Alternative models for the 2023 stock assessment of the Rougheye and Blackspotted rockfish complex in the Gulf of Alaska

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Executive Summary

Gulf of Alaska (GOA) rougheye and blackspotted (RE/BS) rockfish are assessed on a biennial schedule in odd years and managed as a Tier 3 stock. Survey and fishery data are input to a statistical catch-at-age model developed in AD Model Builder (ADMB; Fournier et al. 2012), which generates historical time series of population estimates. Results from this model are input to the standard AFSC projection model, which predicts future population estimates, biological reference points, and recommended harvest levels. Acceptable Biological Catch (ABC) estimates are apportioned to the eastern, central, and western GOA management areas using the two-survey random effects (REMA) model written in ADMB that fits to the GOA bottom trawl survey (BTS) biomass, which informs biomass scale and trend, and the GOA longline survey (LLS) relative population weights (RPW), which informs biomass trend only. In the main body of the document we present alternative statistical catch-at-age models for consideration by GOA Groundfish Plan Team (GPT) and Scientific and Statistical Committee (SSC) in 2023. In Appendix A, we present alternative apportionment models that include an update to the *rema* R library as recommended by the GPT and SSC and an alternative apportionment method that accounts for different abundance trends and population scales indicated by the LLS RPWs and BTS biomass.

The statistical catch-at-age model for GOA RE/BS was last updated in 2015. Since then, the GPT, SSC, and internal reviewers have made numerous comments and recommendations related to the assessment's biological assumptions, data inputs, fleet structure, retrospective patterns, catchability, selectivity, and data weighting in the model. For 2023, we focused on updating the biological assumptions in the assessment, including the prior for natural mortality, estimates of growth (including weight-at-age and the size-age transition matrix), maturity, and ageing error. For natural mortality, we used the updated longevity estimator from Hamel and Cope (2022) based on the maximum age (135 y) estimated from BTS and fishery data in the GOA. We updated the ageing error matrix using methods outlined in Punt et al. 2008 and software in the nwfscSurvey R library. We recommend a new age-based logistic maturity curve using data from a histological study in the GOA (Conrath 2017). Finally, we fit length and weight-based growth curves using updated age, length, and weight specimen data from the GOA BTS and recommend a weight-at-age vector based on the allometric length-weight conversion instead of a weight-based von Bertalanffy growth function.

Summary of Methods

Changes in the input data:
Because updated data were not available, we use the same data available for the last full assessment in 2021. Based on a recommendation from the GOA GPT (September 2022) and SSC (October 2022), biomass estimates from the 1984 and 1987 GOA bottom trawl surveys were removed from the models.

Changes in the assessment methodology:
We present the base model (M15.4_2021) that was used in the 2021 full assessment plus 11 alternative models that include alternative data and modeling assumptions. Most of the models reflect either stepwise

updates to the model with new biological assumptions, or they were run as sensitivities. **The model in bold is preferred by the author for 2023**:

1) M15.4_2021: The accepted ADMB model in the last full assessment (Sullivan et al. 2021). Full specification details can be found here: https://apps-afsc.fisheries.noaa.gov/refm/docs/2015/GOArougheye.pdf
2) M15.4_2021_n80: M15.4_2021 but without 1984 and 1987 BTS data. This is the base model for all subsequent models.
3) M23.a_natmat_2021: M15.4_2021_n80 with an updated natural mortality prior.
4) M23.b_ageerror_2021: M15.4_2021_n80 with an updated ageing error matrix.
5) M23.c_maturity_2021: M15.4_2021_n80 with updated maturity-at-age.
6) M23.d_growth_2021: M15.4_2021_n80 with a new length-age transition matrix and weight-at-age using status quo methods (separate length and weight-based von Bertalanffy growth models) fit to updated BTS data through 2021.
7) M23.e_allom_2021: M23.d_growth_2021 but the weight-at-age vector is based on the allometric length-weight conversion instead of a weight-based von Bertalanffy growth function.
8) M23.full_2021: A combination of M23.a_natmat_2021, M23.b_ageerror_2021, M23.c_maturity_2021, and M23.d_growth_2021
9) **M23.full_allom_2021**: A combination of M23.a_natmat_2021, M23.b_ageerror_2021, M23.c_maturity_2021, and M23.d_allom_2021
10) M23.full_allom_fixM_2021 (*sensitivity*): M23.full_allom_2021 but M is fixed to the updated prior mean of 0.04.
11) M23.full_noGrowth_2021 (*sensitivity*): M23.full_allom_2021 but using the 2015 weight-at-age vector and length-age transition matrix.
12) M23.full_noGrowth_fixM_2021 (*sensitivity*): M23.full_allom_2021 but but using the 2015 weight-at-age vector and length-age transition matrix and fixing M the updated prior mean of 0.04.

Summary of Results

A summary of biological and management reference points for all models in 2021 is below. Note that these values are from the assessment model, not the projection model, and are for illustrating model differences only.

Description	M15.4_2021	M15.4_2021_n80	M23.a_natmat_2021	M23.b_ageerror_2021	M23.c_maturity_2021	M23.d_growth_2021	M23.e_allom_2021	M23.full_2021	M23.full_allom_2021
Age-3+ biomass in 2022	26,053	24,619	72,953	25,284	26,053	15,738	13,158	50,122	44,702
Age-3+ biomass in 2023	25,985	24,550	71,795	25,230	26,031	15,862	13,355	49,440	44,197
SSB in 2022	8,645	8,239	23,850	8,372	7,784	5,093	4,032	13,213	12,771
SSB in 2023	8,621	8,213	23,376	8,350	7,777	5,140	4,116	12,953	12,563
B_{100}	14,776	14,125	27,698	14,553	13,871	12,180	10,886	16,893	16,812
B_{40}	5,911	5,650	11,079	5,821	5,548	4,872	4,355	6,757	6,725
B_{35}	5,172	4,944	9,694	5,094	4,855	4,263	3,810	5,912	5,884
F_{40}	0.0381	0.0377	0.0491	0.0383	0.0333	0.0386	0.0409	0.0541	0.0482
F_{35}	0.0460	0.0455	0.0590	0.0462	0.0399	0.0464	0.0490	0.0654	0.0578
F_{ABC} in 2022	0.0381	0.0377	0.0491	0.0383	0.0333	0.0386	0.0377	0.0541	0.0482
F_{ABC} in 2023	0.0381	0.0377	0.0491	0.0383	0.0333	0.0386	0.0386	0.0541	0.0482

ABC in 2022	788	743	2,779	763	689	470	369	1,936	1,627
ABC in 2023	780	735	2,706	756	683	471	382	1,885	1,593
F_{OFL} in 2022	0.0460	0.0455	0.0590	0.0462	0.0399	0.0464	0.0452	0.0654	0.0578
F_{OFL} in 2023	0.0460	0.0455	0.0590	0.0462	0.0399	0.0464	0.0462	0.0654	0.0578
OFL in 2022	946	892	3,328	916	824	562	441	2,325	1,941
OFL in 2023	937	883	3,240	908	817	564	456	2,265	1,900

Analytic Approach

In each of the following sections, we present the data and methods used to update the biological assumptions in the GOA RE/BS assessment model.

