

# **Bridging the Gulf of Alaska arrowtooth flounder assessment to CEATTLE to improve parameter estimation, account for cannibalism, and increase climate readiness**

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## **Executive Summary**

Recommendations from the Groundfish Plan Team and the Scientific and Statistical Committee (SSC) for the Gulf of Alaska (GOA) arrowtooth flounder (ATF) stock assessment and fishery evaluation (SAFE) over the past several years included investigation of the following elements:

- Recent lower recruitment trends and relationship to environmental conditions in the GOA, including the development of an ESP
- Lack of fit in female survey age and fishery length compositions, including interactions between female natural mortality and selectivity
- Incorporation of predation mortality estimates from the GOA CEATTLE model
- Update growth and age-length conversion matrices

In response to these recommendations and to improve our ability to investigate these concerns, we plan to improve the current GOA ATF assessment model in two main ways. First, we want to bridge from the current Automatic Differentiation Model Builder (ADMB) software to Template Model Builder (TMB) and second we want to include the impact of predation mortality by exploring the multi-species age-structured stock assessment model. We plan to do this by using the CEATTLE (Climate-Enhanced, Age-based model with Temperature-specific Trophic Linkages and Energetics) model that has been expanded for groundfish in the GOA (Holsman et al., 2016, Adams et al., 2022) using TMB (Kristensen et al., 2016).

## **Background**

The current GOA ATF stock assessment model is based on an age-structured model using ADMB software (Fournier et al. 2012). The framework uses automatic differentiation and allows estimation of highly-parameterized and non-linear models. The approach consists of an assessment model, which uses survey and fishery data to generate a historical time series of population estimates, and a projection model which uses results from the assessment model to predict future population estimates and recommended harvest levels. The assessment model is fit to survey abundance data, survey age data, and fishery length composition data with a harvest control rule to model the status and productivity of these stocks and set quotas.

The current operational model using ADMB has been used for the GOA and the Bering Sea and Aleutian Islands (BSAI) ATF stock assessments since 2015 and stems from the "generalized" ADMB model developed for Alaska flatfish (J. Ianelli, pers. comm.). The model incorporates ages 1-20 with 21 and greater in a plus group, estimates age-based selectivity up to age 19 with full selectivity after age 19, and uses 26 length bins starting at 10 cm to a 75 cm plus group and defined at 2 and 3 cm intervals (see last full assessment for more details, Shotwell et al., 2021). A Markov chain Monte Carlo (MCMC) is performed in ADMB to capture variability in recruitment, female spawning biomass, and total (age 1+) biomass. No

spawner-recruit curve is used in the model. Instead, we calculated average recruitment with an estimated lognormal deviation for each year of the model with the exception of the final year. In the final modeled year, recruitment is set to median recruitment. Recruitment deviations are freely estimated but with a modest penalty on extreme deviations from the mean value ( $\sigma_r$  value). Age at recruitment is set to one in the model. Recruitment is informed by subsequent age and length composition and there is little information to inform recruitment in the final few years because selectivity is low for younger ATF. Ages 2-21 are subject to a sex-specific vector of instantaneous rates of natural mortality. Natural mortality is subscripted for sex, as males appear to have higher natural mortality than females in this species (Wilderbuer and Turnock 2009, 0.2 for females, 0.35 for males). Fishery selectivity is estimated as a smooth, age- and sex-specific non-parametric function through age 19. Survey selectivity is modeled using a two parameter ascending logistic function for males and females (four parameters total). Please refer to the most recent full SAFE report (Shotwell et al., 2021) for more details on the current assessment model (hereafter referred to as the ADMB model).

## Justification

Since 2019, recommendations from the Groundfish Plan Team and the SSC for the GOA ATF SAFE have included investigation of the following elements:

- Recent lower recruitment trends and relationship to environmental conditions in the GOA, including the development of an ESP
- Lack of fit in female survey age and fishery length compositions, including interactions between female natural mortality and selectivity
- Incorporation of predation mortality estimates from the GOA CEATTLE model
- Update growth and age-length conversion matrices

The goals of this document are to describe how we intend to start addressing these recommendations by 1) updating the current ADMB model to TMB to improve parameter estimation and 2) accounting for both the impacts of cannibalism and fishery removals in the population dynamics assessment model used for arrowtooth flounder.

TMB (Kristensen et al., 2016) is based on ADMB, but allows for improved estimation of hierarchical non-linear models. TMB, often considered a successor to ADMB, can estimate time-varying parameters (e.g. recruitment deviations) as random effects using marginal maximum likelihood rather than the penalized likelihood used in ADMB. This allows proper estimation of associated variance parameters, which can bias management quantities if misspecified. For example, the current ADMB assessment does not have an explicit recruitment variance parameter, rather the ADMB assessment penalizes annual recruitment deviates by squaring them in the log-likelihood (*i.e.*  $rec\_dev^2$ ). This parameterization implicitly assumes a variance of 0.707, which may not accurately reflect the amount of variability in recruitment. Moving to TMB will allow estimation of recruitment deviates as random effects and allow estimation of age- and sex-specific non-parametric selectivity penalties or other selectivity forms.

Arrowtooth flounder are generalist predators. Analyses from bottom trawl survey diet data show a non-trivial amount of cannibalism particularly on the small to medium (30-299 mm) sizes (Doyle et al., 2018). An ontogenetic shift occurs in ATF diet with smaller fish (<200 mm) consuming primarily euphausiids and capelin to larger fish consuming mostly walleye pollock and increasing amounts of flatfish as they age. Predation on ATF varies with their habitat utilization from pelagic zooplanktivorous predators (e.g., walleye pollock, northern rockfish, Pacific ocean perch) while ATF are small (<30 mm) to increasing amounts of benthic predation (particularly from Pacific cod, Pacific halibut, and larger ATF) as ATF age. The larger ATF (>400 mm) are consumed by the largest predators (e.g., sleeper sharks) (Doyle et al., 2018). Adams et al. (2022) estimated that on average approximately 27,000 to 37,000 t of ATF were consumed

annually by predators in the models explored and that of those species considered (Pacific halibut, ATF, Pacific cod, walleye pollock), ATF was the primary consumer. The fishery has caught between 1,200 to 37,000 mt of ATF between 1977 and 2023. Catch was on average around 17,000 mt since 1991 and has been decreasing from the maximum in 2014 at 37,000 mt to about 10,000 mt since 2021 (see Table 7.3 in Shotwell et al., 2021). In some years cannibalism can largely exceed the removals by the fishery and potentially impact harvest recommendations, highlighting the need to account for the impacts of cannibalism on the population dynamics of ATF (Adams et al., 2022).

A preliminary ecosystem and socioeconomic profile or ESP has recently been created for GOA ATF that includes several mechanistically derived physical and biological indicators to evaluate the impacts of the ecosystem on ATF (Doyle et al., 2018; Shotwell et al., 2022; Ferriss, 2023). Indicators in this report include estimated ATF annual ration, ATF biomass eaten due to cannibalism, and sex-specific natural mortality ( $M$ ) for ages 1 and 2 from the most recent GOA CEATTLE model (Adams et al., 2023) over the years 1977 to 2023. ATF ration averages 9.7 million t and ranges from 8.2-11.4 million t, clearly showing the impact this predator has in the GOA ecosystem. Biomass eaten due to cannibalism ranges from 13,000 t to 49,000 t and averages 26,000 t, supporting the Adams et al., 2022 results. Cannibalism exceeds catch in all years up until 2011 where it becomes comparable to catch. Since 2021, cannibalism has again exceeded catch due to the recent lower harvest levels. Sex-specific  $M$  for ages 1 and 2 are much higher than the ADMB model fixed estimates of 0.2 for females and 0.35 for males (Shotwell et al., 2021). Average  $M$  at age 1 was equal to 0.335 for females (range 0.326 to 0.349) and 0.43 for males (range 0.417 to 0.451). Average  $M$  at age 2 was equal to 0.356 for females (range 0.343 to 0.374) and 0.458 for males (range 0.439 to 0.485). The variable  $M$  by sex and age from the multi-species models from Adams et al., 2023 supports exploring the estimation of sex- and age-specific  $M$  for ATF.

In the GOA, climate can impact the population dynamics of groundfish related to stock assessment through recruitment, bioenergetics/growth, and mortality (Anderson and Piatt, 1999; Clark and Hare, 2022). Additionally, this can have impacts on cannibalism in arrowtooth flounder via temperature-dependent foraging rates, changing species distributions, and shifts in abundance of conspecific predators (Barnes et al., 2018; Holsman and Aydin, 2015). These shifts in predator-prey interactions undermine the assumptions of time-invariant natural mortality (and the equilibrium assumptions of reference points), highlighting the need to evaluate the impact of climate-driven dynamics on management recommendations for ATF. Currently the ADMB model for arrowtooth is not configured for exploration and estimation of climate-linkages. Development of models that can allow incorporation and testing of multiple climate-linkages would be valuable for evaluating future management performance and explaining historical population variability.

## Methods

We use a previously developed climate-enhanced multi-species statistical catch-at-age modeling framework called CEATTLE (Climate-Enhanced, Age-based model with Temperature-specific Trophic Linkages and Energetics, Holsman et al., 2016) that has been expanded for groundfish in the GOA using TMB (Adams et al., 2022, Kristensen et al., 2016) as the basis for the new assessment model explorations for ATF. Developed in part from the underpinnings of multi-species statistical catch-at-age analysis (MSCAA, Jurado-Molina et al., 2005) and multi-species virtual population analysis (MSVPA; Jurado-Molina et al., 2005; Magnusson, 1995), CEATTLE links single-species age-structured models (Table 1) through predation mortality conditioned on the temperature-dependent bioenergetic demand and diet-based prey-selectivity patterns of predators (Curti et al., 2013; Holsman et al., 2016; Kinzey and Punt, 2009). Predation mortality assumes a Holling Type II functional response and parameters are either pre-specified or estimated by fitting to survey and fishery data (Table 2). CEATTLE can be run in single-species mode

by “turning-off” time-varying predation mortality or in multi-species mode by “turning-on” time-varying predation mortality.

### Data

CEATTLE uses the same inputs as the ADMB single-species assessment model (ADMB model, Shotwell et al., 2021) used to provide management advice in addition to diet and bioenergetics data (Adams et al., 2022) (Table 5). Catchability for the AFSC bottom trawl survey is assumed to be 1, and age-at-maturity, weight-at-age, age-length conversion matrix, and ageing error matrix are all estimated outside the model. All data and assumed uncertainties are consistent with the ADMB model. Diet and bioenergetics data were derived from the AFSC stomach sampling program from 1990 to 2015 (Adams et al., 2022, Holsman et al. 2023, Holsman & Aydin 2015). Time-series of bottom temperature derived from the Climate Forecast System Reanalysis for the Pacific cod assessment (Hulson et al., 2023) was used to parametrize consumption and diet composition.

### Model Structure

For arrowtooth flounder in the GOA, the single-species CEATTLE spans 1977 to 2023 and is parameterized similarly to the ADMB model (Adams et al., 2022; Shotwell et al., 2021). The effects of changing climate are accounted for by conducting projections with temperature that determine consumption rates over time. Parameters estimated inside the model include the number-at-age in the first year of the assessment, the number of recruits in subsequent years, the fishing mortality rates for each year, and survey/fishery selectivity. Similar to the ADMB model, separate fishery selectivities were estimated non-parametrically for each age, up to age-19, and the shape of the selectivity curve was constrained to be a smooth function. Survey selectivities were modeled using a two-parameter ascending logistic function. The selectivities by age were estimated separately for females and males. A differential age-invariant natural mortality is assumed or estimated for each sex. CEATTLE assumes multinomial likelihoods for composition data and log-normal likelihoods for index and catch data (Table 3). Despite similarities, the assessment model and CEATTLE have the following differences:

1. In the case of age-composition data, the multinomial in the ADMB model is defined as:

$$NLL = - \sum_i \sum_y n_{f_i1y} \sum_a (\hat{o}_{f_i1ay} + 0.00001) * \ln(o_{f_i1ay} + 0.00001) - \sum_i \sum_y n_{f_i2y} \sum_a (\hat{o}_{f_i2ay} + 0.00001) * \ln(o_{f_i2ay} + 0.00001)$$

where  $\hat{O}_{f_i1ay}$  is the predicted age composition from fleet  $f_i$  for species  $i$  for sex (1 = females; 2 = males) for true age  $a$  and year  $y$ ,  $O_{f_i1ay}$  is the observed true age composition, and  $n_{f_i1y}$  is the sex-specific sample size. The ADMB model, therefore, assumes the input sample sizes are sex-specific, but the observed and true age compositions are calculated relative to both sexes as in Table 1, resulting in a mis-specified multinomial distribution. CEATTLE, instead assumes a single sex-combined input sample size ( $n_{f_iy}$ ) avoiding the mis-specification and allowing the sex ratio to be correctly estimated. Additionally, CEATTLE uses the predicted and observed age composition for observed ages in the multinomial likelihood (accounting for ageing error; see point 4 below).

