\right)\left(1 - \frac{1}{1 + e^{-(a-\alpha_2)/\beta_2}}\right) \tag{6}$$

And the two-parameter logistic equation used was:

$$Sel_{x,i,a} = \left(\frac{1}{1 + e^{-(a-\alpha_1)/\beta_1}}\right) \tag{7}$$

where $Sel_{x,i,a}$ is the species-specific selectivity at age, x = fleet or survey, i = species, a = age class, and α_{1or2} and $\beta_{1\mathrm{or}2}$ are the ascending or descending inflection point and slope parameters, respecitvely.

Predation mortality (M2) is a sub component of total mortality (Z), but more specifically a sub-component of the natural mortality component in Z. The simplest equation to describe this is:

$$Z = F + \ (M1 + M2) \tag{8}$$

where Z is total mortality, F is fishing mortality, M1 is residual natural mortality (natural mortality attributed to non-predation factors, and M2 is predation mortality from the species included in the model (Helgason and Gislason 1979). It is important to remember that species in the model that are considered predators only (e.g. striped bass, bluefish, and spiny dogfish) will only have M1 operating on their population, while species that are considered prey only (e.g. menhaden, Atlantic herring, and weakfish) will have both M1 andM2 operating on their population. A special case for striped bass was developed for this model and is described below.

The M1 value is an important uncertainty in the model. For this project, M1 was parameterized by looking back at the MSVPA information for these same species and determining the portion of natural mortality that was occurring (based on that analysis) from predation. The assumed total natural mortality from the single-species benchmark assessments for the prey species in this model were prorated downward based on this proportion. An additional analysis was undertaken during the 2019 ERP assessment process to look at both the objective function values under different M1 selections and the difference from the output of biomass from VADER and the single-species biomass outputs. Both methods were used to gage the best choices for this parameter in the model, which was determined to be a 20% decrease from the single species total natural mortality assumptions for the prey species.

There is a recursive property in this formulation of M2 in that the biomass data element needed for calculating M2 has total mortality as an element of its calculation, therefore an approximation is used. To approximate the instantaneous rate of M2, the biomass of the predator and the prey items are assumed to come from the beginning of each year, prior to being subject to these various forms of mortality (Van Kirk et al. 2010). The equation for the instantaneous M2 is:

$$M2_{i,a,t} = \frac{1}{N_{i,a,t}W_{i,a,t}} \sum_{j} \sum_{b} CB_{j,b} B_{j,b,t} \frac{\phi_{i,a,j,b,t}}{\phi_{j,b,t}} \tag{9}$$

where $N_{i,a,t}$ = mean number of prey i at age a and at time t, $W_{i,a,t}$ = the weight of prey i at age a at time t, $CB_{j,b}$ = the age-specific (b) consumption-to-biomass ratio for predator species j, $B_{j,b,t}$ = age-specific biomass of predator j, and $\frac{\phi_{i,a,j,b,t}}{\phi_{j,b,t}}$ = the proportion of prey i at age a in all food available to predator j at age b in year t, which is assumed equal to the proportion of food within the stomach of predator j at age b in year t composed of prey i at age a (Lewy and Vinther 2004). Under this formulation, a type-II functional response is assumed where the predator satiates at a high prey biomass, and the satiation reaches an asymptote (doesn't decline at higher densities) (Sparre 1980).

The next steps for the predation calculation are to develop the various components of the above equation. Availability (ϕ) of prey i at age a to predator j at age b is the product of a suitability coefficient ν of prey i at age a to predator j at age b and the prey's age and year specific biomass ($B_{i,a,t}$):

$$\phi_{i,a,j,b,t} = \tilde{\nu}_{i,a,j,b,t} B_{i,a,t} \tag{10.1}$$

There are also species included in the model that are not explicitly modeled via the statistical catch-at-age equations in the formulation. These species interactions are described through the equation:

$$\phi_{other,t} = \tilde{\nu}_{other,t} B_{other,t} \tag{10.2}$$

where B_{other} refers to the biomass of the non-modeled prey with the modeled prey biomasses subtracted out (Sparre 1980):

$$B_{other,t} = B_{eco} - \sum_{i} \sum_{a} B_{i,a,t} \tag{10.3}$$

which is added to the summation of the explicitly modeled prey biomasses after being multiplied by their suitability coefficients. The parameter B_{eco} is the total weight of all of the species in the ecosystem. This component is constant over time and across species and age. The inclusion of this component allows all of the modeled species to be estimated relative to other prey items in the ecosystem. This can lead to efficiencies as the predator species in this project have a diverse diet, modeling all of the potential prey items (including other fish as well as invertebrates) is a large and time intensive task, and adequate data to make inferences about the population dynamics do not exist for all prey species.

The suitability (ν) for each prey item at age is calculated as the product of the size and species-specific preferences of each predator by age class. Here, the size preference and the species preference are assumed independent from each other. The equation for this calculation is:

$$\nu_{i,a,j,b} = \rho_{i,j} g_{i,a,j,b} \tag{10.4}$$

where $\rho_{i,j}$ is the vulnerability of prey species i to predator species j, and $g_{i,a,j,b}$ is the size-preference function of prey i at age a to predator j at age b. The vulnerability, ρ, incorporates all differences in food selection, for example behavioral and spatial differences, that are not attributable to size differences (Gislason and Helgason 1985). As mentioned previously, one of the factors in selecting the species used in this study is that they have significant spatial overlap during the year, making this a reasonable assumption in this case. Species preference is relative to a reference prey species, referred to as "other food" or all of the prey species not explicitly modeled. The vulnerability (ρ) and suitability parameters (ν) are set to one for this "other food" category. The main assumption for using these equations are that the size and the species are the main drivers controlling whether a predator species eats that particular food item and that the other food category is of the preferred size for the predator.

Suitability coefficients (ν) are scaled across all prey species and ages to facilitate comparisons between estimated available prey biomass and food-habits data such that the suitabilities for a predator age class sum to one (Sparre 1980):

$$\tilde{\nu}_{i,a,j,b,t} = \frac{\nu_{i,a,j,b,t}}{\sum_i \sum_a \nu_{i,a,j,b,t} + \nu_{other}} \tag{10.5}$$

The scaling of the suitability coefficients creates a one-to-one direct correspondence between the stomach-contents of the predator and the relative suitable prey biomass.

Size preference ($g_{i,a,j,b}$) of a predator is modeled as a lognormal function of the ratio between predator and prey weights as shown in the following equation:

$$g_{i,a,j,b} = exp\left[-\frac{1}{2\sigma_j^2}\left(ln\frac{w_{j,b}}{w_{i,a}} - \eta_j\right)^2\right] \tag{10.6}$$

where σ and η are size-preference parameters specific to each predator, and w is the age-specific weight of the prey (i) and predator (j) from a specific food habit sample. Another important assumption implicit in this equation is that there is a single size-preference coefficient for a predator for all prey of a given size regardless of species, but g still must differentiate between species and ages given that each prey species has a unique length and weight for a given age (Andersen and Ursin 1977, Helgason and Gislason 1979). As implemented in Curti et al. (2013), the size-preference coefficients are estimated external to the model from empirical food-habit data analysis and are input as known mean and variance parameters.

In this model formulation, the total food available to a given predator in the ecosystem may include species beyond those that are explicitly modeled. One of the benefits of this formulation, as opposed to other formulations that necessitate only using species explicitly modeled in the mathematical framework, is the inclusion of a non-modeled prey component identified as an overarching ecosystem biomass value (B_{eco}).

The final calculation needed to determine the available prey to a predator is defined by:

$$\phi_{j,b,t} = \phi_{other} + \sum_i \sum_a \phi_{i,a,j,b,t} \tag{10.7}$$

This is the divisor from equation 9 and completes the steps needed to calculate predation mortality.

Given this formulation, most of the parameters can be derived by interrogating different data sources, which is preferable to making numerous assumptions. The number and weights-at-age for all modeled species can be collected from both fishery-independent and dependent sources. These are standard sources of information for many stock assessments. The more unique data elements in a multispecies modeling framework are gathered from diet databases, which are now being routinely (and more systematically) collected in various state, academic, and federal fishery-independent surveys. The diet information (food habits) is derived from stomach-content analysis of the species collected, and the parameters described above that are developed from these data are the consumption-to-biomass ratios, the preferred prey items, and preferred prey size. The most notable parameter described above that is not estimated from data is the total ecosystem biomass (non-modeled prey items). Additionally, some of the elements above are not internally estimated in the model, namely the size-preference parameters, but this element is estimated from actual data before being input in to the model, and this input value is modeled with estimates of uncertainty.

One of the attributes of this multispecies model is the statistical estimation process. The estimated model parameters include age-specific abundances in the first year $N_{i, a, t=1}$ (Yr1), annual recruitment in subsequent years $N_{i, a=1, t+1}$ (Age1), annual fully recruited fishing mortality rates $F_{i, t}$, age-specific fishery ($s_{i,a}$) and survey ($r_{i,a}$) selectivity coefficients, and the vulnerability parameters, $\rho_{i,j}$. Due to the estimation of the population in the first year for all species, the model does not depend on an assumption of equilibrium. Single-species statistical models for all species used in this study provide initial estimates of abundance. For all subsequent years, recruitment is estimated as a mean parameter plus a vector of annual deviation parameters that must sum to zero.

All model parameters were estimated with maximum likelihood techniques, programmed in AD Model Builder (ADMB ver 13.2 2012). In addition to the likelihood approach, penalized likelihoods and bounded parameters are also used to supplement some of the statistical estimation. The estimation of model parameters allows the assumption that fishery catch, survey catch and food habits data are subject to observation error, which is a critically important extension of this modeling approach relative to previous multispecies formulations, in particular the virtual population analysis approaches that have been used for multispecies modeling (Helgason and Gislason 1979; Gislason and Helgason 1985; Sparre 1991; Livingston and Jurado-Molina 2000; Tsou and Collie 2001; Garrison et al. 2010).

The total likelihood comprises five components as well as three penalty functions (Table 3). The total fishery and total survey catch were assumed to be lognormally distributed. The catch-at-age proportions for both the fishery and the survey information, and predator food habits (average proportions by weight) were assumed to follow a Dirichlet multinomial distribution. These are common error distribution assumptions for fisheries stock assessments in general and are also the assumptions used for the single-species assessments for most species modeled in this project.

Weightings for the lognormal components were species-specific. The CVs were set such that the uncertainty associated with recreational harvest and discard levels were accounted for and were higher for species with higher recreational catch (i.e. striped bass and bluefish). Additionally, a higher CV was assumed for the survey component due to the interannual variability observed in those datasets, in each case the CV was set consistent with the choice made by the single-species assessment working group. Interannual variability results from variation in availability of the species to the survey gear, changes in survey methodology through time, or the fact that surveys may be taking place in spatially discrete areas at different times of year, therefore it is not necessarily the case that these observed changes in abundance are real, but rather are due to changes in catchability (Pincin et al. 2014). Therefore, it is appropriate to allow some significant statistical inference when predicting the various indices in the model.

For the Dirichlet multinomial function, sample sizes came from two sources depending on the species. In cases where the total samples collected for the composition data were known, those data were used (menhaden and herring). For the other species, the effective sample size as used in the single-species assessments for the various composition data were used. Some adjustments were made to all of these data based on model performance.

Penalty functions were imposed on initial abundances, annual recruitment and age-specific biomasses (Table 3). These penalties were imposed to keep parameter estimates from collapsing to zero or producing estimates that were not biologically feasible. The penalty imposed on initial abundances, $Yr1_{pen}$, was calculated with two methods. The first method prevents age-specific abundances from deviating substantially from those predicted by exponential decay across ages, assuming a total mortality equal to the age-specific average. The second approach penalized deviation from the initial input abundance (Yr1) values taken from the benchmark models for all species. This second approach was used for the final model configuration. The penalty imposed on annual recruitment, Rpen, prevents the coefficient of variation for the log recruitment of any species from becoming greater than a pre-defined threshold value (Rthresh). The threshold selected was based on the recruitment and its associated variability from the benchmark models for the species in this study. The penalty imposed on age-specific biomasses, Bpen, prevents any age-specific biomass from falling below a pre-defined threshold (Bthresh) to prevent the calculations from crashing due to the biomass dropping to zero. The weights for each of these penalties and their corresponding threshold values were selected iteratively.