Natural mortality

Natural mortality (M) is currently estimated in the assessment model using a prior mean of 0.03 and CV=0.1. The mean of 0.03 is based on a study by McDermott (1994), which used gonadosomatic index (GSI) data and the GSI-based M estimator M_{GSI} from Gunderson and Dygert (1988). The McDermott GSI study was conducted prior to the formalization of RE/BS as separate species and used combined data from the Bering Sea, Aleutian Islands, Gulf of Alaska, British Columbia, and the U.S. West Coast. They found M to range between 0.030 and 0.039 depending on if Stage V (late vitellogenesis) and Stage VI (containing at least some oocytes in the migratory nucleus stage) ovaries were used to determine GSI versus strictly Stage VI ovaries. McDermott (1994) recommended GSI estimates determined using Stage VI samples but cautioned this approach could result in an overestimation of GSI and thus M if oocytes hydrate in the migratory nucleus stage before the coalescence of yolk. Sullivan et al. (2022) revisited the GSI data from McDermott (1994) using updated M_{GSI} methods (Gunderson 1997, Hamel 2015) and found M_{GSI} to range between 0.023 and 0.032. These values are substantially lower than the M_{GSI} estimates reported in McDermott (1994) despite using the same GSI inputs, which was an expected outcome based on updates to M_{GSI} methodology over time (Gunderson and Dygert 1988, Gunderson 1997, Hamel 2015).

We updated the M prior based on longevity ($M_{t_{max}}$), where t_{max} is the maximum age for a species (Hamel and Cope 2022). This is based on recommendations from Then et al. (2015), which found that $M_{t_{max}}$ estimators exhibit superior predictive performance relative to growth-based estimators or combined approaches that averaged multiple M estimates. Hamel and Cope (2022) recently reevaluated Then et al. (2015) and Hoenig's (1982, 1983) $M_{t_{max}}$ methods by assuming a logarithmic transformation of M and t_{max} to account for heteroscedasticity in the original Then data set. The updated $M_{t_{max}}$ prior in Hamel and Cope (2022) assumes a lognormal distribution, where the median (mean in log-space) is given

$$M_{t_{max}} = \frac{5.4}{t_{max}},$$

with a standard deviation in log-space of 0.31. We assumed a t_{max} of 135 y, which is based on a specimen collected during the GOA bottom trawl survey in 2009 (Sullivan et al. 2022). The specimen was identified as a male rougheye rockfish, was 64 cm fork length, and weighed 3.342 kg.

The updated prior for $M_{t_{max}}$ based on this approach is 0.04. The updated prior is considerably more variable than the current prior (Figure 1). The 95% confidence intervals for the updated prior include M values between 0.022 and 0.073, whereas 95% confidence intervals for the current prior range between 0.024 and 0.036. Sullivan et al. (2022) considered M estimators based on longevity, von Bertalanffy growth parameters, GSI, and metabolic rates and reported potential M estimates for RE/BS ranging between 0.023 (M_{GSI}) and 0.219 (growth). The M_{GSI} and $M_{t_{max}}$ estimators resulted in the lowest values

for M, and the estimator based on metabolic rate resulted in intermediate values (0.092). The M estimates based on growth resulted in the highest values, which Sullivan et al. (2022) attributed to the fact that rockfish often grow rapidly and can attain maximum sizes at relatively young ages despite their tendency towards extreme longevity. This growth pattern violates the M/k ratio underpinning the M estimator based on growth, and consequently this estimator has been demonstrated to not fit *Sebastes* species well (Thorson et al. 2017). The variability in the results from Sullivan et al. (2022) highlight the uncertainty in M, thus lending support to the updated prior presented here. As a sensitivity, a couple alternative models were also run fixing M at 0.04.

Maturity

Maturity is fixed in the assessment model using a vector of age-specific proportion of females mature. The current maturity schedule is based on maturity-at-length estimated in McDermott (1994), which was converted to maturity-at-age using the size-age transition matrix estimated in 2015 and currently used in the assessment. As described in the natural mortality section, McDermott (1994) was conducted prior to the formalization of RE/BS as separate species and used combined data from the Bering Sea, Aleutian Islands, Gulf of Alaska, British Columbia, and the U.S. West Coast.

We updated the maturity schedule using data collected in 2009 and 2010 during special cruises, standard bottom trawl surveys, and by fishery observers in the GOA (personal communication, Christina Conrath, AFSC, Groundfish Assessment Program; Table 1). These data were identified to species using macroscopic field identification methods and resultant maturity curves show that blackspotted rockfish mature later (age at 50% maturity; a_{50}=27.4 y) and at a slower rate compared to rougheye rockfish (a_{50}=19.5 y; Conrath 2017). These data have not been used in earlier stock assessments because species identification in the study was not verified using genetics (Shotwell and Hanselman 2018). However, these data are preferred over McDermott (1994) because they are specific to the assessment region (GOA), were analyzed using modern histological methods, and have age estimates associated with each specimen. Because no other inputs to the assessment (e.g., growth, natural mortality, etc.) are currently species-specific, we advocate for a combined species approach with an associated sensitivity analysis that evaluates species-specific maturity curves.

We estimated maturity using a generalized linear model approach for logistic regression, where the probability of being mature (p) is a function of age (a):

$$\log\left(\frac{p_a}{1-p_a}\right) = \beta_0 + \beta_1 a,$$

We then derived a_{50} and the instantaneous rate of maturation (δ) using $a_{50} = -\beta_0/\beta_1$ and $\delta = (\beta_0 + \beta_1)/(1 - a_{50})$. Using these derived parameter estimates, maturity-at-age can be attained using

$$p_a = \left(\frac{1}{1+\exp{(\delta(a-a_{50}))}}\right).$$

Models were fit using custom software coded in Template Model Builder. Following methods in Conrath and Hulson (2021), a penalty term of 1e3 was added to negative log-likelihood to constrain maturity predictions at age-0 to equal approximately zero. We evaluated the sensitivity of model results to assuming no penalty term and a penalty term of 1e5. Additionally, we estimated species-specific parameter values for comparison.