2. The non-parametric fishery selectivity penalties ( $\chi_{f_i}$ ) in CEATTLE are sex-invariant (Table 3), while in the ADMB model, these penalties are different for males and females.
3. The log-normal likelihoods used by the CEATTLE model include a log-normal bias correction and exclude an added constant of 0.0001 that was included in the ADMB model. CEATTLE also

utilizes the complete probability distribution rather than the simplified form used in the ADMB model.

4. To account for ageing error, the ADMB model multiplies the observed age composition data by the ageing error matrix  $\hat{O}_{f_i1ay} = \hat{O}_{f_i1\hat{a}y}AE_{i\hat{a}a}$ . However, CEATTLE multiplies the expected true age composition by the ageing error matrix to derive the expected observed age-composition  $O_{f_i1\hat{a}y} = O_{f_i1ay}AE_{i\hat{a}a}$ .
5. Multinomial distribution weights for the ADMB model are not updated with new data (weights in the 2017 assessment are the same in 2021). However, CEATTLE calculates McAllister and Ianelli (1997) weights allowing for easy sample size tuning. CEATTLE can also be easily updated so that composition weights are directly estimated using the dirichlet-multinomial distribution.

## Models

We present four bridging models to demonstrate the major transitions from the ADMB platform to the multi-species CEATTLE model:

1. ADMB model: current operational single-species ADMB based assessment from the 2021 SAFE (Shotwell et al., 2021) and updated catch to 2023 (Shotwell et al., 2023).
2. TMB single-spp (species) fixed natural mortality ( $M$ ) model: the single-species TMB based CEATTLE model that fixes sex-specific  $M$  (females = 0.2 and males = 0.35) and treats annual recruitment as random effects.
3. TMB single-spp (species) estimated  $M$  model: the single-species TMB based CEATTLE model that estimates sex-specific  $M$  and treats annual recruitment as random effects.
4. TMB multi-spp (species) model: the “multi-species” CEATTLE based cannibalism model that estimates sex-, age-, and time-varying  $M$  due to cannibalism from ATF ( $M2$ ), sex-specific residual mortality ( $MI$ ), and treats annual recruitment as random effects.

The sex-specific residual mortality ( $MI$ ) in the “multi-species” CEATTLE model represents mortality due to predation from other species, disease, senescence, etc. We also created a series of sub-models to demonstrate bridging between the ADMB model and the TMB model in CEATTLE (between models 1 and 2 listed above). Please see the appendix for details on this section of the model bridging exercise. Due to differences in likelihood specifications between the ADMB model and CEATTLE, likelihood components are not directly comparable, however, see the appendix for a more extensive bridging.

## Results

Both the ADMB and single-species CEATTLE model that fixed sex-specific  $M$  (models 1 & 2) showed similar if not exactly similar trends in recruitment, spawning stock biomass, and biomass (Figure 1). The single-species model that estimated  $M$  and the multi-species CEATTLE model that included cannibalism (models 3 & 4) led to higher estimates of recruitment and biomass, owing to higher estimates of total natural mortality for younger age-classes (Figure 2). The single-species model that estimated  $M$  estimated it to be 0.296 for females and 0.383 for males, which is higher than the 0.2 and 0.35 assumed by the current assessment. The multi-species model that estimated sex-, age-, and time-varying mortality, mortality due to cannibalism ( $M2$ ) only impacted ages 1-6 for females and ages 1-7 for males. For females, total mortality estimated on average as age-1 = 0.335, age-2 = 0.356, age-3 = 0.351, age-4 = 0.321, age-5 = 0.31, and age-6 = 0.307 between 1977 and 2023. For males, total mortality estimated on average as age-1 = 0.43, age-2 = 0.458, age-3 = 0.455, age-4 = 0.408, age-5 = 0.395, age-6 = 0.39, and age-7 = 0.389 between 1977 and 2023 (Figure 2). However, both the single-species model that estimated  $M$  and the multi-species model led to lower estimates of spawning stock biomass than the ADMB model due to higher estimates of mortality for older fish. In the multi-species model residual mortality (*e.g.* total natural mortality for age-8+ fish) was

estimated as  $MI = 0.307$  for females and  $MI = 0.388$  for males. This was also higher than the natural mortality of 0.2 and 0.35 assumed by the assessment for females and males, respectively. The multi-species model also estimated that cannibalism peaked in 2001 to 49,122 t, but has decreased in recent years as biomass has decreased (Figure 3).

The single-species CEATTLE model that estimated  $M$  led to the lowest log-likelihood among the CEATTLE models evaluated (Table 6). However, the multi-species CEATTLE model led to a lower log-likelihood than the single-species model that fixed  $M$  (Table 6), owing to an improved fit to the survey biomass, survey age-composition, and fishery length-composition data (Figures 4-6). Both the single-species model that estimated  $M$  and the cannibalism model had similar log-likelihoods for the data components, but differed in likelihood penalties. Both the ADMB and single-species CEATTLE model that fixed  $M$  (models 1 & 2) had similar Pearson and OSA residual patterns (Figure 4 & 5). OSA residuals from the survey age composition data were smaller for the single-species model that estimated  $M$  and the cannibalism model (Figure 5). Females from the survey age-data early in the time series had a positive trend for the 1979 cohort across all models (Figure 4). All models fit the 22nd length bin from males poorly from the fishery length composition data (Figure 6). Due to the large residuals from the fishery length-composition data, OSA residuals did not converge. Both the ADMB and single-species CEATTLE model that fixed  $M$  (models 1 & 2) had similar estimates of survey and fishery selectivity (Figure 7). Selectivity in the single-species model that estimated  $M$  and the multi-species model (Models 3 & 4) was more asymptotic for the fishery than in the single-species models that fixed  $M$  (Models 1 & 2; Figure 7). All models had similar fits to the survey index data (Figure 8). There were no severe retrospective patterns in the single- or multi-species models across 10 annual peels (Figure 9). The single-species model that estimated  $M$  and the multi-species model were consistent in their estimates of  $M$  and  $MI$ , respectively, across peels (Figure 10). The single-species model that estimated  $M$  had slightly lower Mohn's rho (0.08) than the single-species model that fixed  $M$  and the multi-species model (both at 0.09). However, across both single- and multi-species CEATTLE models, treating annual recruitment deviates as random effects led to lower retrospective bias than when treating them as penalized deviates assuming  $\sigma_R = 0.707$ . Profiling  $\sigma_R$  when treating recruitment deviates as random effects or as penalized deviates indicated an inability to estimate  $\sigma_R$  in ADMB (Figure 11) because the highest density was at  $\sigma_R = 0$ .

## Discussion and Recommendation

Estimating the single-species arrowtooth flounder stock assessment in TMB using CEATTLE has multiple benefits when compared to the current ADMB model. CEATTLE was developed with three goals in mind: 1) flexibly and easily recreate single-species AFSC groundfish assessments in TMB, 2) allow easy model development and reparameterization (*i.e.* multiple observation models can easily be estimated and compared), and 3) allow estimation of time- and age-varying predation mortality for trophically linked species. Currently, the ADMB assessment has a few elements that are mis-specified that are not present in CEATTLE (differences 1, 4, and 5 above). These can be easily corrected in ADMB, however, CEATTLE also allows for correct estimation of recruitment by treating recruitment deviates as random effects. Likelihood profiles of  $\sigma_R$  show that estimating variance in recruitment is not possible in ADMB. Additionally, comparison of CEATTLE models estimated using penalized maximum likelihood and marginal maximum likelihood show that estimation of  $\sigma_R$  has impacts on derived quantities used for management. Treating recruitment deviates as random effects also leads to lower retrospective bias than estimating the models using penalized maximum likelihood. Bridging also suggests that estimation using CEATTLE is able to find a better fit to the data than the current ADMB model (see Appendix). Using CEATTLE, improvements to the model could be explored including using the marginal maximum likelihood approach to estimate the non-parametric selectivity penalties or explore other time-varying selectivity functions that may better fit the composition data. We therefore recommend using TMB as the assessment platform via CEATTLE moving forward for GOA ATF.

Accounting for cannibalism in the population dynamics of arrowtooth flounder using CEATTLE demonstrated a better fit to the observed data than the single-species CEATTLE and ADMB models that fixed  $M$ . Natural mortality was estimated to be higher than the values assumed by the assessment when estimated in both single- and multi-species frameworks. As a result fishery selectivity was estimated to be more asymptotic than when  $M$  was fixed. Additionally, cannibalism in most years has been more than removals by the fishery. However, given the difficulty in defining Tier 3 reference points for multi-species models, using the multi-species CEATTLE model for the assessment may not make sense. Rather, the multi-species model could be used to inform estimates of mortality in the single-species assessment and supplement the assessment by informing on the impacts of both fishery removals and cannibalism on the stock (*i.e.* project the multi-species model with the recommended ABC). For future iterations, it would be useful to update the time-series of diet data in the model, and explore including other time-varying elements (e.g., weight-at-age data, age-length conversion matrices, diet data). All of which can be easily implemented in CEATTLE and are currently used for other models. Therefore, our recommendations for future assessments include:

- Move the stock assessment model to Template Model Builder (TMB) to correctly treat recruitment deviates as random effects and explicitly estimate the associated variance parameter.
- Estimate sex-specific, but age- and time-invariant natural mortality ( $M$ ).
- Update the weight-at-age and length-at-age transition matrices with recent data and explore the potential for time-varying growth in the assessment model.
- Update the aging error matrix with recent age data.
- Utilize the multi-species model to inform age- and (possibly) time-varying  $M$ .
- Explore model sensitivity to different assumptions of catchability (*i.e.* catchability is estimated).

## Code and data

<https://github.com/grantdadams/GOA-ATF-ESP/tree/master>

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## Tables

**Table 1.** General population dynamics equations in CEATTLE for species  $i$ , sex  $s$ , age  $a$ , and length  $l$  in year  $y$ , and for survey or fishery  $f_i$ . See Table 4 for parameter definitions.