1.2 Results

Diagnostics

Model fits are compared to the observed data as a diagnostic test to show the internal performance of the model. Additionally, the output is also compared with a run that had the trophic calculations turned off (representing multiple simplified single-species assessments). Several diagnostic plots are presented to verify that the model is fitting observed data reasonably well.

The predicted total annual fishery catch closely followed observed catches with only minor differences for all species (Figure

1). Some lack of fit to the catch data for weakfish and spiny dogfish is evident.

The fits were less exact for the total annual survey catch, but the multispecies output did follow temporal trends in the observed time series fairly well (Figures 2 - 7).

For both fishery (Figure 8 – Figure 13) and survey (not shown for brevity) age proportions, the predicted trends captured much of the interannual variability seen in the observed dataset. The model does a good job at capturing the age proportions for the catch, with Atlantic herring and spiny dogfish being two species where it does not fit as well in a relative sense. The model does poorly in some instances at predicting the survey age proportions. The model predicts more older menhaden than are observed in the population for the NAD and SAD surveys. The model overpredicts the youngest ages of striped bass in the MRIP CPUE survey and the fit declines as the ages increase for the CT LISTS survey. The model does not fit the youngest age class for bluefish in either survey used in the model. The fit to the Albatross and Bigelow surveys for Atlantic herring is poor for the youngest age class. Finally, the fit to the Albatross survey for spiny dogfish decreases with increasing age.

Food-habits data were fit without much statistical weight on the input data. This was done to acknowledge the fact that the food habit data are limited for the species examined in this project. Even with this low weight, there was good correspondence between the input values and predicted data, with the multispecies statistical model predicting smoother curves of increasing proportion of diet for prey items in the food habits of the predators (not shown for brevity).

Contributions of the different data elements to the objective function are presented in Table 4. This information indicates that the fishery catch age composition data contributes the most to the objective function value, followed by the fishery-independent survey age-composition, and then the total fishery-independent survey fit. There is also some contribution from the penalty functions, namely from the initial year penalty function, but these are minor contributions relative to the rest of the information. By species, menhaden followed by striped bass, contribute the most to the objective function value.

Population Estimates

Population abundance produced by the multispecies statistical model follows trends that are in line with the understanding from our current benchmark assessments for these species (Figures 14 and 15). For menhaden, the population begins at a high level in the early part of the time series and then declines until the mid-1990s. The population then increases and oscillates up and down without trend until the end of the time series. The VADER model predicts a lower decline and then a slower recovery than does the single species model. Striped bass begins at a low population abundance. Striped bass population abundance then climbs until the late 1990s and has been variable around this higher level until the end of the time series, with a decreasing trend. The VADER model predicts an earlier increase in population numbers than the single species model does, but has a consistent decline in the most recent years.

Estimated predation mortality (M2) varied between the prey species in this study, by prey age, and through time. One example for menhaden is shown in Figure 16. Three predators in this study are predators only, and are not prey nor do they undergo cannibalism (in the model), so time and age varying predation mortality is only being estimated for menhaden, weakfish, and Atlantic herring. Predation mortality is highest for age-0 menhaden (called age-1 in the model) and decreases sequentially as age increases. Predation mortality increases for menhaden beginning in the early 1990s, peaking in the mid-2000s, and declines towards the end of the time series. At its peak, the predation mortality on age-0 menhaden is greater than 2 in several years. The terminal year estimate of M2 for menhaden is near 1 for age-0 and is 0.5 on average for all other age classes.

Dynamic M1 for striped bass

The main critique from the 2019 peer review of the VADER model was that it lacked bottom up feedback. The concept of bottom-up feedback in ecosystem models emphasizes how prey abundance can influence predator growth and mortality. To look into the empirical information to determine if this relationship could be modeled, explorations focused on identifying whether relationships exist between prey availability and predator growth (e.g., weight-at-age or length-at-age metrics). This exploratory work is recounted in detail in working paper SEDAR 102-WP-09.

The one area that seemed to have a statistical effect was in the striped bass length at age dataset. Schiano et al (2025) developed a simulation model which had bottom up feedback functionality between menhaden and striped bass which had a connection to length-at-age for striped bass. These calculations were built into VADER and are presented as an exploration of this type of effect in the VADER model explicitly for striped bass.

As seen in Figure 17, having the dynamic M1 calculation turned on creates a very different abundance trajectory than that seen in the single species model. It produces large amount of fish earlier in the time series. This is an interesting exploration, but more work is needed on exactly which age classes this calculation should occur on (not all age classes were represented in the data used for the calculation constants), and this is still deterministic in that the calculation is working directly off of the empirical weight-at-age input into the model. Future work can focus on trying to build a function that can dynamically calculate this effect, perhaps working from the parameters developed in the SEDAR 102-WP-09 working paper.

1.3 Conclusion

The VADER model continues to demonstrate strong potential as a viable multispecies assessment framework, producing results that align well with those of established single-species stock assessment models. Its performance reinforces its value as a tool for capturing ecosystem dynamics in fisheries management. A more comprehensive set of model outputs will be presented at the upcoming review meeting to further evaluate its robustness and utility. Notably, the addition of a dynamic natural mortality (M1) component for striped bass represents a meaningful advancement in the model's evolution. Continued development of this dynamic M1 framework is recommended to further refine its ecological realism and responsiveness to prey-predator interactions.

1.4 References

Helgason, T., and H. Gislason. 1979. VPA-analysis with special interaction due to predation. ICES CM 10.

Gislason, H. 1999. Single and multispecies reference points for Baltic fish stocks. ICES Journal of Marine Science 56(5): 571-583.

_______, and T. Helgason. 1985. Species interaction in assessment of fish stocks with special application to the North Sea. Dana 5(2): 1-44.

Sparre, P. 1980. A goal function of fisheries (legion analysis). ICES CM 1980/G:40.

_______. 1991. Introduction to multispecies virtual population analysis. In ICES Marine Science Symposium (Vol. 193, pp. 12-21).

Livingston, P.A., and J. Jurado-Molina. 2000. A multispecies virtual population analysis of the eastern Bering Sea. ICES Journal of Marine Sciences 57(2): 294-299.

Lewy, P., and M. Vinther. 2004. A stochastic age-length-structured multispecies model applied to North Sea stocks. ICES CM 2004/FF:19.

Van Kirk, K.F., T.J. Quinn, and J.S. Collie. 2010. A multispecies age-structured assessment model for the Gulf of Alaska. Canadian Journal of Fisheries and Aquatic Sciences 67(7): 1135- 1148.

Curti, K. L., J. S. Collie, C. M. Legault, and J. S. Link. 2013. Evaluating the performance of a multispecies statistical catch-at-age model. Canadian Journal of Fisheries and Aquatic Sciences 70(3): 470-484.

Moustahfid, H., J. S. Link, W. J. Overholtz, and M. C. Tyrrell. 2009b. The advantage of explicitly incorporating predation mortality into age-structured stock assessment models: an application for Atlantic mackerel. ICES Journal of Marine Science 66(3): 445-454.

Garrison, L. P., and J. S. Link. 2000. Dietary guild structure of the fish community in the Northeast United States continental shelf ecosystem. Marine Ecology Progress Series 202:231–240.

_______, J. S. Link, D. P. Kilduff, M. D. Cieri, B. Muffley, D. S. Vaughan, A. Sharov, B. Mahmoudi, and R. J. Latour. 2010. An expansion of the MSVPA approach for quantifying predator – prey interactions in exploited fish communities. ICES Journal of Marine Science 67:856–870.

Elliot, J.M, and Persson, L. 1978. The estimation of daily rates of food consumption for fish. Journal of Animal Ecology 47: 977-990.

Quinn, T.J., and R.B. Deriso.1999. Quantitative fish dynamics. Oxford University Press.

Tsou, T.S., and J.S. Collie. 2001. Estimating predation mortality in the Georges Bank fish community. Canadian Journal of Fisheries and Aquatic Sciences 58(5): 908-922.

Auster, P.J., and J.S. Link. 2009. Compensation and recovery of feeding guilds in a northwest Atlantic shelf fish community. Marine Ecology Progress Series 382: 163-172.

Byron, C.J., and J. Link. 2010. Stability in the feeding ecology of four demersal fish predators in the US Northeast Shelf Large Marine Ecosystem. Marine Ecology Progress Series 406:239-250.

Link, J. S. 2010. Adding rigor to ecological network models by evaluating a set of pre-balance diagnostics: A plea for PREBAL. Ecological Modelling 221(12):1580–1591.

_______, and F. P. Almeida. 2000. An overview and history of the food web dynamics program of the Northeast Fisheries Science Center, Woods Hole, Massachusetts.

_______, W. Overholtz, J. O'Reilly, J. Green, D. Dow, D. Palka, C. Legault, J. Vitaliano, V. Guida, M. Fogarty, J. Brodziak, L. Methratta, W. Stockhausen, L. Col, and C. Griswold. 2008. The Northeast U.S. continental shelf Energy Modeling and Analysis exercise (EMAX): Ecological network model development and basic ecosystem metrics. Journal of Marine Systems 74: 453–474. Elsevier B.V.

Buchheister, A., and R. J. Latour. 2015. Diets and trophic guild structure of a diverse fish assemblage in Chesapeake Bay, USA. Journal of Fish Biology 86:967–992.

_______, T. J. Miller, and E. D. Houde. 2017a. Evaluating ecosystem-based reference points for Atlantic Menhaden. Marine and Coastal Fisheries 9:457–478.

Wigley, S.E., H.M. McBride, and N.J. McHugh. 2003. Length-weight relationships for 74 fish species collected during NEFSC research vessel bottom trawl surveys, 1992-9. NOAA Tech Memo NMFS NE 171; 26 p.

Walters, C.J., and D. Ludwig. 1994. Calculation of Bayes posterior probability distributions for key population parameters. Canadian Journal of Fisheries and Aquatic Sciences 51(3): 713- 722.

Andersen, K.P., and E. Ursin. 1977. A multispecies extension to the Beverton and Holt theory of fishing, with accounts of phosphorus circulation and primary production. Meddr. Danm. Fisk. Havunders. (N.S.) 7: 319-435.

Pincin, J. S., M. J. Wilberg, L. Harris, and A. Willey. 2014. Trends in relative abundance of fishes in Maryland's coastal bays during 1972-2009. Estuaries and Coasts 37: 791-800.

Schiano, S., Nesslage, G., Collie, J., Costa, N. L. L., Drew, K., Latour, R. J., McNamee, J., Schueller, A., & Wilberg, M. J. (2025). Trends in Atlantic striped bass growth in the mid-Atlantic, USA. Transactions of the American Fisheries Society, 154(3), 262–277. https://doi.org/10.1093/tafs/vnaf006

Tables

Table 1. Symbols and terms used in the VADER model formulation.