The combined RE/BS maturity model with a penalty of 1e3 resulted in an a_{50} of 23.17 y and a δ of -0.164 (Table 2). The resultant maturity curve suggests that RE/BS mature more slowly and at older ages compared to the current assessment, which has an a_{50} of 18 y (Figure 2). The model with no penalty had

a slower maturation rate and smaller a_{50}, whereas the model with the higher penalty (1e5) had a faster maturation rate and higher a_{50} (Table 2). Similar to Conrath (2017), the species-specific models suggest that rougheye rockfish mature earlier and at a faster rate compared to blackspotted rockfish (Table 2, Figure 2).

Ageing error

Ageing error, or the uncertainty in an age reader's interpretation of annuli on a fish's otolith relative to the true age of the animal, is represented in the assessment as a matrix that specifies the probability of the fish of a true age a being aged at age a'. The current ageing error matrix was first adopted in 2015 and was developed using 1,589 age reader and tester pairs from 1984, 1987, 1990, 1993, 1996, 1999, 2003-2007, and 2009 bottom trawl surveys. It assumes that break-and-burn ages were unbiased and that uncertainty around the true age was normally distributed. The current ageing error matrix is used to fit both bottom trawl survey and fishery age composition data.

Here we update the ageing error matrix using both bottom trawl survey and fishery data through 2021 using a total of 2,974 reader and tester pairs (Table 3). Fishery data are appropriate to use in this case because RE/BS older than ~25 y are better represented in the fishery data, whereas younger RE/BS are better represented in the survey data (right-hand panels in Figure 3). We examined length-age and weight-age plots and removed one outlier from the data set (highlighted as the red star middle and bottom left-hand panels in Figure 3)).

We re-evaluated the assumption that the current ageing process is unbiased by examining unique reader-tester pairs and the frequency for which the final age equals the reader age. We found that the full data set included 22 unique reader and tester pairs based on seven unique readers (Table 4). On average, the final age was equal to the reader age only 55% of the time and this ranged between 36% and 100% of the time depending on the unique reader and tester pair (Table 4). These results make assessing individual bias very challenging, because neither reader nor tester could be considered unbiased and the final read cannot be used to assess precision because the final read is not an independent variable. For these reasons, we recommend maintaining the current assumption that RE/BS age data are unbiased. Ideally, age reader bias would be revisited for this assessment using an unbiased reference data set as described in Punt et al. (2008).

We updated the ageing error matrix using the *nwfscAgeingError* R library based in ADMB that is commonly used at the Northwest Fisheries Science Center and has been applied to several Alaskan stocks including GOA flathead sole and GOA pollock (Punt et al. 2008; Thorson et al. 2012). We compared the following models which differed in the parametric relationship between ageing error and true age: 1) M.1.0_LinearSD_NoBias: a 1-parameter linear relationship of the standard deviation (SD) with true age; 2) M.2.0_CurvilinearSD_NoBias: a 3-parameter Hollings-form relationship of SD with true age; 3) M.3.0_CurvilinearCV_NoBias: a 3-parameter Hollings-form relationship of coefficient of variation (CV) with true age. We then compared models using Akaike Information Criterion (AIC), where the model with the lowest AIC is considered superior in terms of fit and parsimony.

The best model by AIC assumed a curvilinear relationship between SD and true age (M.2.0_CurvilinearSD_NoBias), and we recommend using this ageing error matrix in 2023 (Table 5, Figure 4). The resulting SDs from all alternative models were generally higher than the currently assumed SD, though the curvilinear models generally scaled SD similarly to the current model at older ages (Figure 5). The curvilinear functional form is a sensible choice for long-lived species, where we may expect the rate of increasing imprecision to asymptote at older ages.

Growth

The weight-at-age vector and length-age transition matrix are treated as fixed, static inputs to the stock assessment model. These inputs were last updated in 2015 (Shotwell et al. 2015). Currently, length-at-age is obtained using the von Bertalanffy growth model fit in ADMB:

$$L_a = L_\infty(1 - \exp(-k(age - t_0))),$$

Inputs to the model are the observed length-at-age mean and standard deviation (SD) from bottom trawl survey data, correcting for length-stratified sampling as specified in Bettoli and Miranda (2001). There is assumed to be a linear relationship between the observed SD of length-at-age and log-transformed age. Using the predicted SD of length-at-age from this linear model, the length-age transition matrix is constructed for the probability of different size classes for each age (Figure 6).

Weight-at-age is obtained by first fitting the allometric length-weight relationship:

$$W = \alpha L^\beta.$$

The β parameter was then fixed in the weight-based formulation of the von Bertalanffy model fit in ADMB:

$$W_a = W_\infty(1 - \exp(-k(age - t_0)))^\beta,$$

Inputs to this model are the observed weight-at-age mean and SD from bottom trawl survey data, correcting for length-stratified sampling as specified in Bettoli and Miranda (2001).

Data were updated using bottom trawl survey data between 1990 and 2021. A comparison of the old (2015) and new (2021) length-at-age and weight parameters are below:

Old (2015) length-at-age parameters: L_∞= 49.6 cm, k =0.09, t_0=-0.69, n=6,738
New (2021) length-at-age parameters: L_∞= 54.2 cm, k =0.07, t_0=-1.5, n=7,638

Old (2015) weight-at-age parameters: W_∞= 1,639 g, k =0.12, t_0=-0.38, β = 3.086, n=5,806
New (2021) weight-at-age parameters: W_∞= 1,843 g, k =0.10, t_0=-0.88, β = 3.097, n=7,063

In addition to status quo growth method with updated data, we also considered an alternative method that calculates the weight-at-age vector using the allometric conversion of length-at-age to weight-at-age (Figure 7). This method is preferred because it reduces potential conflict between weight-at-age and length-at-age trajectories.

Model Results

Before updating biological assumptions in the model, the 1984 and 1987 bottom trawl survey data (biomass and age compositions) were removed. Removing the 1984 and 1987 bottom trawl survey age and abundance index data from the base model (M15.4_2021_n80 vs. M15.4_2021) resulted in slightly higher estimates of bottom trawl survey catchability (Figure 8C) and in turn a decrease in the scale of the population (Figure 8D). Then, the biological updates were incorporated one-by-one into the new base model with no 1980s trawl survey data. The longline and bottom trawl survey abundance indices for the GOA rougheye/blackspotted assessment model have relatively flat but downward trending trajectories, and changes to the data and biological assumptions of the model subtly improve the overall fit to these data (Figures 8A and 9A).