Definition	Equation
Initial abundance	$N_{isa1} = \{ \underline{R}_{f_i} e^{(-\sum_{j=1}^{a-1} M_{1isj} + \tau_{ia})} \rho_{i1} \text{ if } a < A_i$ $N_{isA_i1} = \frac{\underline{R}_{f_i} e^{(-\sum_{j=1}^{a-1} M_{1isj} + \tau_{ia})} \rho_{i1}}{(1 - e^{(-M_{1isA_i})})} \text{ if } a = A_i$
Recruitment	$N_{is1y} = R_{isy} = \underline{R}_i e^{\tau_{iy}} \rho_{i1}$
Numbers at age	$N_{isa+1y+1} = N_{isay} e^{-Z_{isay}}$ $N_{isA_iy+1} = N_{isA_i-1y} e^{-Z_{isA_i-1y}} + N_{isA_iy} e^{-Z_{isA_iy}}$
Survey biomass (kg)	$CP\widehat{UE}: B_{f_iy} = \sum_s \sum_a N_{isay} e^{-Month_{f_i} * Z_{isay}} W_{f_i say} sel_{f_i say} q_{f_i y}$
Catch-at-age	$C_{f_i say} = \frac{F_{f_i say}}{Z_{isay}} (1 - e^{-Z_{isay}}) N_{isay}$
Total catch (kg)	$C^*_{f_i y} = \sum_s \sum_j \frac{F_{f_i say}}{Z_{isay}} (1 - e^{-Z_{isay}}) N_{isay} W_{f_i say}$
Age-1+ biomass (kg)	$B_{iy} = \sum_s \sum_{a \geq 0} N_{isay} W_{B_{iy}}$
Spawning biomass at age (kg)	$SB_{iay} = N_{i1ay} e^{-Month_{ssb_i}/12 * Z_{i1ay}} W_{ssb_i 1ay} \delta_{ia}$
Total mortality at age (single-species)	$Z_{isay} = M_{1isa} + \sum_{f_i} F_{f_i say}$
Total mortality at age (multi-species)	$Z_{isay} = M_{1isa} + M_{2isay} + \sum_{f_i} F_{f_i say}$
Fishing mortality at age and fleet	$F_{f_i say} = \underline{F}_{f_i} e^{\epsilon_{f_i y}} sel_{f_i say}$
Projected fishing mortality	$F_{f_i say} = F_{Target_i} sel_{f_i say} \psi_{f_i}$
Predicted age composition	$\hat{O}_{f_i s \hat{a} y} = \frac{\sum_a C_{f_i say} AE_{i \hat{a} a}}{\sum_s \sum_{\hat{a}} \sum_a C_{f_i say} AE_{i \hat{a} a}} \text{ if } f_i = \text{fishery}$ $\hat{O}_{f_i s \hat{a} y} = \frac{\sum_a N_{isay} e^{-Month_{f_i} * Z_{isjy}} sel_{f_i say} AE_{i \hat{a} a}}{\sum_s \sum_{\hat{a}} \sum_a N_{isay} e^{-Month_{f_i} * Z_{isjy}} sel_{f_i say} AE_{i \hat{a} a}} \text{ if } f_i = \text{survey}$
Predicted length composition	$\hat{O}_{f_i s l y} = \frac{\sum_{\hat{a}} \sum_a C_{f_i say} AE_{i \hat{a} a} ATM_{isal}}{\sum_s \sum_l \sum_{\hat{a}} \sum_a C_{f_i say} AE_{i \hat{a} a} ATM_{isal}} \text{ if } f_i = \text{fishery}$ $\hat{O}_{f_i s l y} = \frac{\sum_{\hat{a}} \sum_a N_{isay} e^{-Month_{f_i} * Z_{isay}} sel_{f_i say} AE_{i \hat{a} a} ATM_{isal}}{\sum_s \sum_l \sum_{\hat{a}} \sum_a N_{isay} e^{-Month_{f_i} * Z_{isjy}} sel_{f_i say} AE_{i \hat{a} a} ATM_{isal}} \text{ if } f_i = \text{survey}$

**Table 2.** Predation mortality equations for predator species  $p$ , sex  $b$ , age  $j$ , and prey species  $i$ , sex  $s$  and age  $a$ . For parameter definitions see Table 4.

Definition	Equation
Predation mortality	$M_{2_{isay}} = \sum_{pbj} \left( \frac{N_{pbjy} \delta_{pbjy} \hat{S}_{pbjisa}}{\left( \sum_{isa} (\hat{S}_{pbjisa} B_{isay}) + B_p^{other} (1 - \sum_{isa} (\hat{S}_{pbjisa})) \right)} \right)$
Predator-prey suitability	$S^{pbjisa} = \frac{1}{n_y} \sum_y \left( \frac{\frac{U_{psaisa}}{w_{isay} N_{isay}^{H_i}}}{\sum_{isa} \left( \frac{U_{pbjisa}}{w_{isay}} \right) + \frac{1 - \sum_{isa} U_{pbjisa}}{B_p^{other}}} \right)$
Individual specific ration ( $kg\ kg^{-1}\ yr^{-1}$ )	$\delta_{pbjy} = \varphi_{pbjy} \alpha_p^\delta W_{pbjy}^{(1+\beta_p^\delta)} f(T_y)_p$
Temperature scaling algorithms	$f(T_y)_p = V^X e^{(X(1-V))}$
...	$V = (T_p^{cm} - T_y) / (T_p^{cm} - T_p^{co})$
...	$X = (Z^2 (1 + (1 + 40/Y)^{0.5})^2) / 400$
...	$Z = \ln(Q_p^c) (T_p^{cm} - T_p^{co})$
...	$Y = \ln(Q_p^c) (T_p^{cm} - T_p^{co} + 2)$

**Table 3.** Components of the likelihood function for species  $i$ , sex  $s$ , age  $a$ , or length  $l$  during year  $y$  for survey  $s$  or fishery  $f$ . For parameter definitions see Table 4.

Description	Equation
<b>Data components</b>	
Survey biomass	$\ln(B_{fiy}) \sim N\left(\ln(\hat{B}_{fiy}) - \frac{\sigma_{fiy}^2}{2}, \sigma_{fiy}^2\right)$
Total catch	$\ln(C_{fiy}^*) \sim N\left(\ln(\hat{C}_{fiy}^*) - \frac{\sigma_{fiy}^2}{2}, \sigma_{fiy}^2\right)$
Age composition	$-\sum_i n_{fiy} \sum_s \sum_{\hat{a}} \sum_y (\hat{O}_{fis\hat{a}y} + 0.00001) \\ * \ln(O_{fis\hat{a}y} + 0.00001)$
Length composition	$-\sum_i n_{fiy} \sum_s \sum_l \sum_y (\hat{O}_{fisl y} + 0.00001) \\ * \ln(O_{fisl y} + 0.00001)$
<b>Penalties</b>	
Non-parametric selectivity	$\sum_i \sum_s \sum_a^{A_i-1} \chi_{fi} \left[ \ln\left(\frac{e^{\psi_{fisa}}}{e^{\psi_{fisa+1}}}\right) - \ln\left(\frac{e^{\psi_{fisa+1}}}{e^{\psi_{fisa+2}}}\right) \right]^2 \\ \chi_{fi} = 0 \quad \text{if } e^{\psi_{fisa}} \leq e^{\psi_{fisa+1}}$
Recruitment deviate	$\tau_{iy} \sim N\left(-\frac{\sigma_{Ri}^2}{2}, \sigma_{Ri}^2\right)$
Fishing mortality deviate	$\epsilon_{fiy} \sim \epsilon_{fiy} * \epsilon_{fiy}$

**Table 4.** Parameter definition for CEATTLE.

Category	Parameter	Definition
Index	$i$	Species
	$s$	Sex
	$a$	Age
	$\hat{a}$	Observed age
	$A$	Plus group
	$l$	Length
	$y$	Year
	$Y$	Last year of estimation (not projection)
	$p$	Predator species
	$b$	Predator sex
	$j$	Predator age
	$k$	Predator length
	$f_i$	Fleet/survey
Population model	$R_{isy}$	Recruitment
	$\bar{R}_i$	Mean recruitment
	$\tau_{iy}$	Annual recruitment deviate
	$\delta_{ia}$	Maturity-at-age
	$\rho_{ia}$	Sex-ratio
	$M1_{isa}$	Residual mortality yr <sup>-1</sup>
	$M2_{isay}$	Predation-mortality yr <sup>-1</sup>
	$F_{f_i say}$	Fleet-specific fishing mortality yr <sup>-1</sup>
	$F_{isay}$	Total fishing mortality yr <sup>-1</sup>
	$Z_{isay}$	Total mortality yr <sup>-1</sup>
	$\bar{F}_{f_i}$	Mean fishing mortality yr <sup>-1</sup>
	$\epsilon_{f_i y}$	Annual fishing mortality deviate
	$\psi_{f_i}$	Fishing mortality apportionment per fleet
	$N_{isay}$	Numbers-at-age
	$\bar{N}_{isay}$	Average numbers-at-age
	$SB_{ijy}$	Spawning-stock-biomass (kg)
	$B_{isay}$	Biomass (kg)
	$\bar{B}_{isay}$	Average biomass (kg)
Predation model	$\hat{S}_{pbjisa}$	Predator-prey suitability
	$H_i$	Holling functional response parameter
	$B_p^{other}$	Biomass of “other prey” (kg)
	$T_y$	Observed bottom temperature (°C)
	$T_p^{co}$	Thermal optima for consumption (°C)
	$T_p^{cm}$	Thermal limit of consumption (°C)
	$Q_p^c$	Rate at which consumption increased over relatively low water temperatures
	$\alpha_p^\delta, \beta_p^\delta$	Weight specific intercept and slope of maximum consumption
	$\varphi_{pbj}$	Scalar for maximum to observed consumption
	$\bar{U}_{pbj,isa}$	Average proportion of prey-at-age in the stomach of a predator-at-age
Observation model		
	$CP\bar{U}\bar{E}: B_{f_i y}$	Survey/fishery relative biomass (kg)
	$sel_{f_i say}$	Selectivity

	$q_{fiy}$	Catchability
	$W$	Weight (kg)
	$C_{fisy}$	Catch-at-age
	$C^*_{fiy}$	Total catch (kg)
	$\hat{O}_{fisy}/\hat{O}_{fisy}$	Predicted age/length composition
	$AE_{i\hat{a}a}$	Ageing error matrix
	$ATM_{isal}$	Age-transition matrix (growth trajectory)
	$\hat{S}_{pbjisa}$	Predator-prey suitability

**Table 5.** Time-series and sources of data used in CEATTLE model

<b>Source</b>	<b>Data type</b>	<b>Data collection cycle</b>
NMFS bottom trawl survey	Absolute biomass	Triennial and Biennial (1984-2021)
	Age composition	1984-2019
	Diet composition	1990-2015
Holsman and Aydin (2015)	Bioenergetic demand	1990-2015
Fishery	Total catch	Annual (1977-2023)
	Length composition	1977-2020

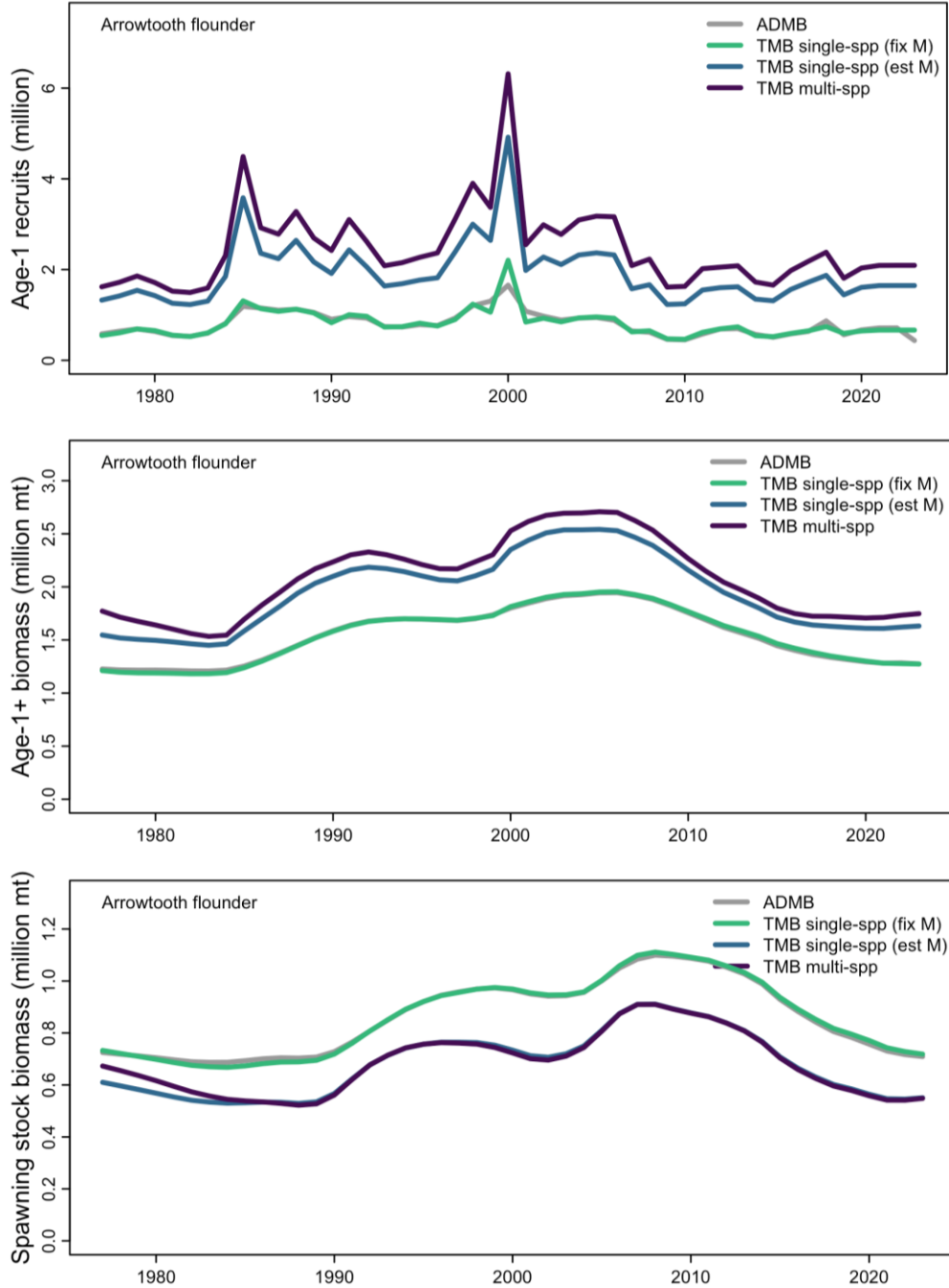
**Table 6.** Model comparison table. Note, likelihoods from the ADMB model are not comparable with CEATTLE.