Symbol	Definition
i	Species (used to designate prey species)
a	Age class (used to designate prey species age)

j	Predator species
b	Predator species age
t	Year
k	Fishery independent index
n	Number of indices
l	Vector of species-specific surveys
m	Month
$N_{i,a,t}$	January 1 abundance-at-age (10^6 fish)
$Z_{i,a,t}$	Instantaneous total mortality-at-age per year
$C_{i,a,t}$	Fishery catch-at-age (commercial and recreational harvest and dead discards, 10^6 fish)
$F_{i,a,t}$	Instantaneous fishing mortality-at-age per year
$s_{i,a}$	Fishery selectivity-at-age
$FIC_{i,a,t}$	Fishery independent catch (CPUE)
q_i	Fishery independent catchability
$r_{i,a}$	Fishery independent survey selectivity-at-age
$Sel_{x,i}$	Selectivity generated by logistic or double logistic functions
α_1, α_2, β_1, β_2	Logistic and double logistic ascending or descending limb parameters
$M_{i,a,t}$	Instantaneous natural mortality
$M0_{i,a}$	Residual natural mortality (time invariant)
$M2_{i,a,t}$	Instantaneous natural mortality due to predation
$W_{i,a,t}$	Average annual species-specific weight-at-age
$CB_{j,b}$	Consumption to biomass ratio (time invariant)
$B_{i,b,t}$	Biomass-at-age (10^6 kg)
$\phi_{i,a,j,b,t}$	Available prey biomass (10^6 kg)
$\tilde{\nu}_{i,a,j,b,t}$	Scaled prey suitability
$\nu_{i,a,j,b}$	Prey suitability
B_{eco}	Total ecosystem biomass (10^6 kg)
$\rho_{i,j}$	Prey species preference

Table 1 (Continued). Symbols and terms used in the VADER model formulation

Symbol	Definition
$g_{i,a,j,b}$	Predator size preference
η_j	Preferred predator to prey weight ratio
$B_{other,t}$	Total biomass of other food
$P_{i,a,t}$	Proportion-at-age
I	Dataset
LL_I	Log likelihood of dataset I
D_I	Objective function weighting for dataset I
TC	Total fishery catch (10^3 mt)
TS	Total survey catch (CPUE)
CP	Fishery catch age proportions
SP	Survey catch age proportions
FH	Food habits proportions
Pen_i	Total likelihood penalty for each species
Pwt_p	Objective function weighting for penalty p
Yr1pen	Year 1 abundance penalty
Rpen	Recruitment penalty
Bpen	Biomass penalty
Yr1	Year 1 abundance-at-age
Rthresh	Threshold value for the CV of log recruitment variability
Bthresh	Threshold value for age-specific biomass
Age1	Recruitment

Table 2. Indices used for each species for the Base and Alternate runs of the VADER model.

Bluefish		
	Used in Base run	Used in sensitivity run
NEFSC Albatross		X
MRIP CPUE	X	X
NC PSIGNS/P915	X	
Composite YOY	X	
Weakfish		
	Used in Base run	Used in sensitivity run
MRIP CPUE	X	
DE 30’ Trawl	X	
NJ Ocean Trawl		X (offshore)
Composite YOY	X	
NC PSIGNS/P915		X (inshore)
Atlantic Herring		
	Used in Base run	Used in sensitivity run
Shrimp Survey		X
NEFSC Fall Albatross (1985-2008)	X	
NEFSC Fall Bigelow (2009-2017)	X	
Striped bass		
	Used in Base run	Used in sensitivity run
Composite YOY	X	
MD Spawning Stock		X
MRIP CPUE	X	
CT LISTS	X	
Atlantic menhaden		
	Used in Base run	Used in sensitivity run
SAD	X	X
MAD	X	X
NAD	X	X
Composite YOY	X	X
Spiny Dogfish		
	Used in Base run	Used in sensitivity run
NMFS Trawl (converted to Albatross units)	X	X

Table 3. Components of the VADER model likelihood function by assumed distributions and including penalty functions for the VADER model. Small constants (10^{-3}) are added to the lognormal and multinomial calculations to keep the calculations from terminating if they reach zero.

Equation	Definition
$\mathrm{LL}_{\mathrm{Total}} = \mathrm{LL}_{\mathrm{TC}} + \mathrm{LL}_{\mathrm{TS}} + \mathrm{LL}_{\mathrm{CP}} + \mathrm{LL}_{\mathrm{SP}} + \mathrm{LL}_{\mathrm{FH}} + \sum_{i} Pen_i$	Total log likelihood
$LL_I = \sum_{t,i} \frac{1}{2} \ast ln\left(\frac{\hat{I} + 10^{-4}}{I + 10^{-4}}\right)^{ln(cv^2)}$	Lognormal distribution component
$LL_I = -\Gamma(nsamp \ast e^{dpar}) - \sum_{t,i,a} \Gamma\left((nsamp \ast I) + \left((nsamp \ast e^{dpar}) \ast \hat{I}\right)\right) + \sum_{t,i,a} \Gamma\left((nsamp \ast e^{dpar}) \ast \hat{I}\right)$	Dirichlet multinomial distribution component
$Pen_i = Pwt_{Yr1_i} \ast Yr1pen_i + Pwt_{Age1_i} \ast Rpen_i + Pwt_{B_i} \ast Bpen_i$	Total penalty
$Yr1pen_i = \sum_{a} (N_{i,a,t=1} - Yr1_{i,a})^2$	Year 1 penalty
$Rpen_i = 0.01 \ast (CV(N_{i,a=1,t}) - Rthresh_i)^2$	Recruitment penalty. Applied when the CV > *Rthresh*
$Bpen_i = \sum_{a,t} 0.01 \ast (B_{i,a,t} - Bthresh_i)^2$	Biomass penalty. Applied when *B* < *Bthresh*

Table 4. Contributions of the various components by species to the VADER model objective function value

Likelihood component	Menhaden	Striped Bass	Bluefish	Weakfish	Atlantic Herring	Spiny Dogfish
Total fishery catch	2.5	7.0	5.4	51.8	1.5	0.1
Total survey catch	28.2 27.2 22.7 35.5	70.4 111.6 150.6	26.2 33.7 182.1	63.8 82.3 80.7	16.1 24.3	81.4
Fishery catch age proportions	4,658.2	8,795.9	3,971.7	3,068.2	1,205.1	9,990.4
Survey catch age proportions	1,724.1 588.0 3,534.1	2,312.6 507.8	1,982.2 730.1	1,504.9 1,061.0	658.7 255.6	1,029.9
Food habits	0	793.7	480.3	534.2	0	1,192.3
Year 1 penalty	8.4e-005	9.8	0.2	27.2	6.0e-005	1.3
Recruitment penalty	0	0	0	0	0.05	0
Biomass penalty	0	0	0	0	0	0
Total Likelihood Value	10,620.6	12,749.6	7,411.7	6,446.9	2,161.3	12,294.0

Figures

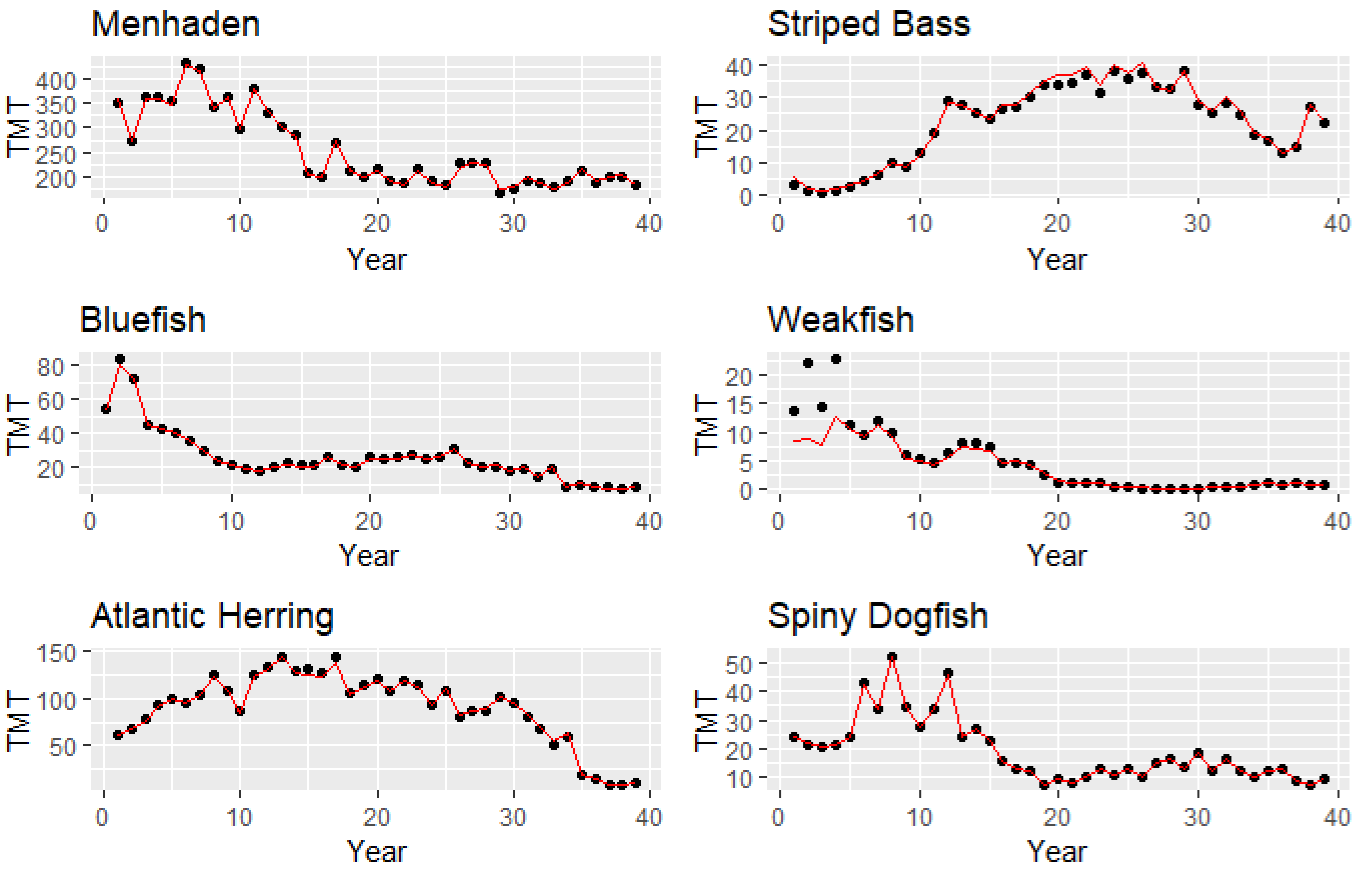

Figure 1. Observed (circles) and predicted multispecies (solid red line) total annual catch from the VADER model.

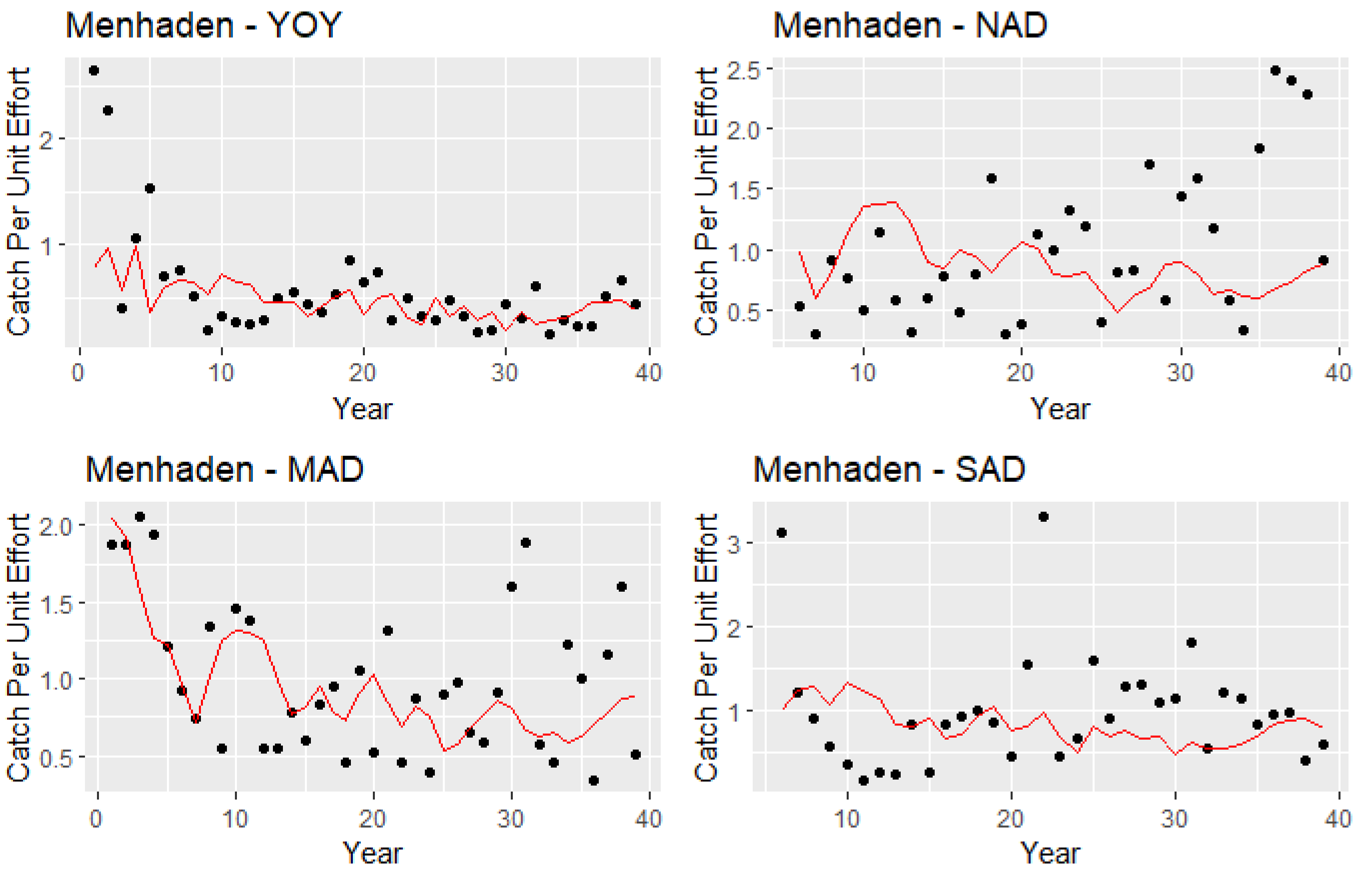

Figure 2. Observed (circles) and predicted multispecies (solid red line) indices of abundance for Atlantic menhaden from the VADER model.