Updating the *M* prior (M23.a_natmat_2021) had the largest influence on assessment model results, leading to a near three-fold increase in the scale of the population relative to M15.4_2021_n80 (Figure 9D). Updates to the length-age transition matrix and weight-at-age vector (M23.d_growth_2021 and M23.e_allom_2021) decreased the scale of the population and increased estimates of fishing mortality over time (Figure 9D). As expected, *M* was negatively correlated with both the bottom trawl and longline survey catchabilities, leading to lower estimates of these parameters in the models with updated *M* (M23.a_natmat_2021, M23.full_2021, and M23.full_allom_2021; Figure 9C). Notably, *M* was estimated to be much higher than the prior mean of 0.04 in the full models (approximately 0.062 for both M23.full_2021 and M23.full_allom_2021; Figure 9C).

Finally, the all biological updates were incorporated into two separate "full" models, one using the status quo method for estimating the length-age transition matrix (M23.full_2021) and the second using the allometric conversion to calculate weight-at-age from length-at-age (M23.full_allom_2021). Results from these two models reflected a compromise between the increase in scale caused by the new *M* prior and the decrease in scale caused by the updated growth assumptions in the model. Updates to the length-age transition matrix and weight-at-age (M23.d_growth_2021 and M23.e_allom_2021) result in increased total likelihoods (Table 6). In part this can be attributed to degraded fits to the age and length composition data (Figures 10-13). For the length compositions, the degraded fit is primarily 40-55 cm length bins and in the plus group (Figures 12 and 13). Notably, the selectivity curves are simpler in the full models and therefore potentially more biologically defensible (Figure 9B).

Sensitivity results

Three alternative models were run that either fixed M at the updated prior mean (0.04) and/or used the 2015 weight-at-age vector and length-age transition matrix. Models with fixed M (M23.full_allom_fixM_2021 and M23.full_noGrowth_fixM_2021) were most similar to the base model (Figure 14). This result was expected given M15.4_2021_n80 estimates M be 0.034. Models that did not update the weight-at-age vector and length-age transition matrix (M23.full_noGrowth_2021 and M23.full_noGrowth_fixM_2021) differed considerably when M was estimated or not. The model where M was estimated (M23.full_noGrowth_2021) resulted in the highest estimates of stock scale relative to all other models (Figure 14).

Recommendation and Rationale

We recommend M23.full_allom_2021 for use in 2023. This model configuration reflects updated assumptions for natural mortality, maturity, ageing error, and growth based on the most current available data and recommended practices in stock assessment. While we acknowledge M23.full_allom_2021 results in degraded fits to data relative to the base model, it is the preferred model from which to address additional GPT and SSC recommendations related to catchability, selectivity, fleet structure and data weighting in future assessment cycles. The author welcomes feedback and alternative recommendations from reviewers.

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Tables

Table 1. Sample sizes by year and month for the rougheye (RE) and blackspotted (BS) rockfish maturity data in Conrath (2017).

	BS		RE		
	2009	**2010**	**2009**	**2010**	**Combined**
January	0	121	0	105	226
February	0	0	7	8	15
March	1	0	21	28	50
April	0	0	3	0	3
May	6	2	3	0	11
June	27	0	15	2	44
July	4	0	12	0	16
August	1	0	31	0	32
September	0	0	4	0	4
October	0	0	2	0	2
November	66	0	54	0	120
December	68	0	74	0	142
Total	173	123	226	143	**665**

Table 2. Parameter estimates (with standard error) for the alternative maturity models considered, including alternative penalties on the negative log-likelihood for age-0 fish (NoPen=no penalty) and models fit to all rougheye and blackspotted (REBS) data compared to species-specific models. Conrath_REBS_Pen=1e3 is the author-preferred model.

Model	Age at 50% maturity (a_{50})	Maturation rate (δ)
Conrath_REBS_NoPen	21.34 (0.92)	-0.095 (0.010)
Conrath_REBS_Pen=1e3	**23.17 (0.55)**	**-0.164 (0.008)**
Conrath_REBS_Pen=1e5	24.08 (0.36)	-0.323 (0.008)
Conrath_BS_Pen=1e3	27.32 (0.79)	-0.174 (0.012)
Conrath_RE_Pen=1e3	19.38 (0.59)	-0.230 (0.014)

Table 3. Annual sample sizes for bottom trawl survey and fishery age reader and tester pairs.

Year	Survey	Fishery	Total
1984	73	0	73
1987	64	0	64
1990	0	81	81
1993	233	0	233
1996	182	0	182
1999	155	0	155
2003	291	0	291
2004	0	85	85
2005	81	0	81
2006	0	180	180
2007	94	0	94
2008	0	60	60
2009	186	61	247
2010	0	47	47
2011	79	0	79
2012	0	83	83
2013	205	0	205
2014	0	92	92
2015	59	0	59
2016	0	78	78
2017	257	0	257
2018	0	70	70
2019	86	0	86
2020	0	40	40
2021	52	0	52
Total	**2,097**	**877**	**2,974**

Table 4. Unique reader and tester pairs, with the number of specimens (N) for which the final age equaled the reader age, total N, and percent for which final age equaled reader age.

Reader Name	Tester Name	N Final Age = Reader Age	Total N	Percent Final Age = Reader Age
Chris Gburski	Betty Goetz	315	615	51%
Charlie Piston	Betty Goetz	222	448	50%
Irina Benson	Betty Goetz	141	232	61%
Charlie Piston	Chris Gburski	85	157	54%
Delsa Anderl	Charles Hutchinson	79	145	54%
Charlie Piston	Irina Benson	78	144	54%
Irina Benson	Chris Gburski	79	143	55%
Chris Gburski	Charlie Piston	73	128	57%
Chris Gburski	Irina Benson	57	127	45%
Charles Hutchinson	Betty Goetz	78	123	63%
Charles Hutchinson	Irina Benson	87	116	75%
Charlie Piston	Charles Hutchinson	74	115	64%
Dan Foy	Betty Goetz	67	112	60%
Chris Gburski	Delsa Anderl	25	70	36%
Charles Hutchinson	Delsa Anderl	40	59	68%
Charles Hutchinson	Charlie Piston	34	56	61%
Delsa Anderl	Charlie Piston	37	53	70%
Irina Benson	Charlie Piston	24	50	48%
Chris Gburski	Charles Hutchinson	17	42	40%
Betty Goetz	Irina Benson	17	25	68%
Betty Goetz	Charles Hutchinson	9	9	100%
Betty Goetz	Chris Gburski	5	5	100%
Total	**Total**	**1,643**	**2,974**	**55%**

Table 5. Model selection results for the ageing error analysis.