	ADMB	CEATTLE Single-spp (fix M)	CEATTLE Single-spp (est M)	CEATTLE multi-spp
Platform	ADMB	TMB	TMB	TMB
<i>Likelihoods</i>				
Catch	4.31803e-08	-97.51	-97.38	-94.38
Fishery length composition	816.17	83.32	63.94	63.76
Survey biomass	27.86	1.16	-3.94	-4.44
Survey age composition	276.91	43.36	40.49	40.54
Recruit deviations	5.04	24.30	19.26	21.96
Selectivity penalties	7.30	9.91	6.48	6.95
F regularity	21.20	20.44	21.08	22.20
<b>Joint NLL</b>	<b>177.67</b>	<b>84.99</b>	<b>49.94</b>	<b>56.61</b>
Marginal NLL		96.47	66.18	68.92
Number of parameters	158	92	94	94
<i>Estimates</i>				
$q$ -trawl	1	1.0	1.0	1.0
Mean Recruitment (thousand)	801,987	806,846	1,921,099	2,451,550
$\sigma_r$	0.707	0.477	0.445	0.462
2023 total biomass (t)	1,276,460	1,273,952	1,631,329	1,747,704
2023 spawning biomass (t)	696,871	718,708	550,638	548,410
$B_{100\%}$ (t)	1,018,700	1,684,452	2,045,104	2,141,534
$B_{40\%}$ (t)		673,781	818,042	856,614
$SSB_{100\%}$ (t)		984,431	752,438	738,569
$SSB_{40\%}$ (t)	407,478	393,772	300,975	295,428

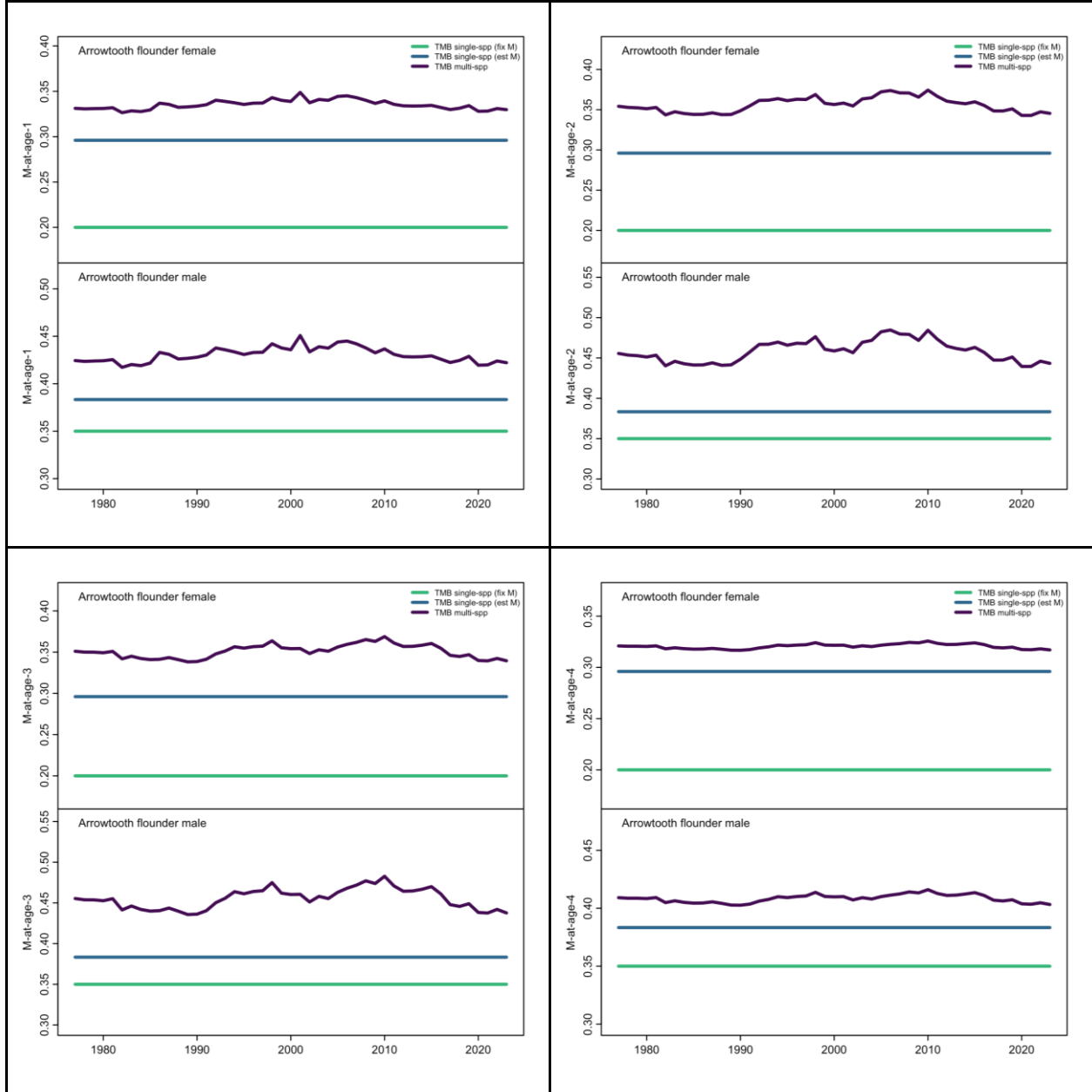


## Figures

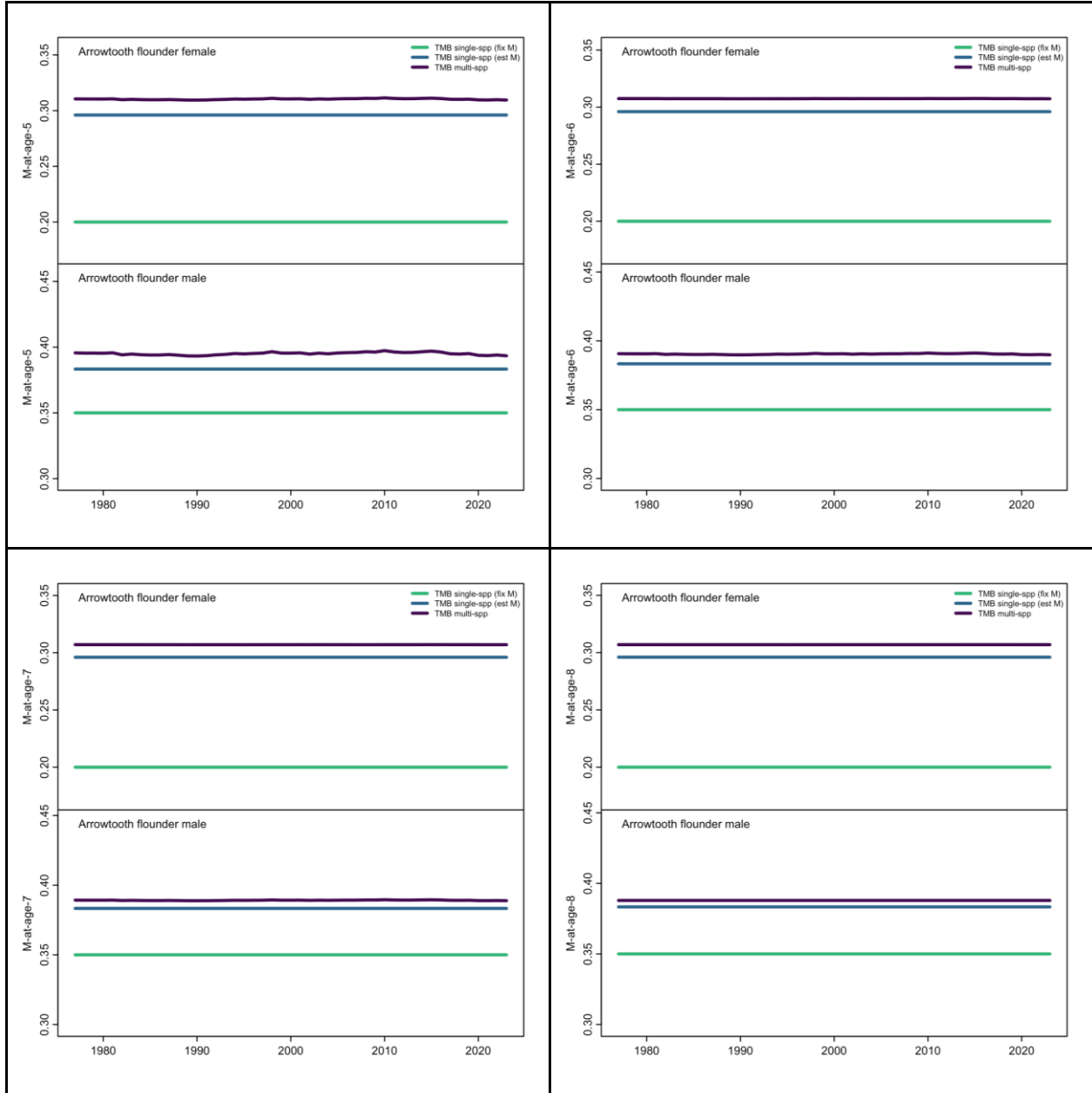
**Figure 1.** Time-series of estimated age-1 recruitment (millions; top panel), total biomass (million mt; middle panel), spawning stock biomass (million mt; bottom panel) as determined from the 2023 ADMB assessment, CEATTLE single-species fixed M and estimated M, and multi-species (cannibalism) models.