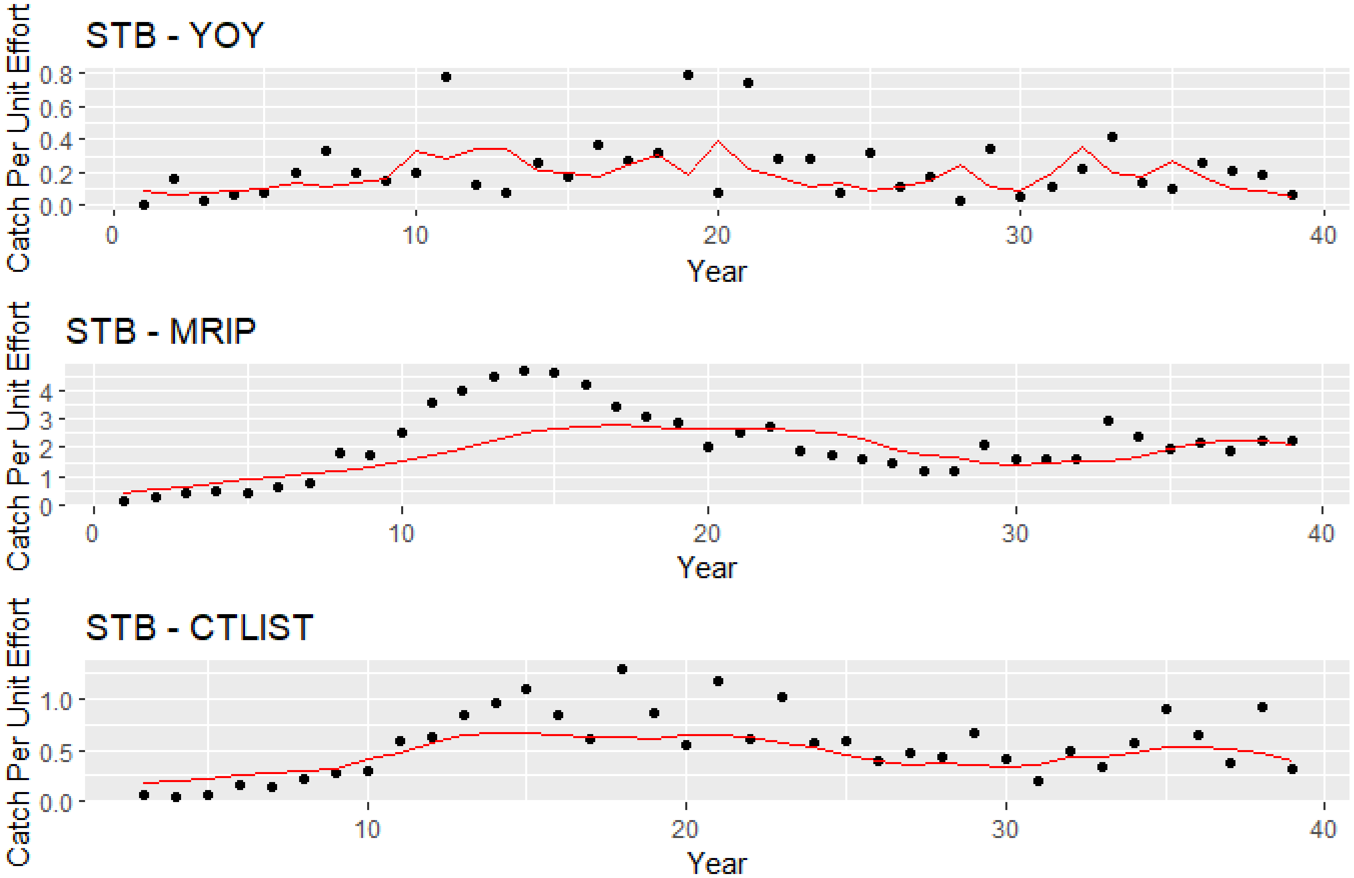

Figure 3. Observed (circles) and predicted multispecies (solid red line) indices of abundance for Atlantic striped bass from the VADER model.

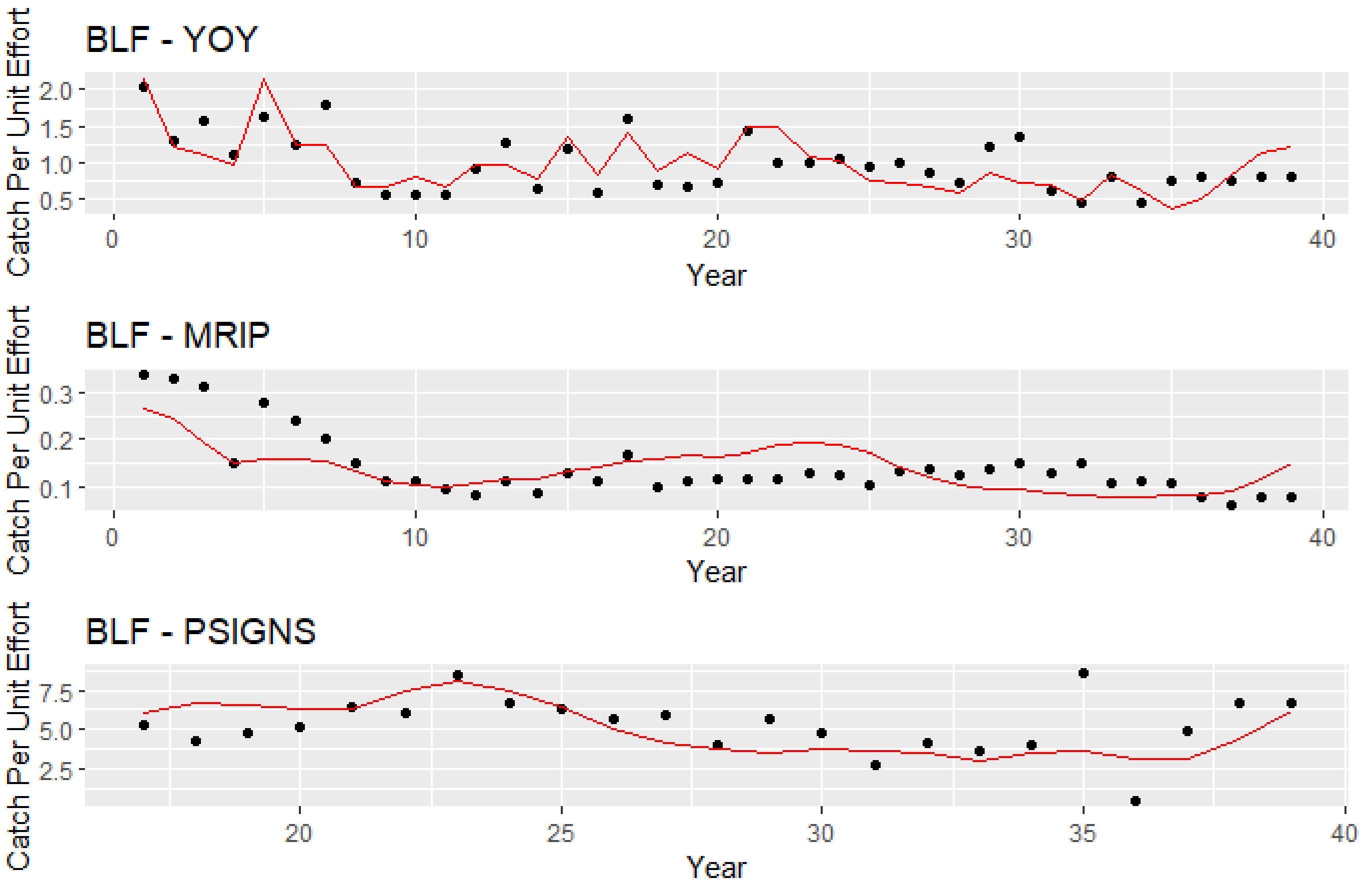

Figure 4. Observed (circles) and predicted multispecies (solid red line) indices of abundance for bluefish from the VADER model.

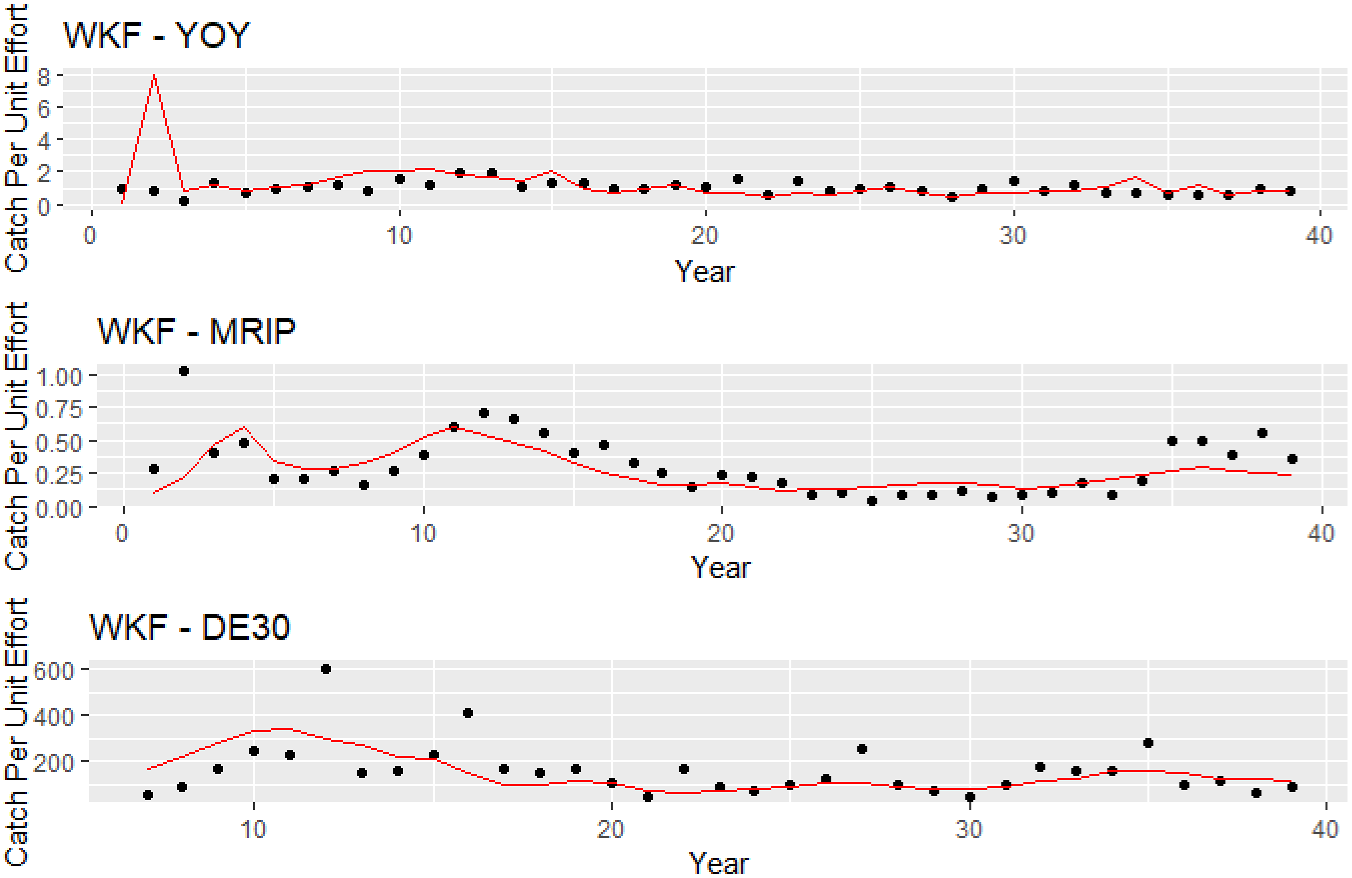

Figure 5. Observed (circles) and predicted multispecies (solid red line) indices of abundance for weakfish from the VADER model.