Model	AIC	deltaAIC
M.1.0_LinearSD_NoBias	30744.0	12.3
M.2.0_CurvilinearSD_NoBias	30731.7	0.0
M.3.0_CurvilinearCV_NoBias	30732.3	0.6

Table 6. Likelihood components for all models without the 1984 and 1987 trawl survey data.

Likelihood component	M15.4_2021_n80	M23.a_natmat_2021	M23.b_ageerror_2021	M23.c_maturity_2021	M23.d_growth_2021	M23.e_allom_2021	M23.full_2021	M23.full_allom_2021
Penalties/Priors	2.2	1.2	2.6	2.2	15.4	15.4	8.0	7.9
Catch	0.1	0.0	0.1	0.1	0.3	0.3	0.0	0.0
Trawl survey biomass	12.2	13.0	12.2	12.2	10.4	10.5	10.8	11.1
Longline survey abundance	19.6	19.6	19.5	19.6	17.7	18.0	15.1	15.3
Fishery ages	30.6	29.8	29.9	30.6	54.1	53.9	40.9	40.7
Trawl survey ages	29.6	29.4	31.1	29.6	33.4	32.9	31.0	30.8
Fishery lengths	70.5	69.8	69.9	70.5	83.1	83.3	144.3	144.3
Longline survey lengths	98.4	97.3	97.8	98.4	123.9	124.0	256.5	256.6
Total	**263.2**	**260.1**	**263.1**	**263.2**	**338.2**	**338.2**	**506.6**	**506.8**