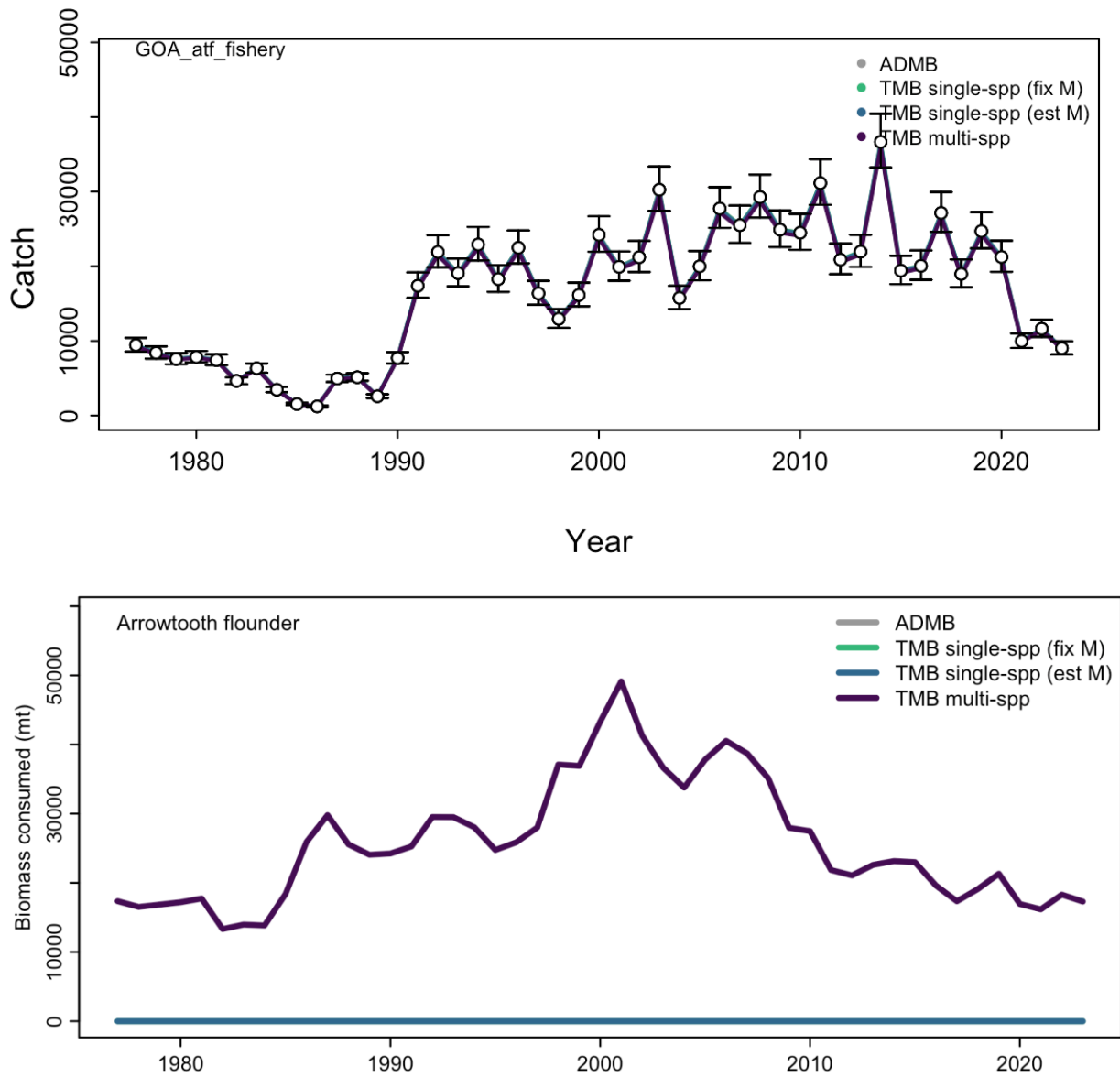
**Figure 2a.** Time-series of total natural mortality at age-1 (top-left panel), age-2 (top-right panel), age-3 (bottom-left panel), and age-4 (bottom-right panel) from the single- and multi-species (cannibalism) CEATTLE models. For the single-species ADMB and CEATTLE single-species with fixed  $M$ , natural mortality is set at 0.2 for females and 0.35 for males.



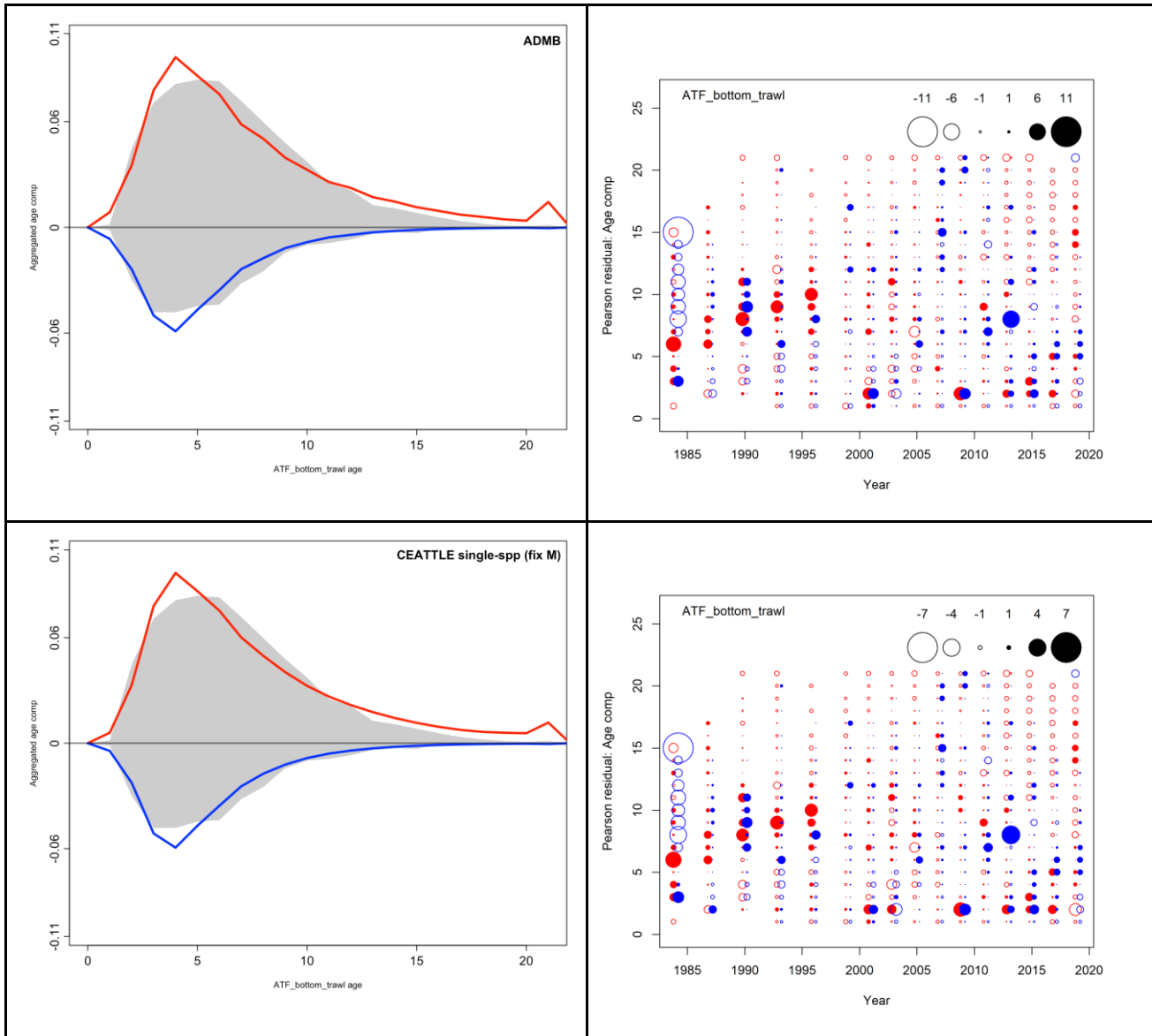
**Figure 2b.** Time-series of total natural mortality at age-5 (top-left panel), age-6 (top-right panel), age-7 (bottom-left panel), and age-8 (bottom-right panel) from the single- and multi-species (cannibalism) CEATTLE models. For the single-species ADMB and CEATTLE single-species with fixed  $M$ , natural mortality is set at 0.2 for females and 0.35 for males.

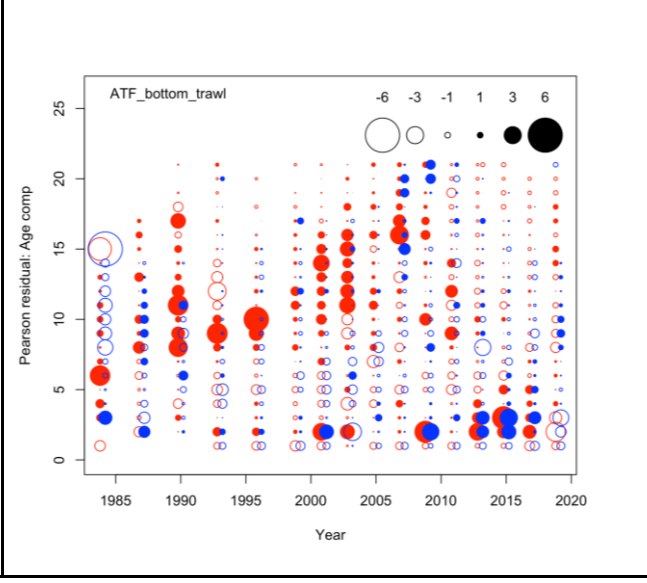
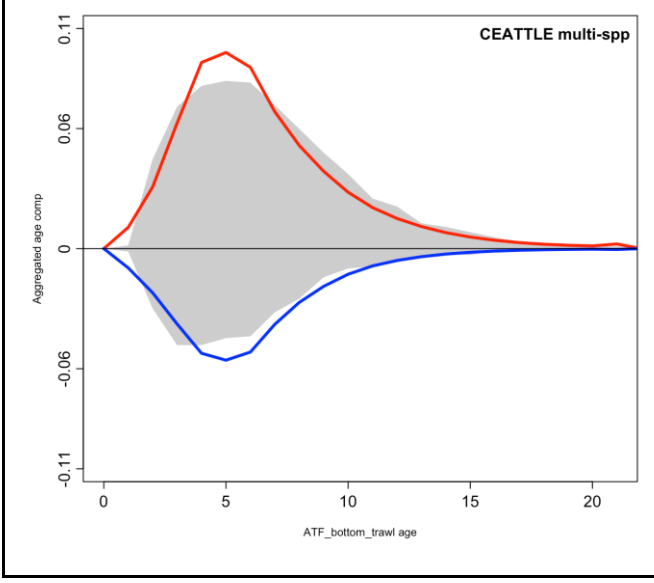
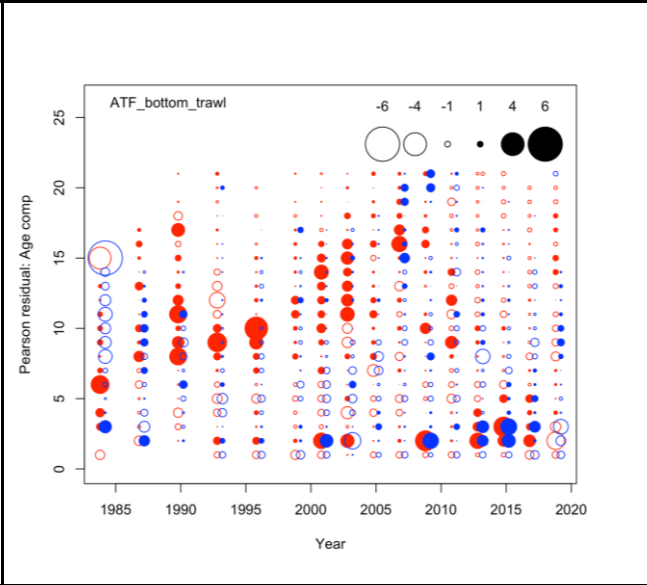
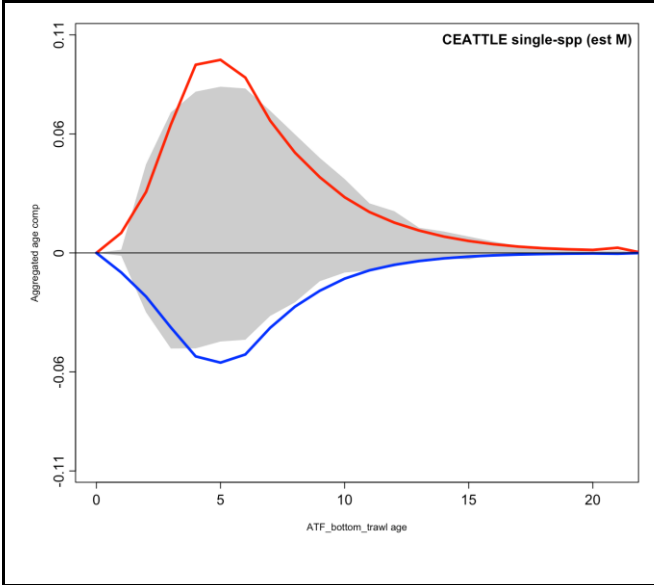


**Figure 3.** Time-series of estimated and observed catch (mt) and biomass consumed (mt) as prey as determined from the 2023 ADMB assessment and CEATTLE single- and multi-species (cannibalism) models.