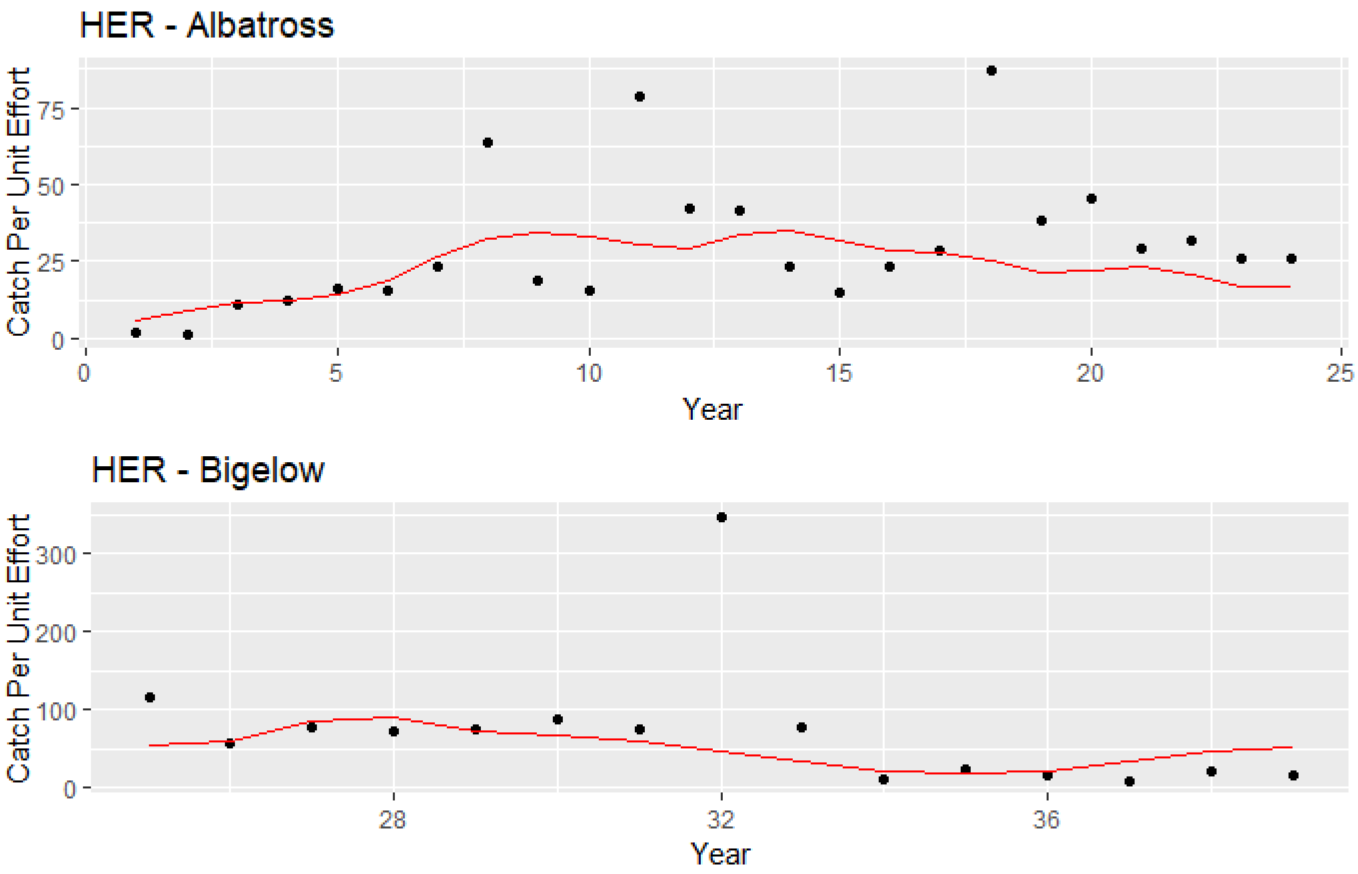

Figure 6. Observed (circles) and predicted multispecies (solid red line) indices of abundance for Atlantic herring from the VADER model.

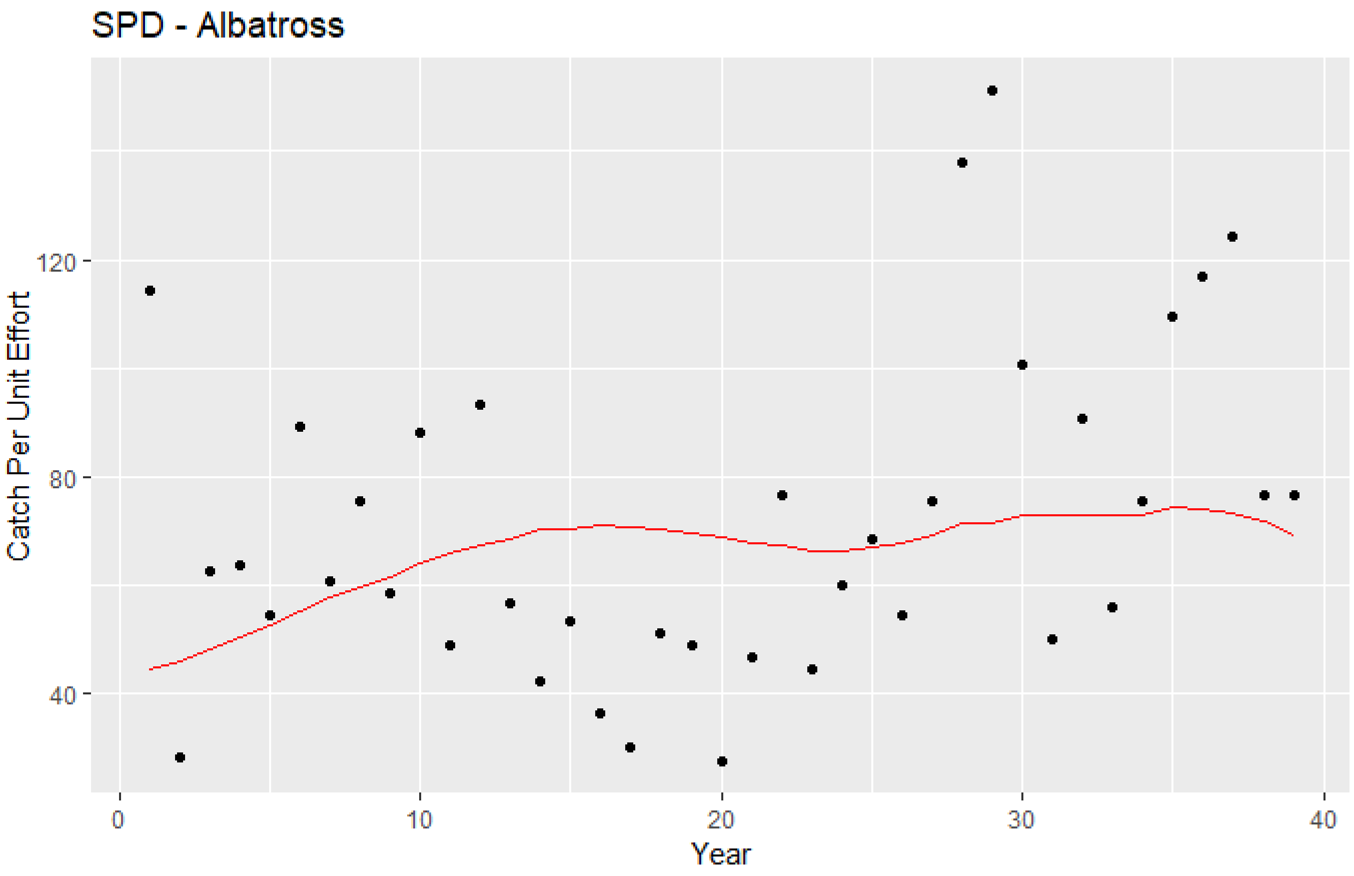

Figure 7. Observed (circles) and predicted multispecies (solid red line) indices of abundance for spiny dogfish from the VADER model.

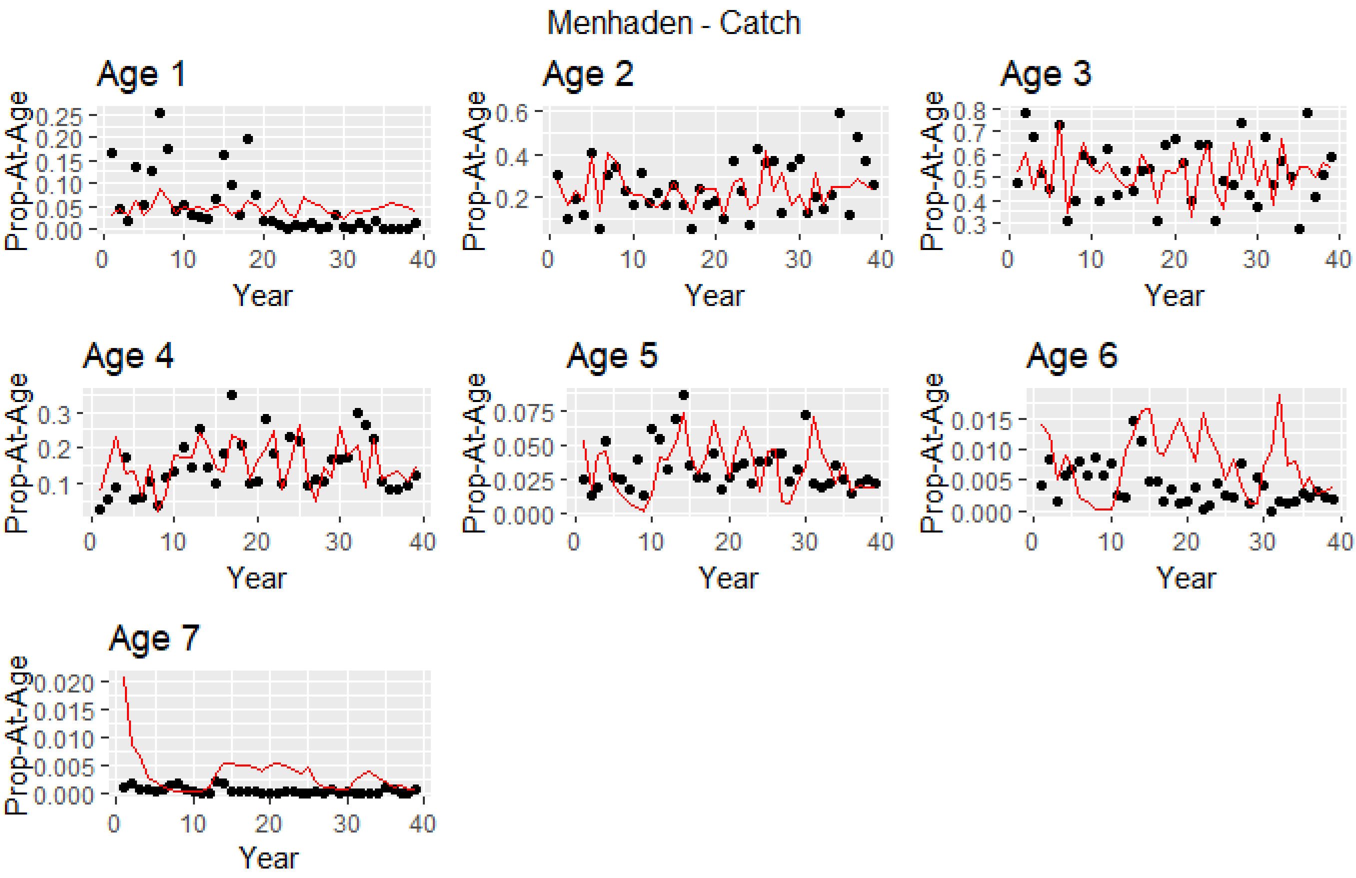

Figure 8. Observed (circles) and predicted multispecies (solid red line) total catch age proportions for Atlantic menhaden from the VADER model.