Figures
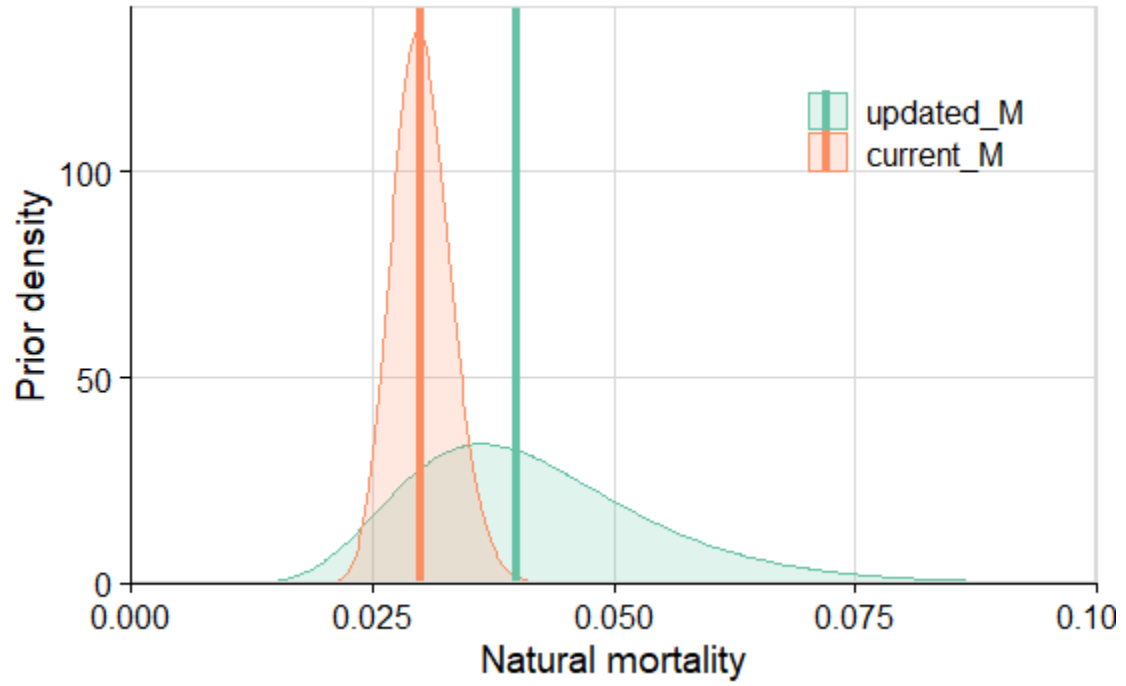
Figure 1. A comparison of the updated and current natural mortality (M) prior.
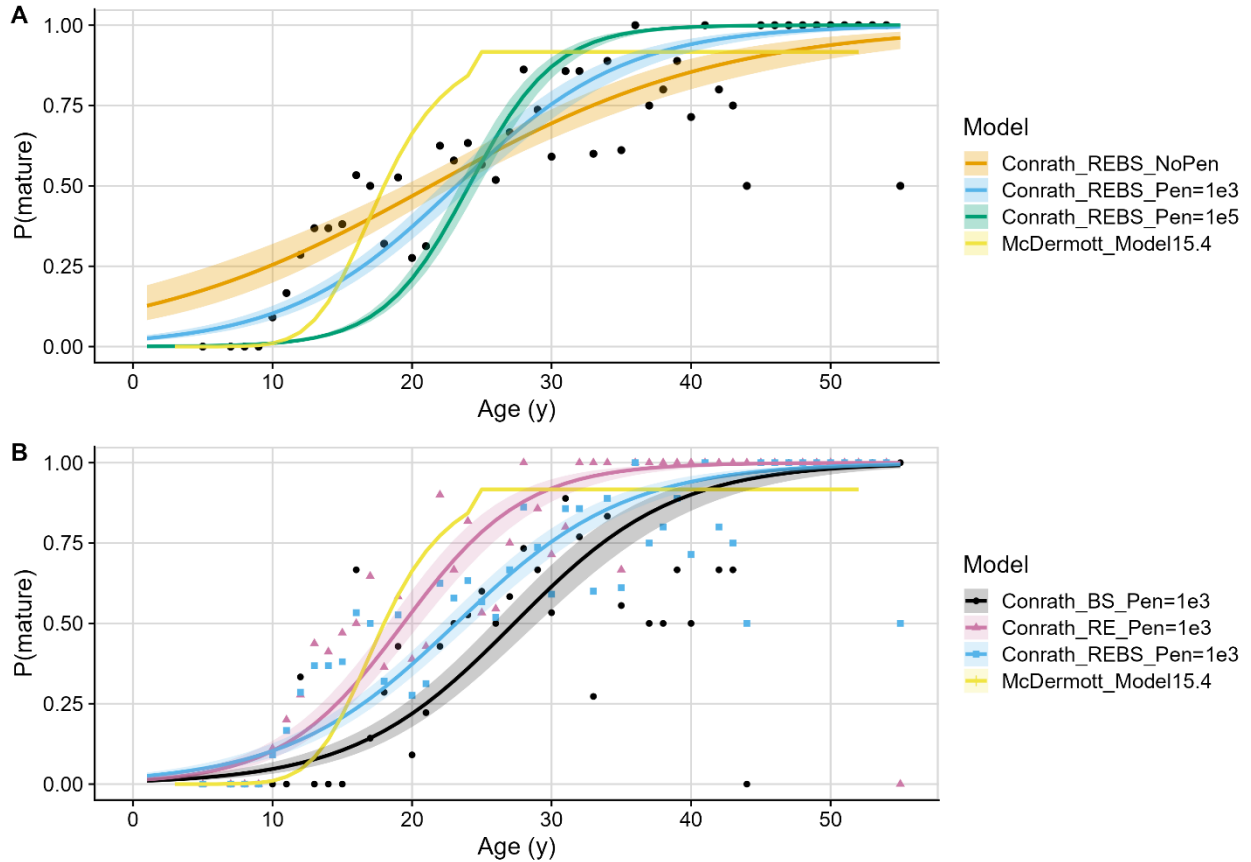
Figure 2. Maturity-at-age predictions based on Conrath (2017) data (points) compared to the maturity-at-age vector assumed in the current assessment model (McDermott_Model15.4). The top panel (A) shows model results for alternative penalties on the negative log-likelihood for age-0 fish, where NoPen=no penalty. The bottom panel (B) compares results when a single model was fit to all rougheye and blackspotted (REBS) data to species-specific models. Conrath_REBS_Pen=1e3 is the author-preferred model.