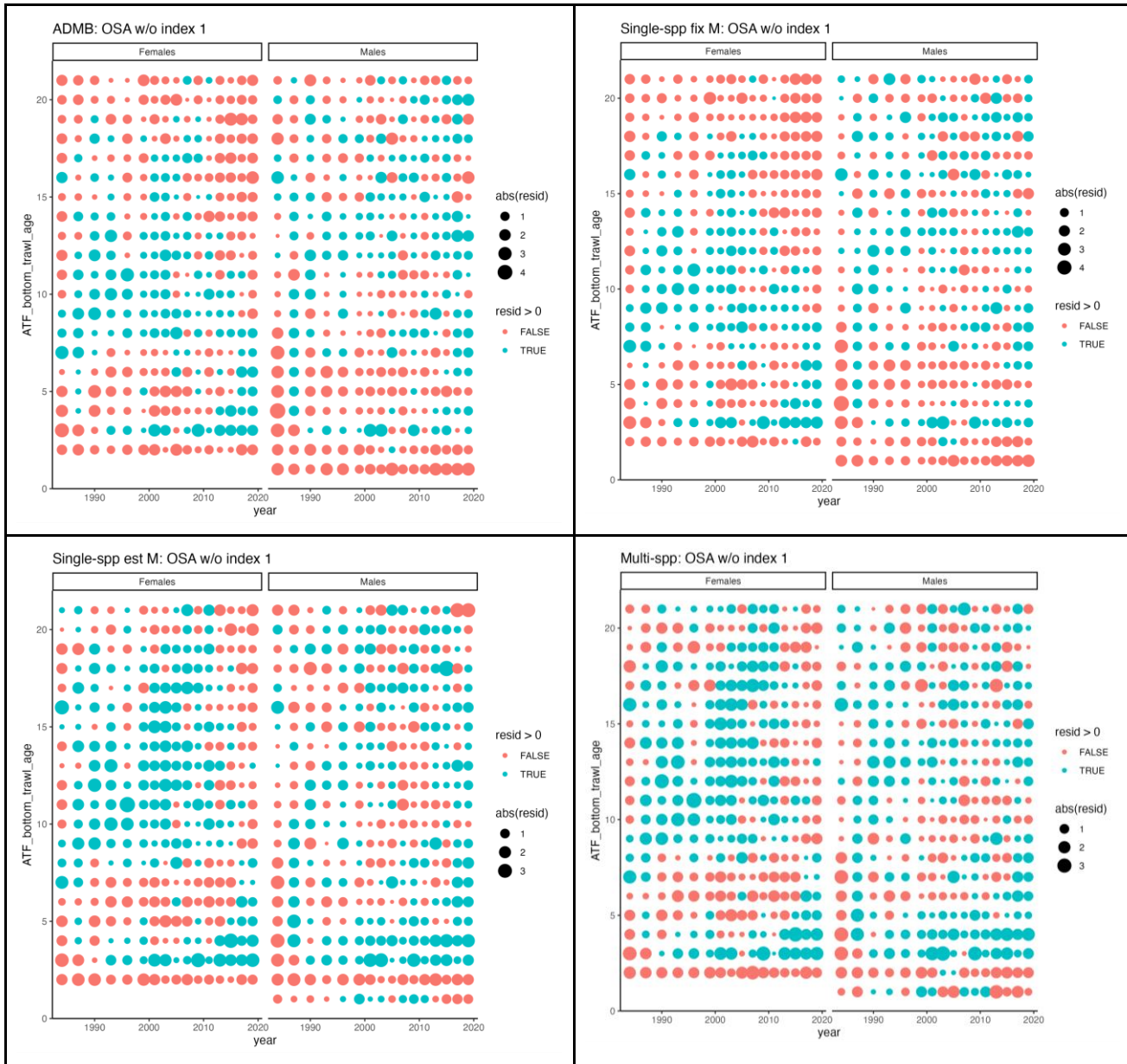


**Figure 4.** Fits to aggregated and pearson residuals of observed and expected bottom trawl survey age-composition data between the ADMB model and CEATTLE single- and multi-species models. Females are red and males are blue. NOTE: difference in z-scale.

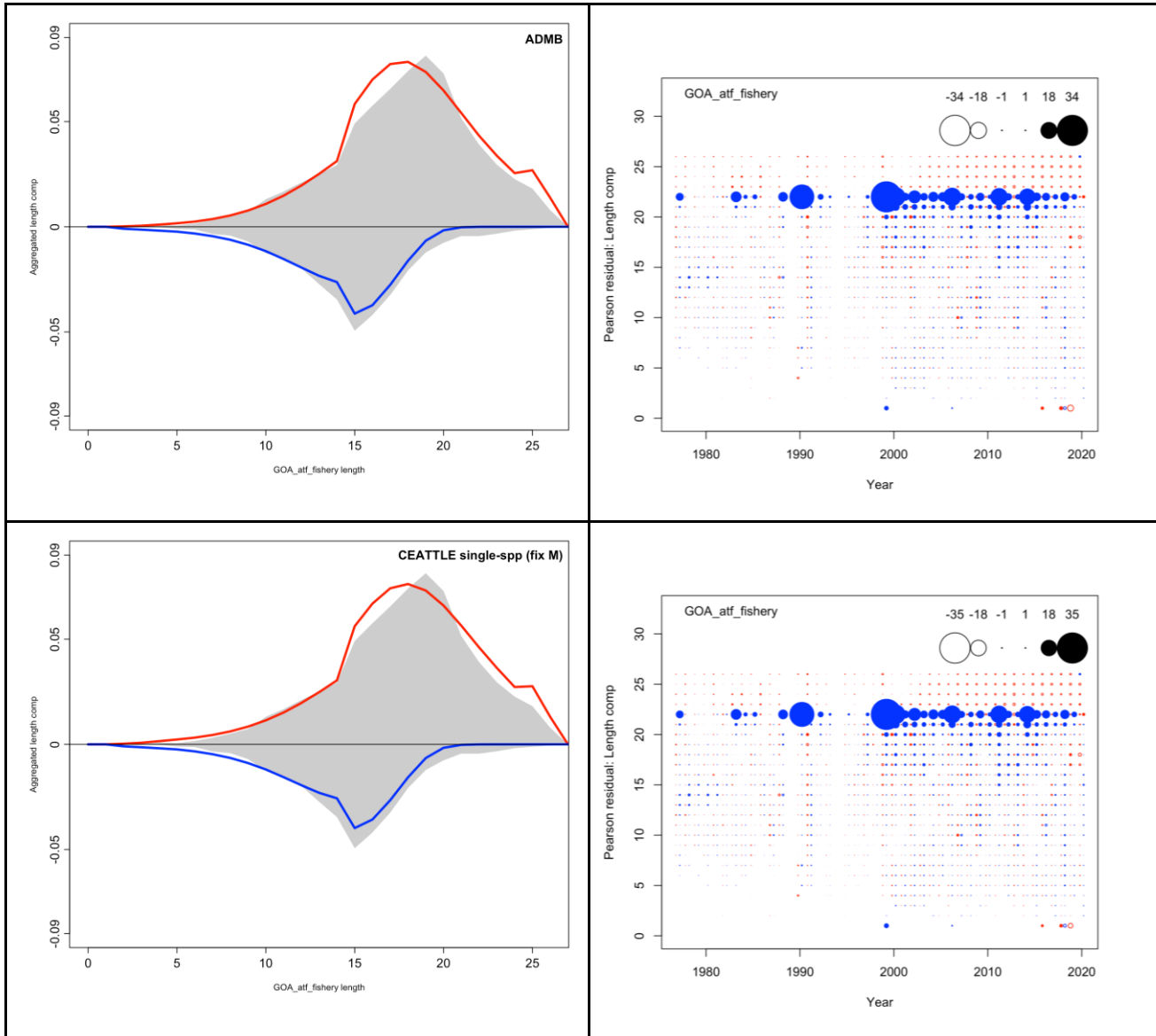




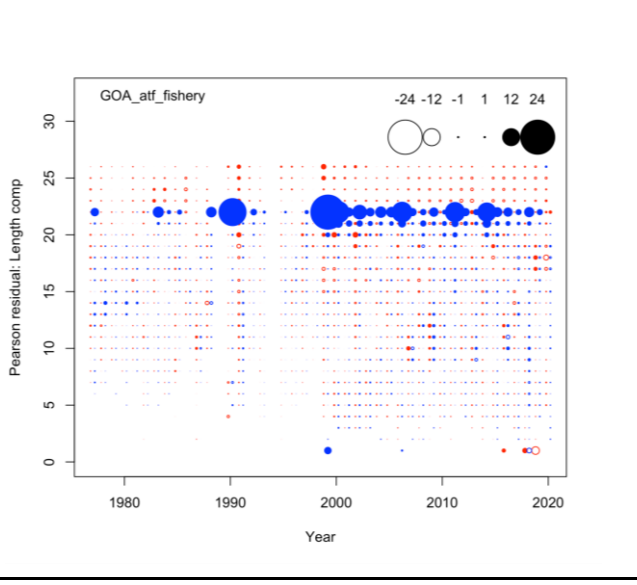
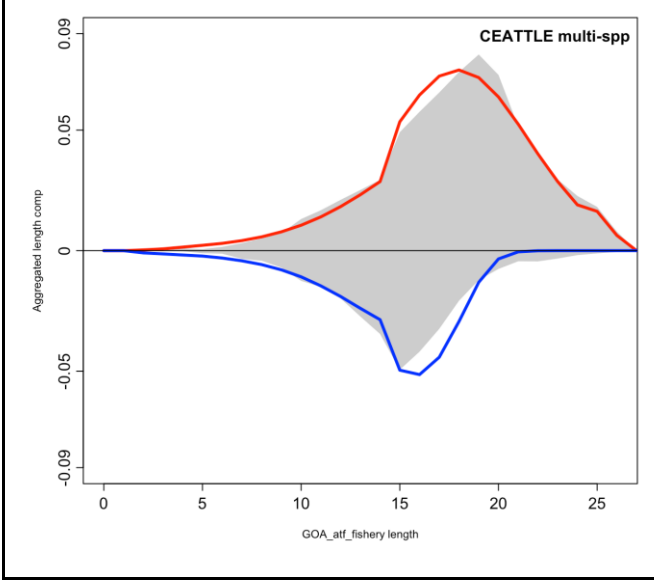
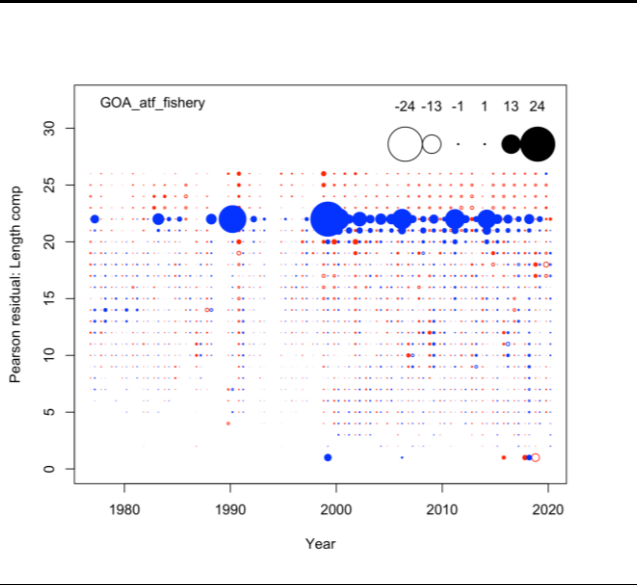
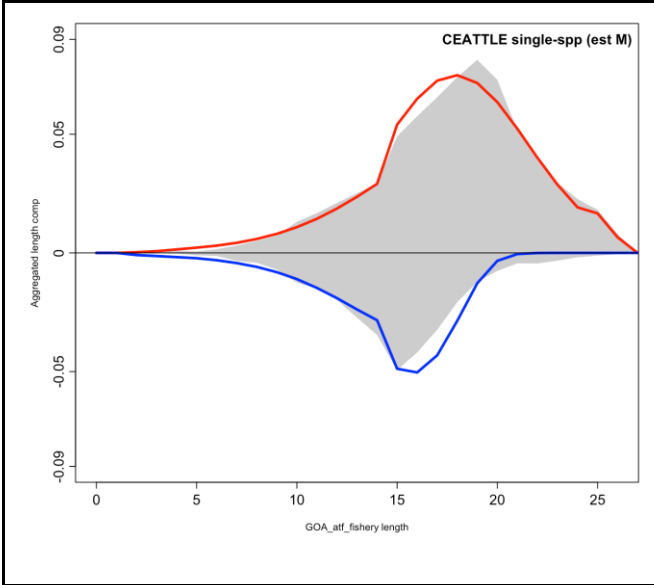
**Figure 5.** One step ahead (OSA) residuals of observed and expected bottom trawl survey age-composition data between the ADMB model and CEATTLE single- and multi-species models. NOTE: difference in z-scale.