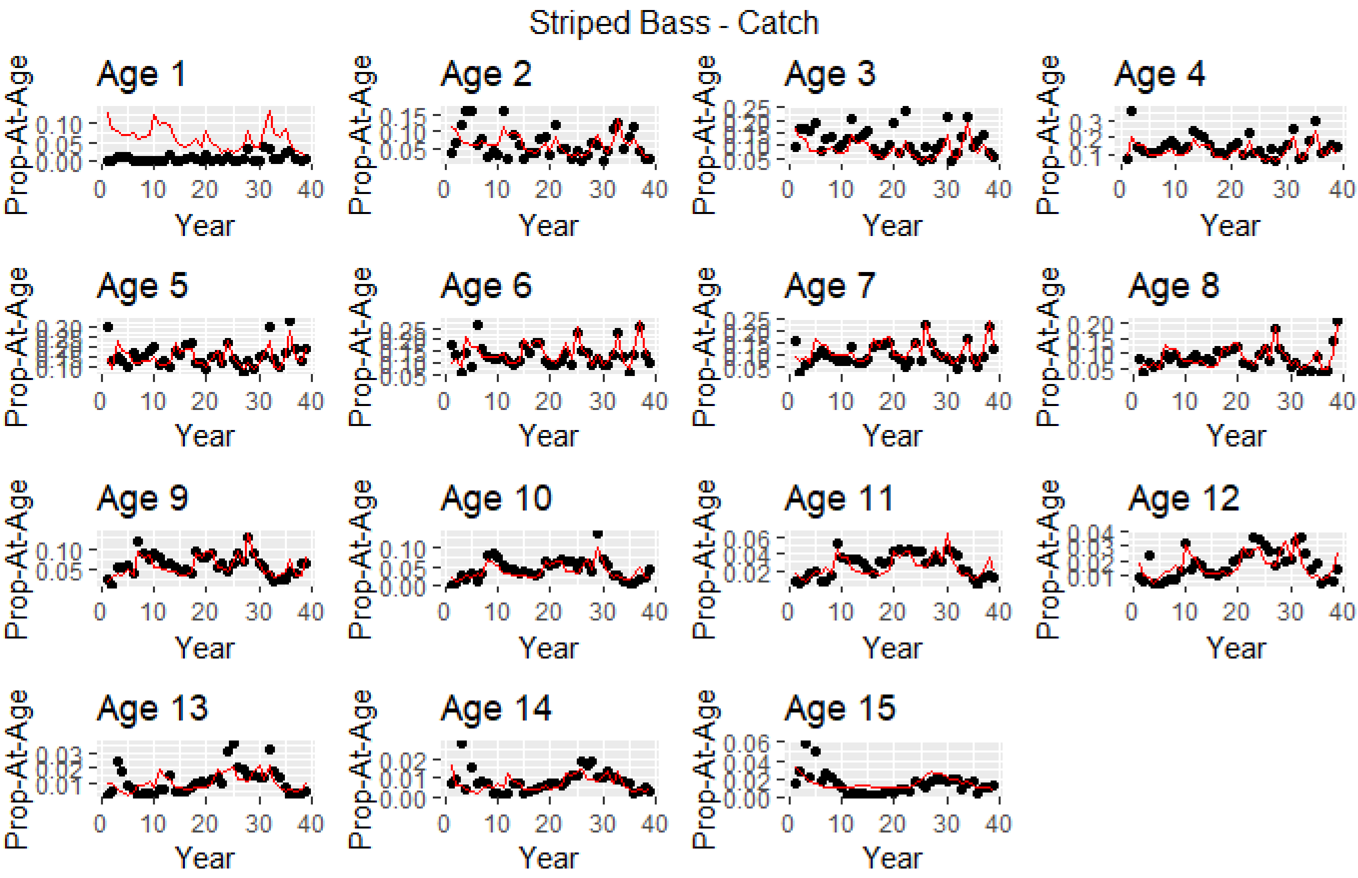

Figure 9. Observed (circles) and predicted multispecies (solid red line) total catch age proportions for Atlantic striped bass from the VADER model.

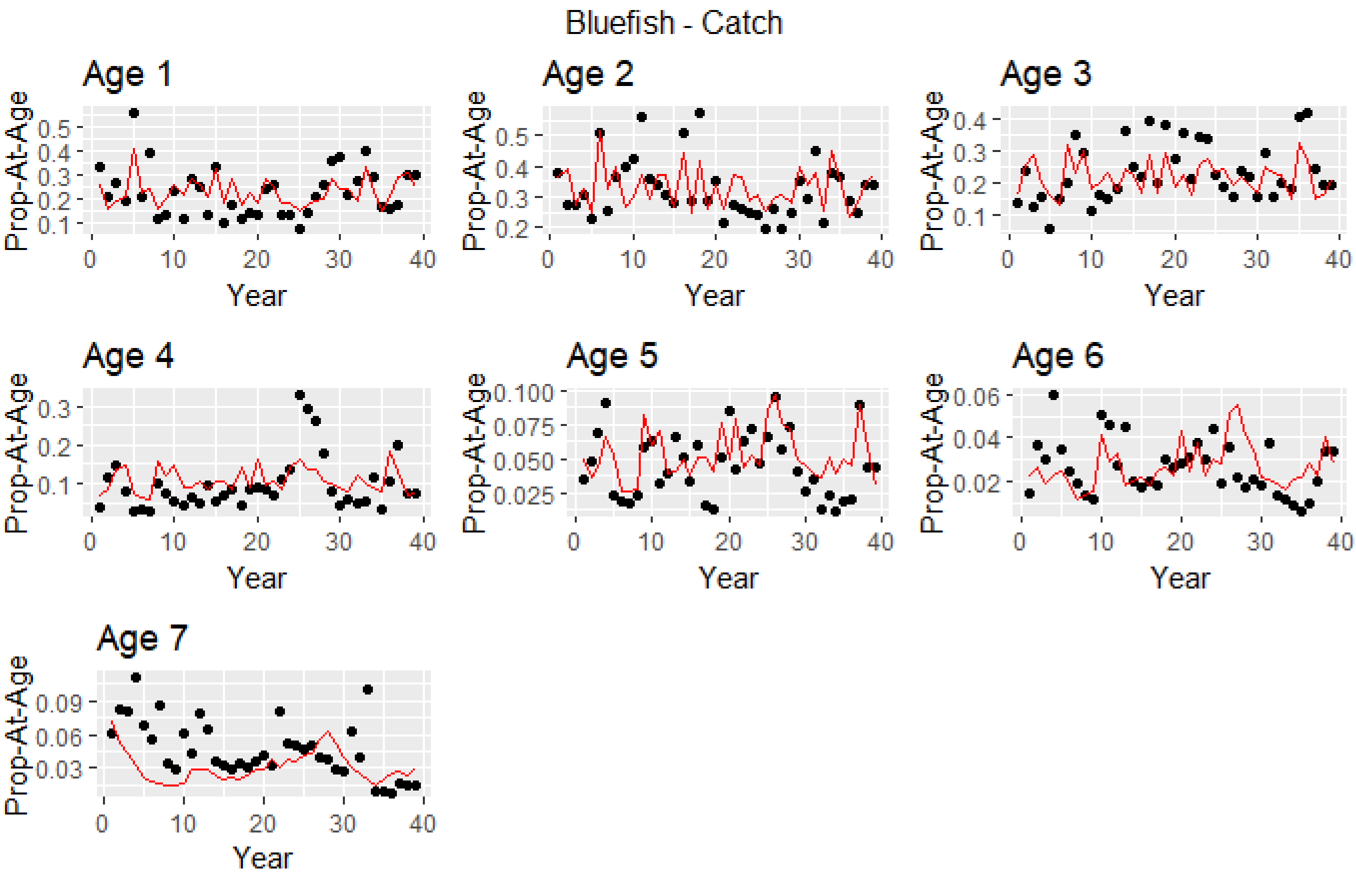

Figure 10. Observed (circles) and predicted multispecies (solid red line) total catch age proportions for bluefish from the VADER model.

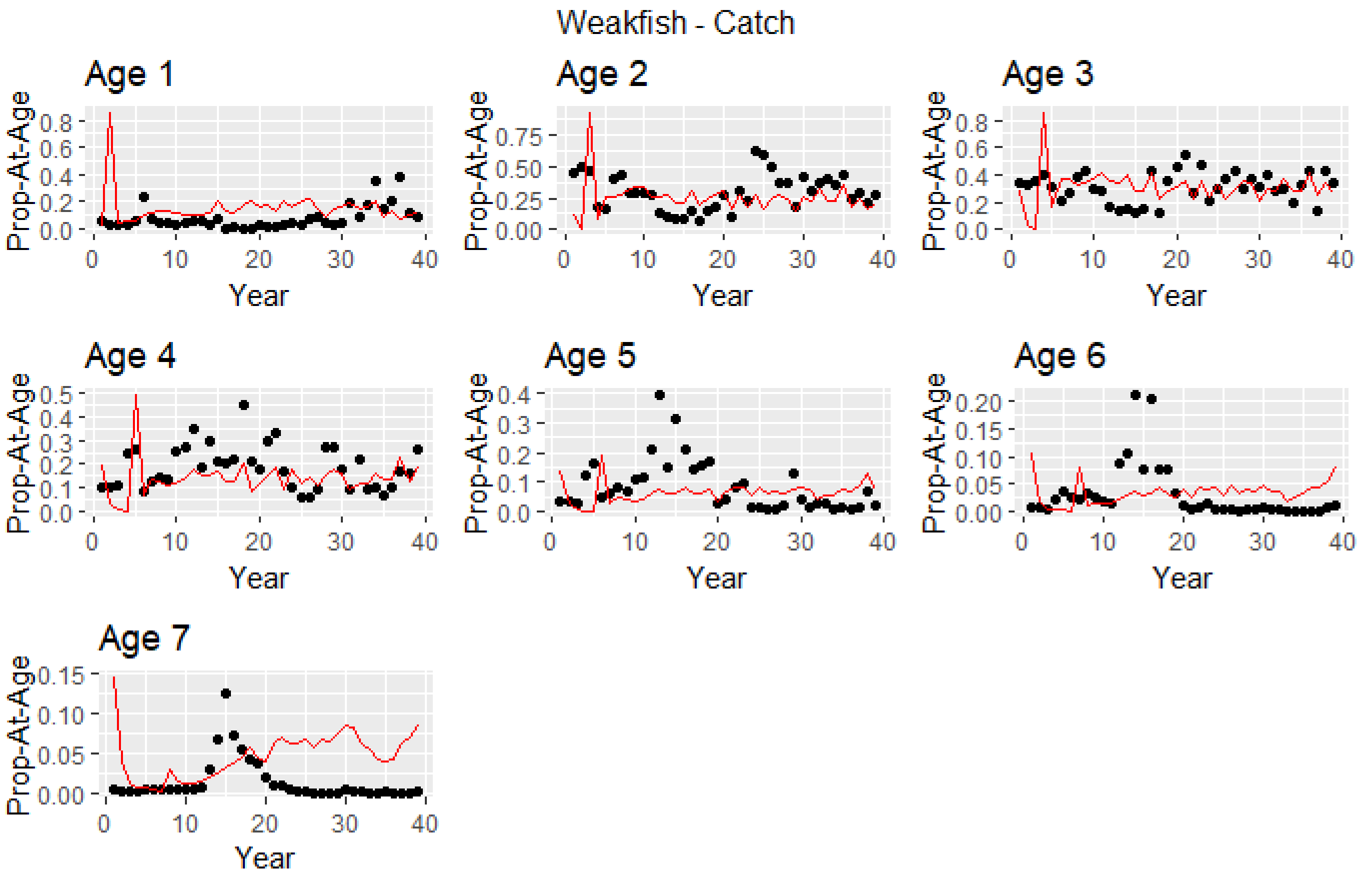

Figure 11. Observed (circles) and predicted multispecies (solid red line) total catch age proportions for weakfish from the VADER model.