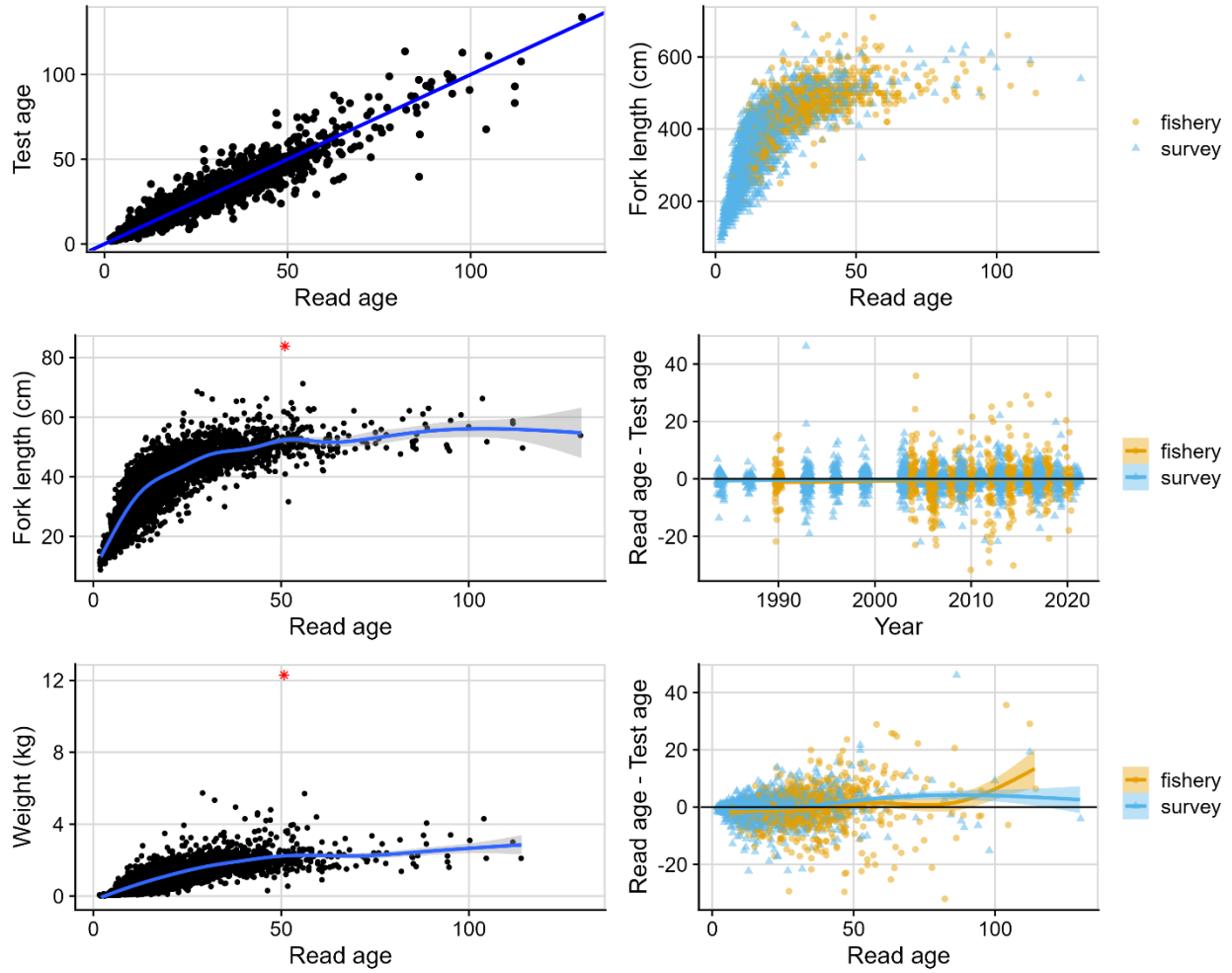
Figure 3. Diagnostic figures for the ageing error analysis. The figures on the left show the relationship between test and read age (top), length and age (middle), and weight and age (bottom). The red star in the middle and bottom left-hand figures was deemed an outlier and removed from the analysis. The right-hand figures are separated by data type, with fishery data in orange and bottom trawl survey data in blue. The top figure shows length and age (top), difference between read age and test age by year (middle), and difference between read age and test age by read age (bottom). Smoothed lines in all plots are the results from a loess moother using ggplot2 in R.