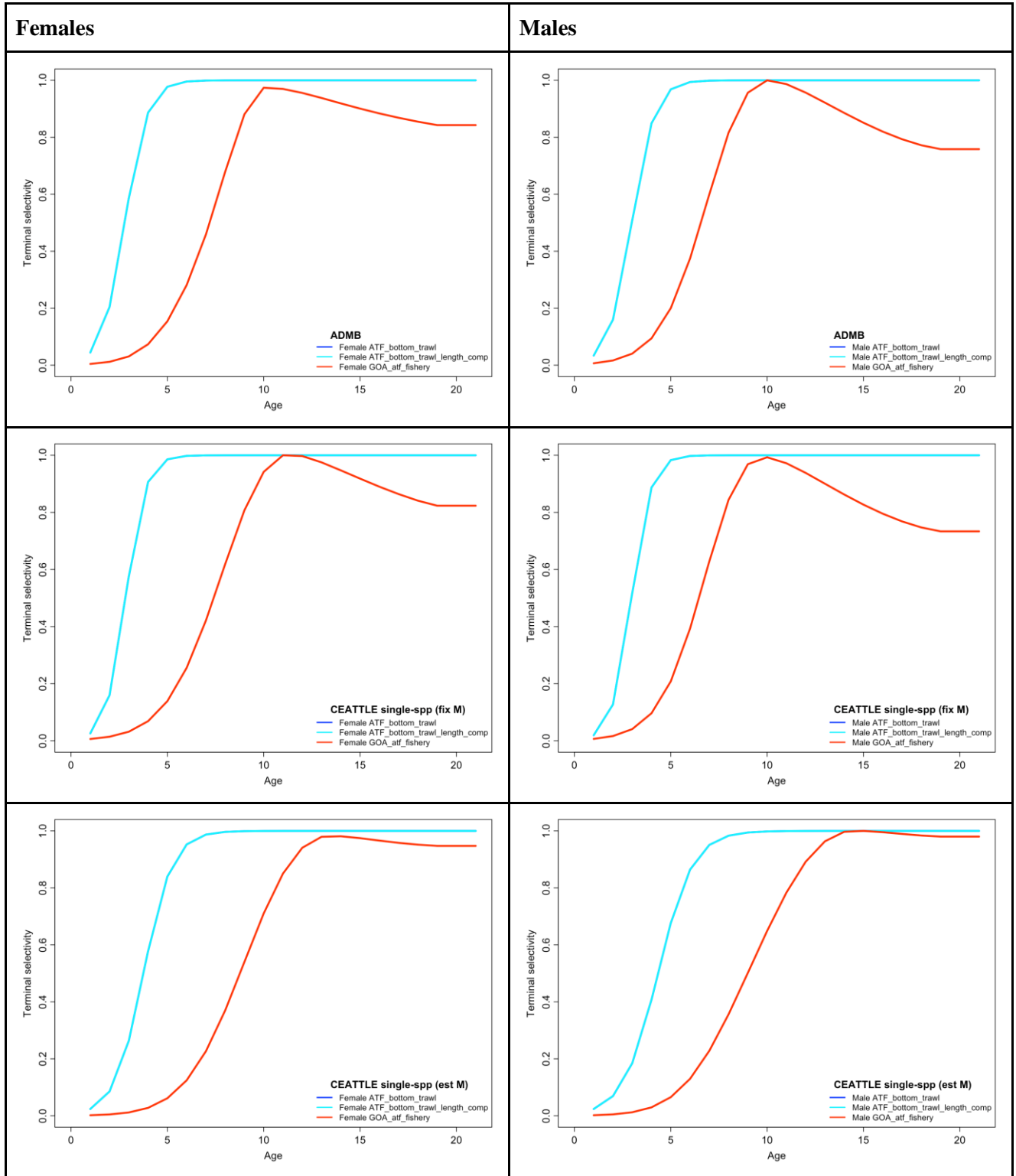
**Figure 6.** Fits to aggregated and pearson residuals of observed and expected fishery length-composition data between the ADMB model and CEATTLE single- and multi-species models. Females are red and males are blue. NOTE: difference in z-scale.

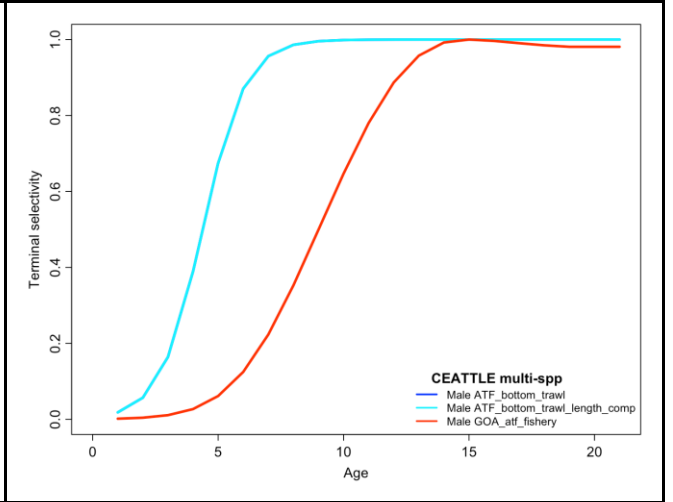
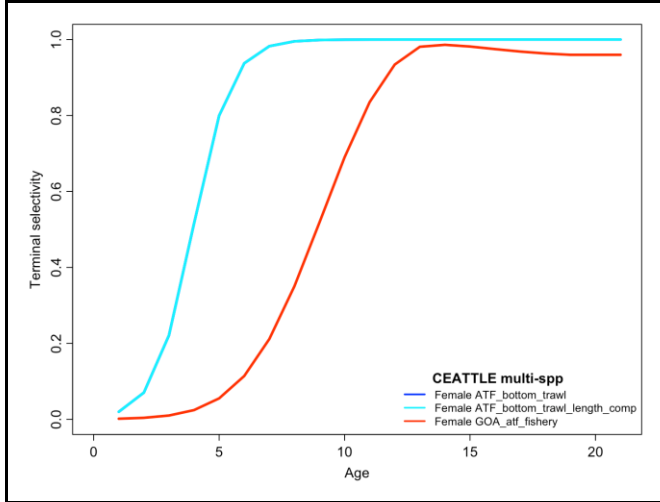