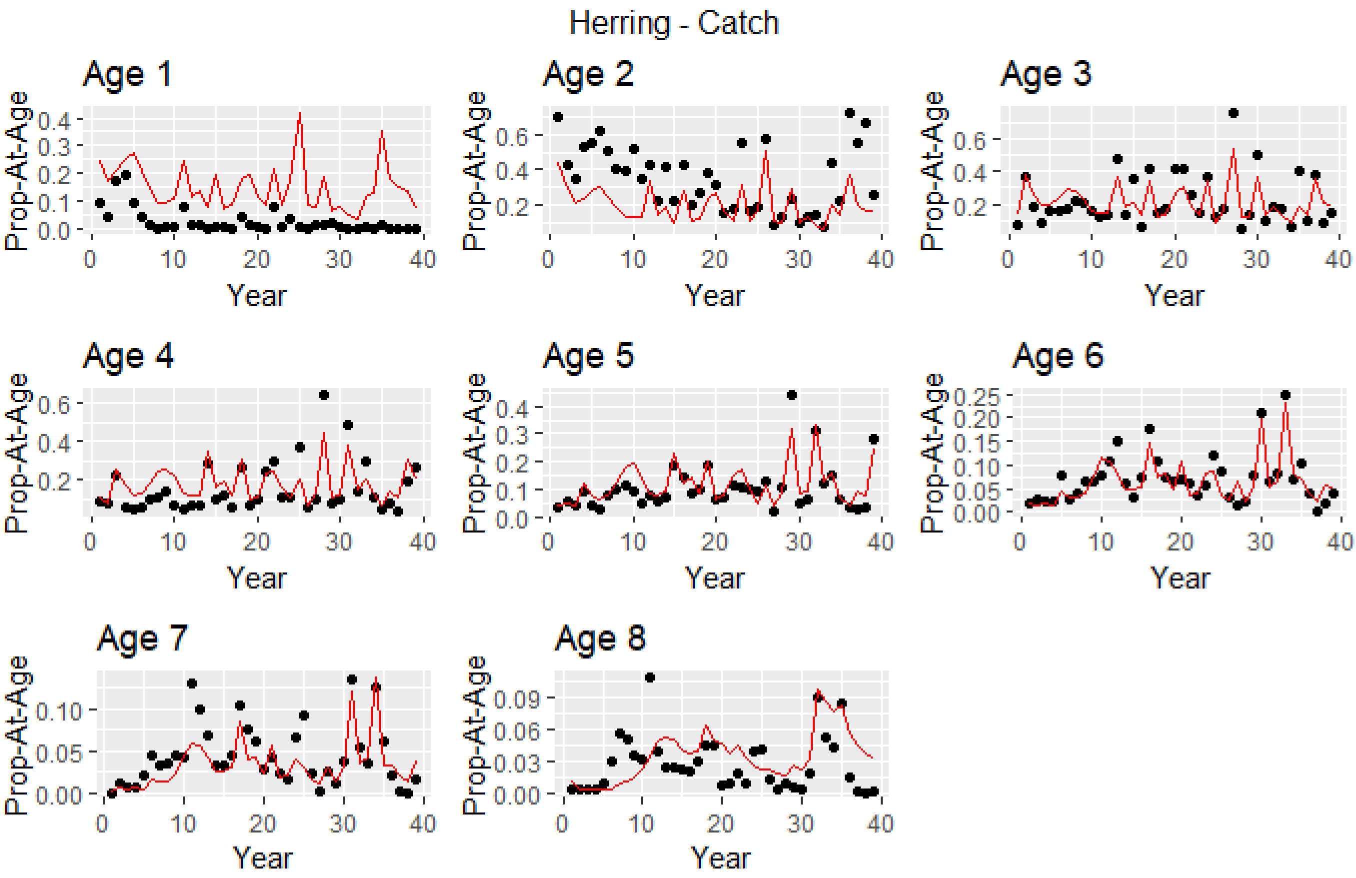

Figure 12. Observed (circles) and predicted multispecies (solid red line) total catch age proportions for Atlantic herring from the VADER model.

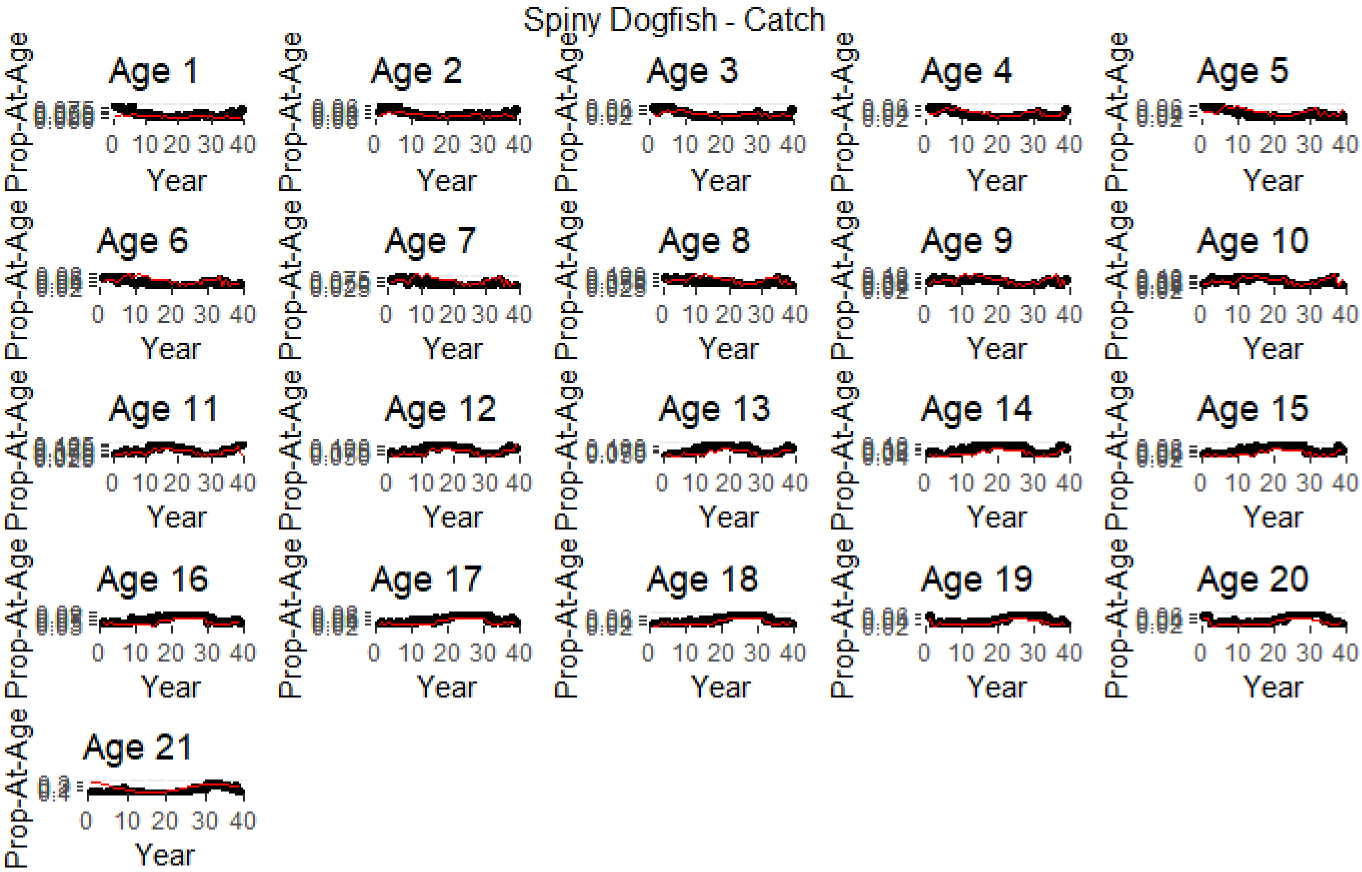

Figure 13. Observed (circles) and predicted multispecies (solid red line) total catch age proportions for spiny dogfish from the VADER model.

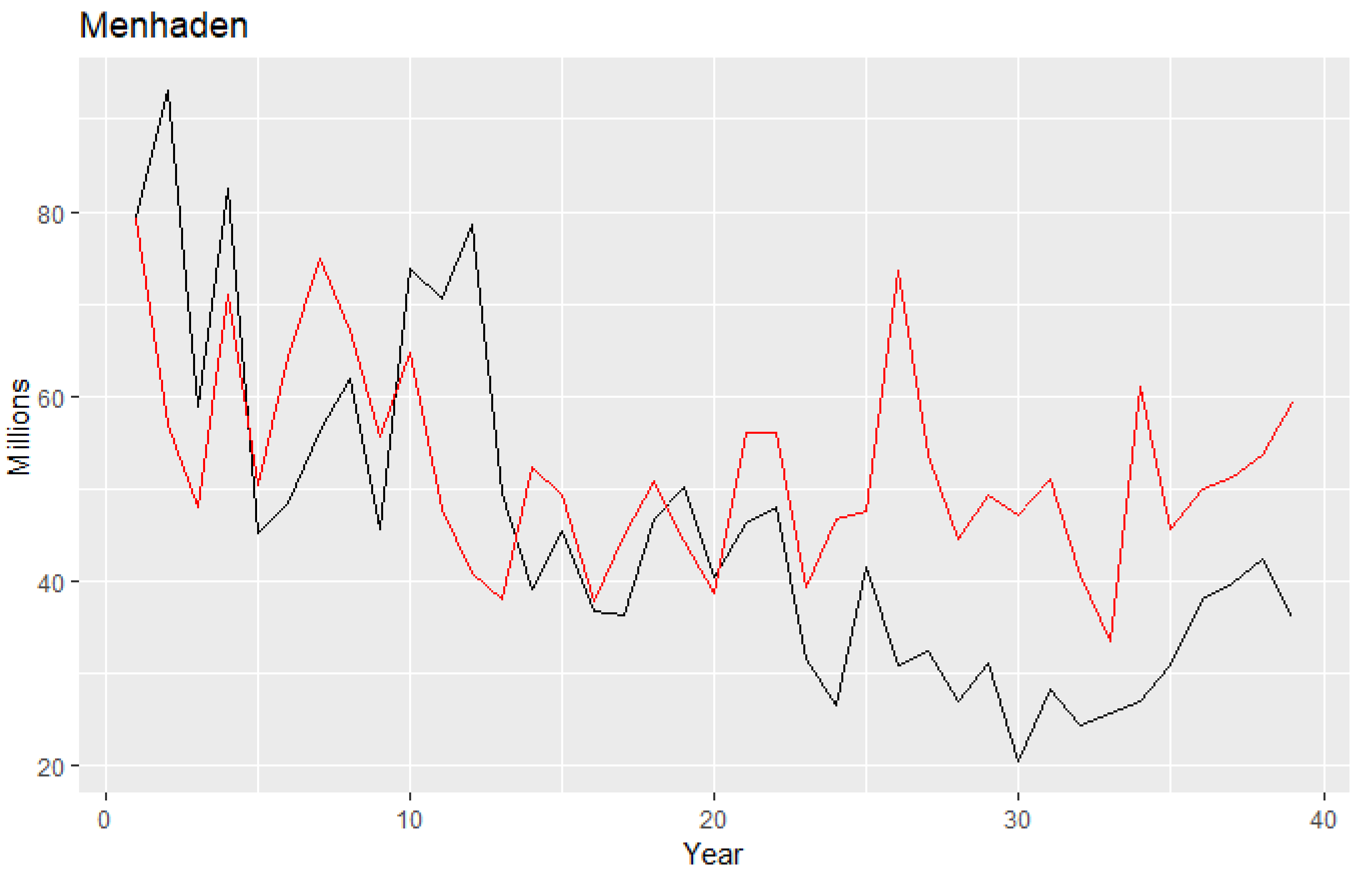

Figure 14. Predicted annual total abundance for menhaden from the single species assessment (red) and the VADER model (black).

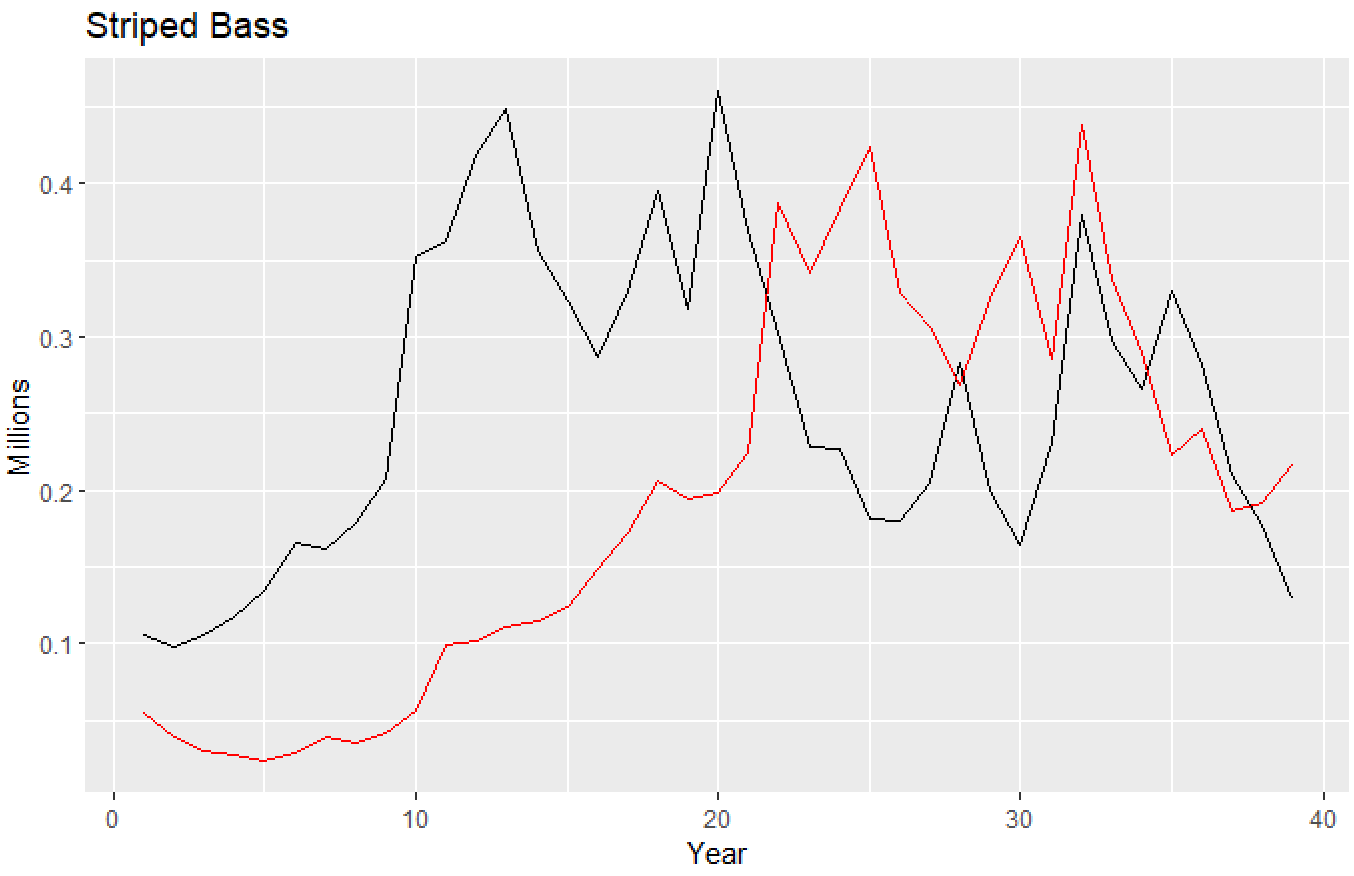

Figure 15. Predicted annual total abundance for striped bass from the single species assessment (red) and the VADER model (black).

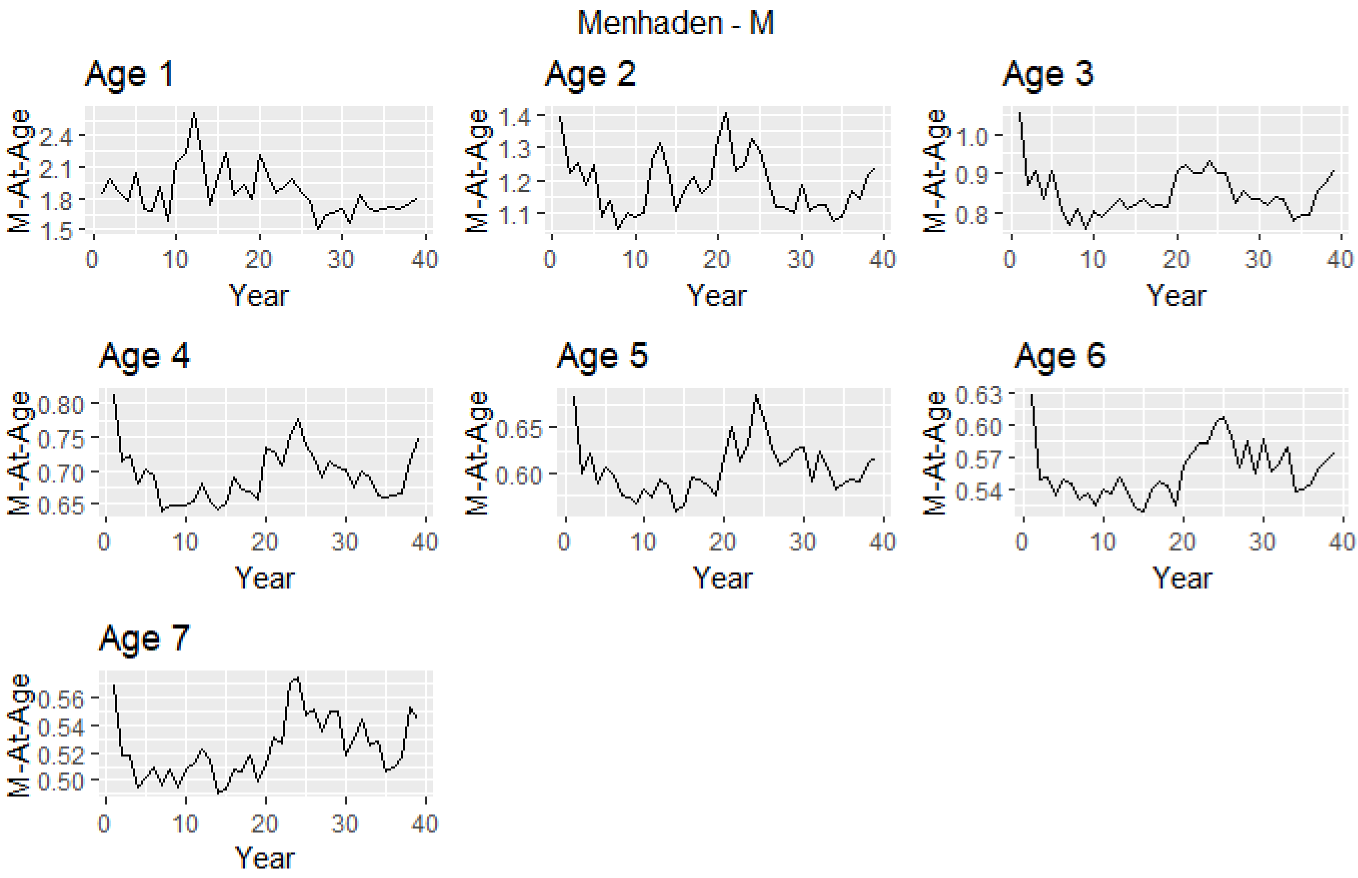

Figure 16. Predicted annual natural mortality for menhaden.

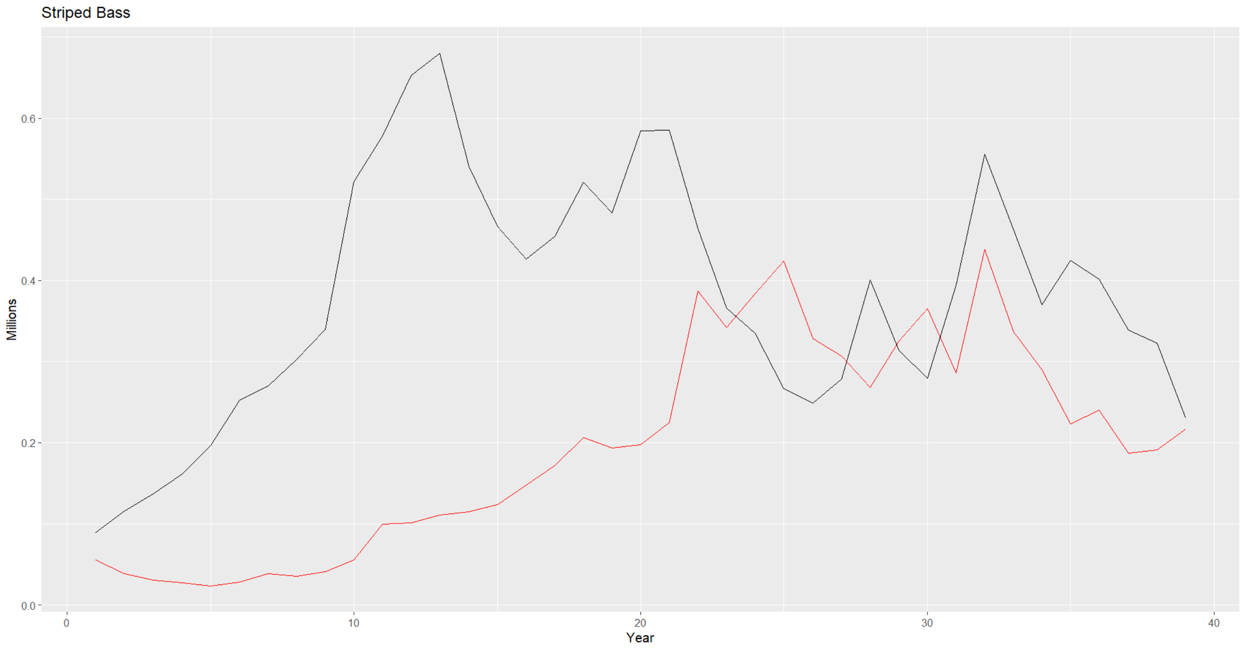

Figure 17. Predicted annual numbers for striped bass from the single species model (red) and the VADER model with dynamic M1 calculation turned on (black).