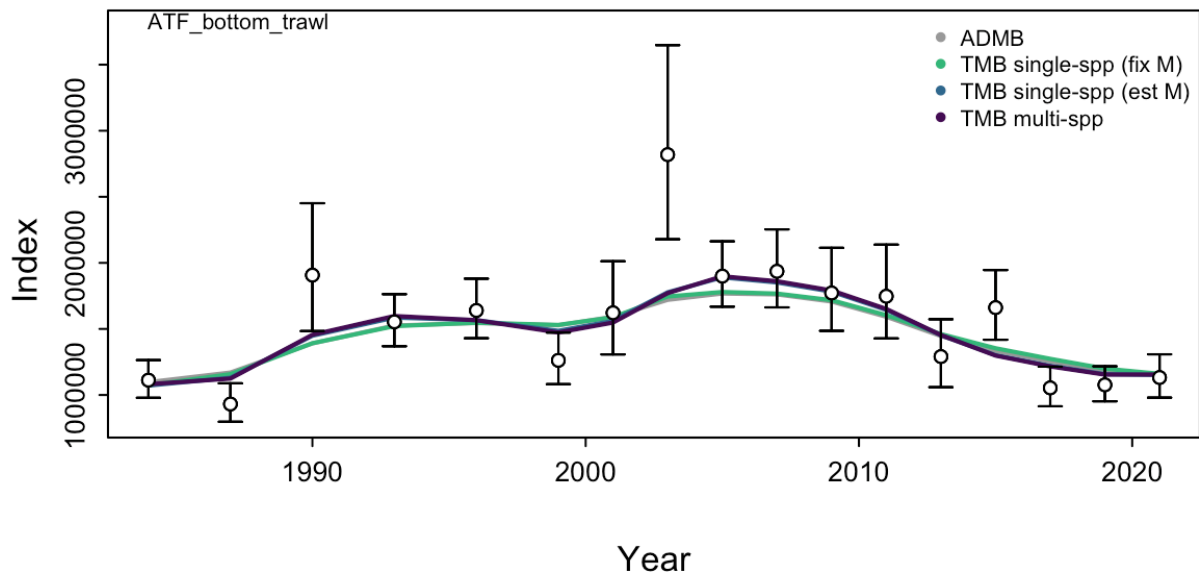


**Figure 7.** Estimated selectivity between the ADMB model and CEATTLE single- and multi-species models.

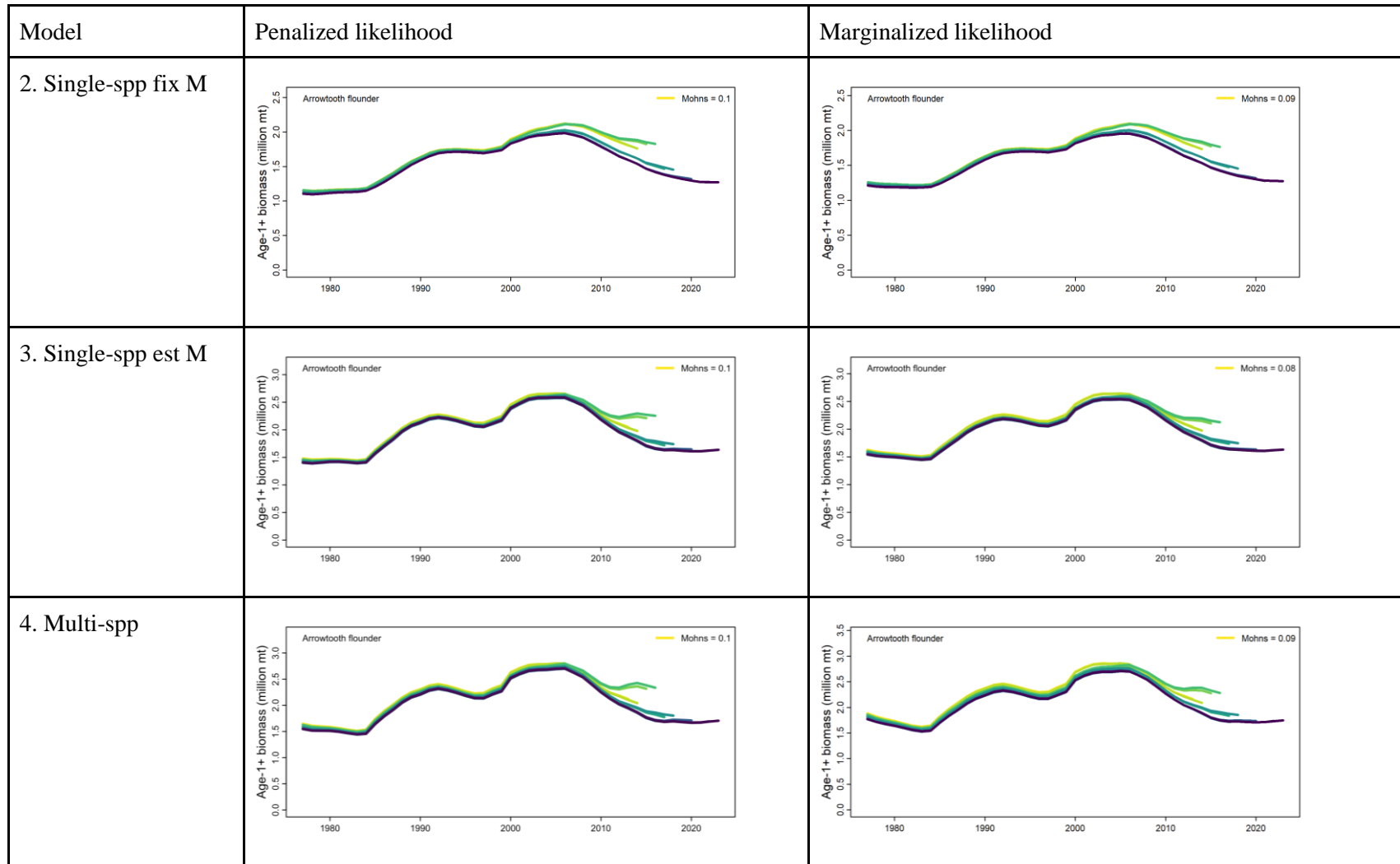




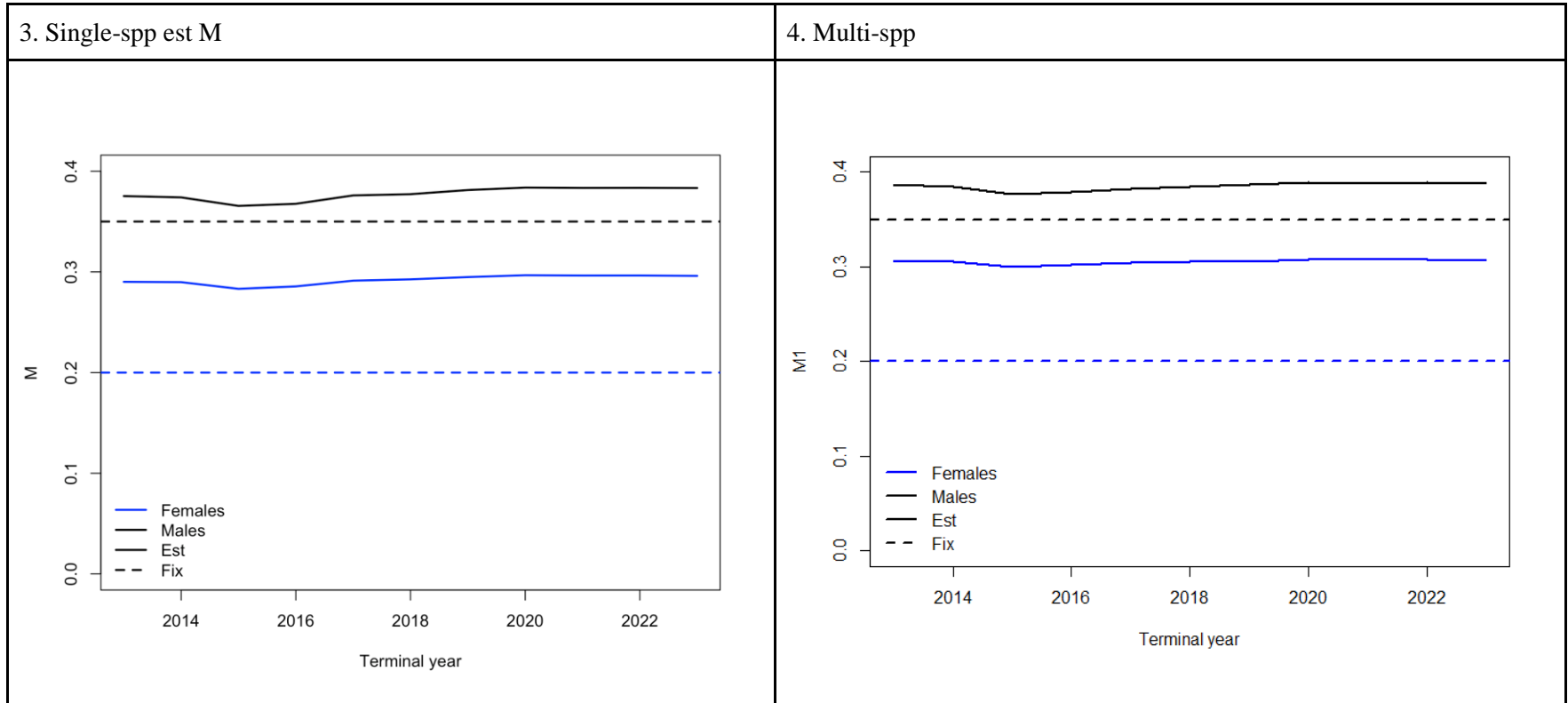
**Figure 8.** Observed (circles) and expected (lines) AFSC trawl survey biomass across the ADMB model and CEATTLE single- and multi-species models.



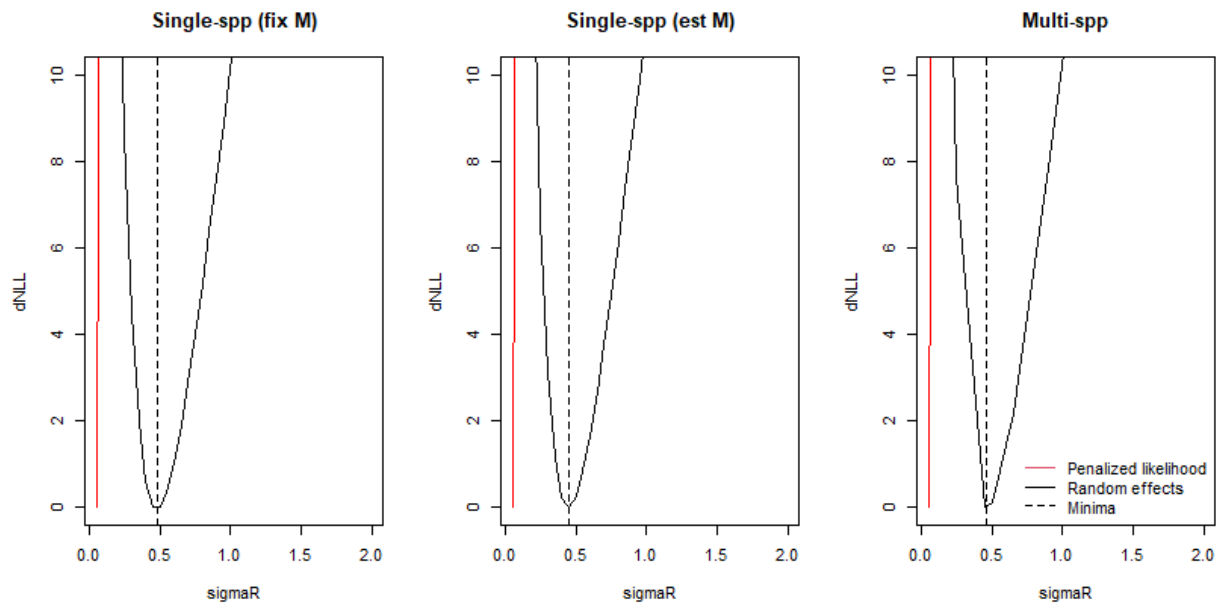
**Figure 9.** Retrospective spawning age-1+ total biomass estimates across CEATTLE single- and multi-species models. Mohn's rho is indicated in the upper right hand corner. The left column are models where recruitment deviates are treated as penalized deviates (similar to ADMB) and the right column are models where recruitment deviates are treated as random effects.



**Figure 10.** Retrospective estimates of total natural mortality ( $M$ ) and residual natural mortality ( $M1$ ) for CEATTLE single-species models that estimated  $M$  and multi-species models where recruitment deviates are treated as random effects.



**Figure 11.** Likelihood profiles for variance in recruitment ( $\sigma_{R}$ ) across CEATTLE single- and multi-species models where recruitment deviates are treated as penalized deviates (similar to ADMB) or as random effects.



## Appendix

### *Model bridging*

A series of models were developed to bridge the ADMB model to CEATTLE and evaluate the impacts of the previous four differences on model outputs:

- *Base model*: a base 2023 ADMB model. This model uses the 2021 SAFE assessment parametrization and extends the model and catch series to 2023, rather than use a separate projection module.
- *Bridging model 1*: The 2023 ADMB model with the multinomial likelihood correctly specified by setting the fishery length sample size for males to the same value as females and where the non-parametric selectivity penalties are set the same for males and females (40 and 100). Note, setting the penalties to 10 and 200 (female specification) for both sexes did not result in a converged model.
- *Bridging model 2*: CEATTLE where the maximum likelihood parameter estimates from *bridging model 1* are used as fixed inputs. Structurally, this model is exactly the same as *bridging model 1* but likelihood components are fully specified and include the log-normal bias correction.
- *Bridging model 3*: CEATTLE where the model parameters are estimated using TMB.
- *Bridging model 4*: ADMB model where the maximum likelihood parameter estimates from *bridging model 3* (CEATTLE) are used as fixed inputs.
- *Bridging model 5*: Same as model 3, however, the ageing error matrix is correctly applied to the expected true age-composition.
- *Bridging model 6*: Same as model 4, however, the recruitment deviates are treated as random effects and the associated variance parameter is estimated.

### *Results*

All single-species bridging models showed similar if not exactly similar trends in recruitment, spawning stock biomass, and biomass (Figure S1). Bridging model 1 and 2 had the same derived quantities, given that the parameters from the ADMB model were input into CEATTLE. This included total predicted catch, selectivity, and predicted survey biomass. Similarly, the likelihood component for non-parametric selectivity penalties were the same between bridging model 1 and 2 (Table S1). However, other likelihood components differed because CEATTLE uses the full probability distribution rather than simplified forms. Bridging model 2 and 3 had overlapping estimates of recruitment, spawning stock biomass, and biomass indicating that the minor changes in the log-likelihood formulations and optimization between ADMB and CEATTLE. Bridging model 3 resulted in a lower negative log-likelihood than when using the maximum likelihood parameter estimates from ADMB, suggesting that optimization is improved in TMB. Similarly, bridging model 4 (CEATTLE parameters input into ADMB) had lower negative log-likelihood components for survey index and fishery length data than bridging model 2, but due to high penalties on catch fits in ADMB, had a higher total negative log-likelihood. Correcting the specification of the ageing error matrix resulted in a higher log-likelihood, but estimates of total biomass and spawning biomass from bridging model 5 were extremely similar to bridging model 3. For bridging model 6, treating recruitment deviates as random effects resulted in a lower variance parameter ( $\sigma_R = 0.48$ ) than the value implicitly assumed by ADMB ( $\sigma_R = 0.707$ ). This resulted in slightly elevated estimates of biomass and spawning stock biomass in the first 10 years of the time series.



**Table S1.** Model comparison of the bridging models.

	<i>Base</i>	<i>1</i>	<i>2</i>	<i>3</i>	<i>4</i>	<i>5</i>	<i>6</i>
<b>Platform</b>	<i>ADMB</i>	<i>ADMB</i>	<i>TMB</i>	<i>TMB</i>	<i>ADMB</i>	<i>TMB</i>	<i>TMB</i>
<i>Likelihoods</i>							
Catch	4.32e-08	6.41e-07	-97.28	-97.52	0.00205	-97.52	-97.51
Fishery length composition	816.17	841.17	85.23	83.08	823.03	83.25	83.32
Survey biomass	27.86	28.16	1.84	0.82	27.19	-0.31	1.16
Survey age composition	276.91	275.98	32.67	32.93	278.16	42.80	43.36
Recruit deviations	5.04	5.03	47.57	44.41	6.06	45.51	24.30
Selectivity penalties	7.30	8.72	8.73	9.91	9.91	10.39	9.91
F regularity	21.20	21.31	21.31	19.35	19.35	19.19	20.44
<b>Joint NLL</b>	<b>177.67</b>	<b>181.95</b>	<b>100.08</b>	<b>92.97</b>	<b>195.81</b>	<b>103.31</b>	<b>84.99</b>
Marginal NLL							96.47
Number of parameters	158	158	158	158	158	158	92
<i>Estimates</i>							
<i>q</i> -trawl	1	1	1.0	1.0		1.0	1.0
Mean Recruitment (thousand)	801,987	800,286	806,206	815,324	800,286	814,450	806,846
$\sigma_r$	0.707	0.707	0.707	0.707	0.707	0.707	0.48
$F_{40\%}$							
2023 total biomass (t)	1,273,800	1,270,450	1,284,926	1,279,433	1,265,700	1,272,617	1,273,952
2023 spawning biomass (t)	709,254	710,935	710,935	713,886	713,886	712,504	718,708
$B_{100\%}$ (t)			1,684,224	1,702,520		1,700,424	1,684,452
$B_{40\%}$ (t)			673,690	681,008		680,170	673,781
$SSB_{100\%}$ (t)			984,753	995,141		993,804	984,431
$SSB_{40\%}$ (t)			393,901	398,056		397,522	393,772
$ABC_{F40\%}$ (t)							

**Figure S1.** Time-series of age-1 recruitment (millions; top panel), total biomass (million mt; upper middle panel), spawning stock biomass (million mt; lower middle panel), and catch (mt; bottom panel) as determined from the ADMB and bridging models.