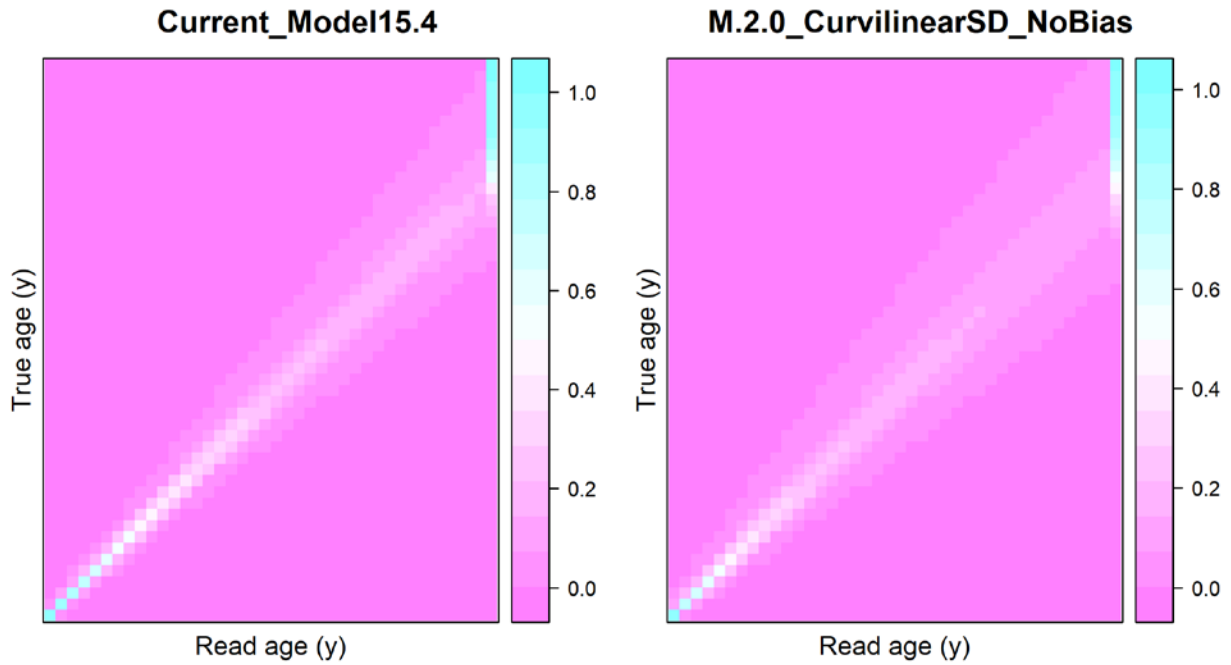
Figure 4. A comparison of the current ageing error matrix (Current_Model15.4) and the recommend ageing error matrix (M.2.0_CurvilinearSD_NoBias). In the assessment model the ageing error matrix is asymmetric because the number of modeled ages (ages 3-52) differs from the number of ages for which data are specified (ages 3-42).
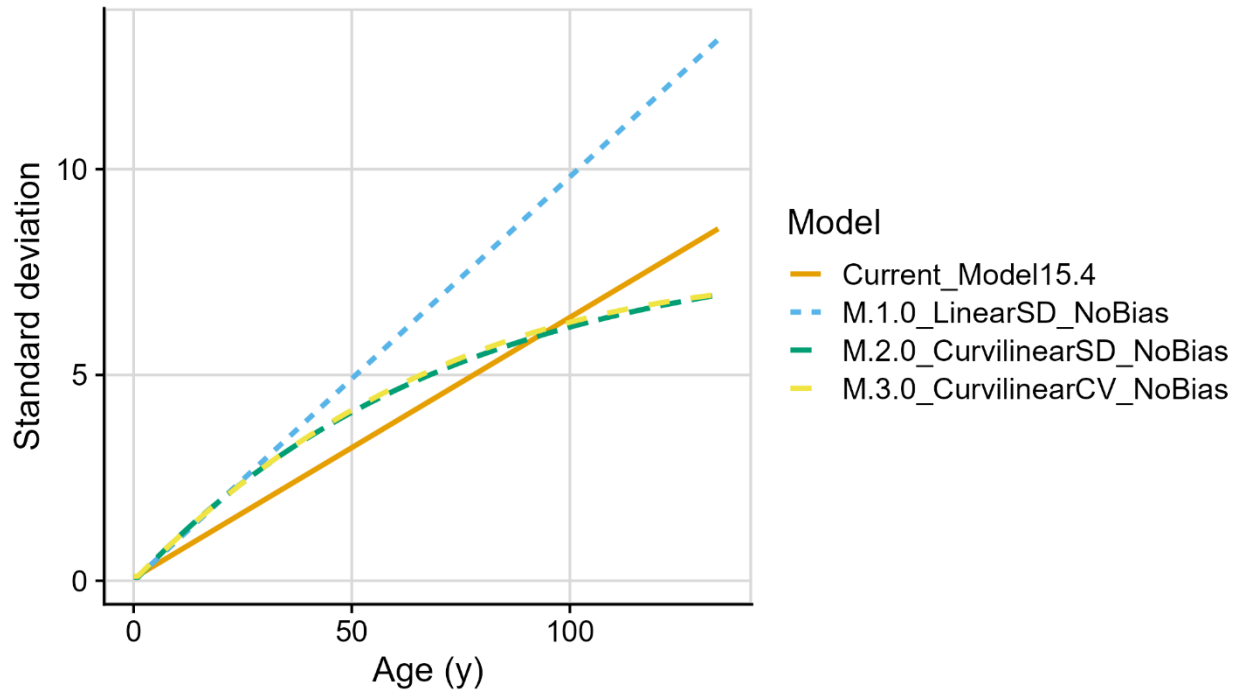
Figure 5. A comparison of the standard deviation by age for the alternative ageing error models.
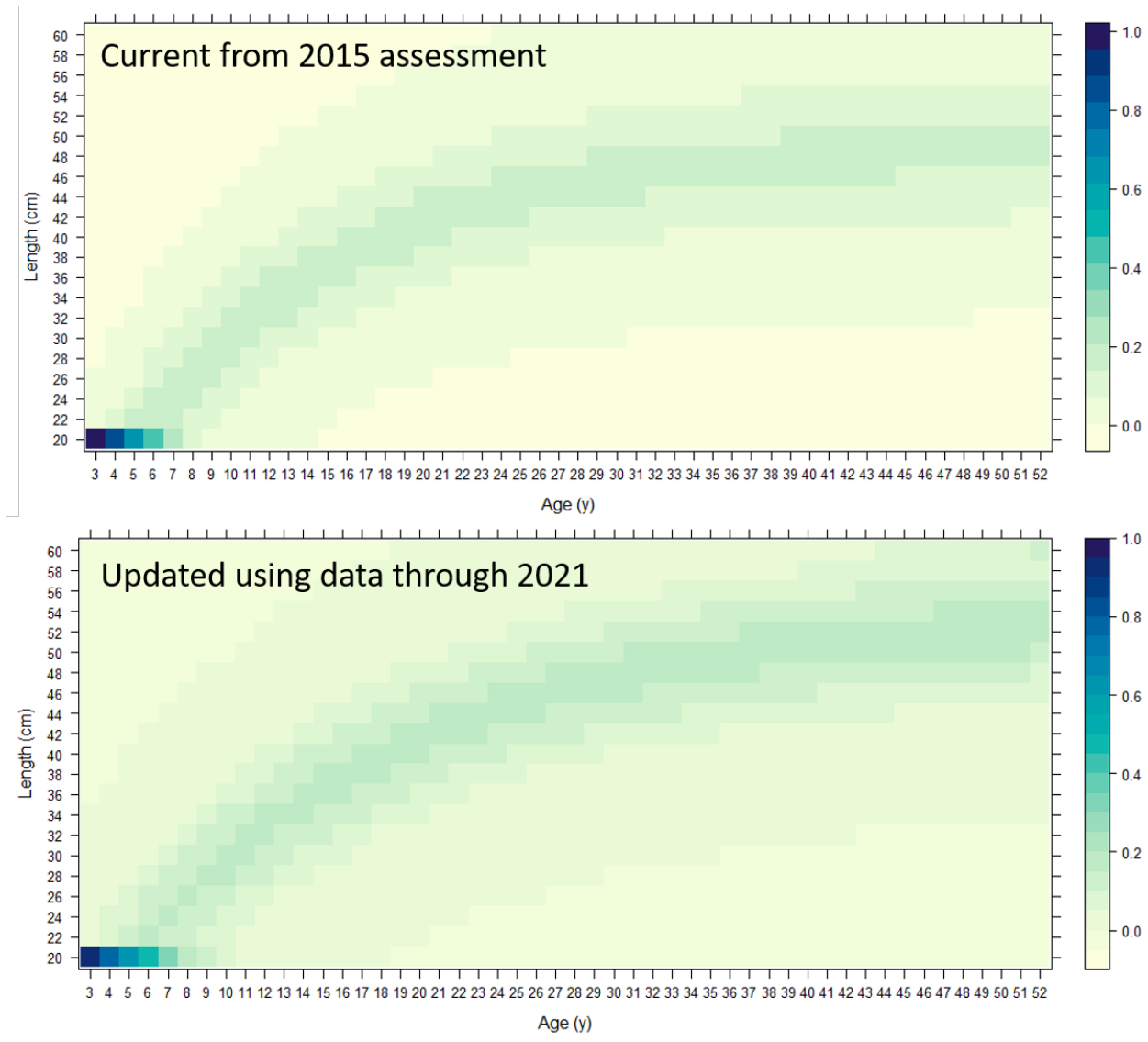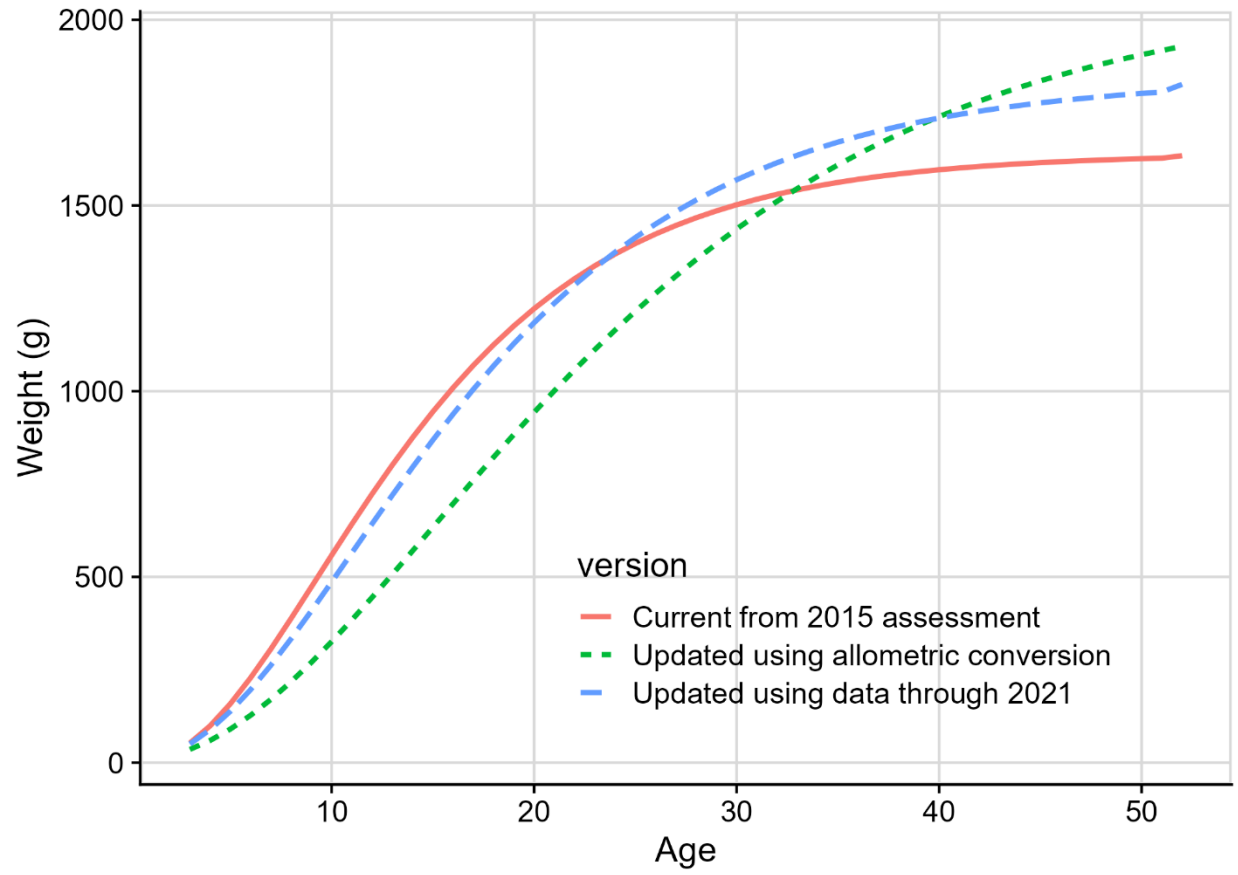
Figure 6. A comparison of the current and updated length-age transition matrices.

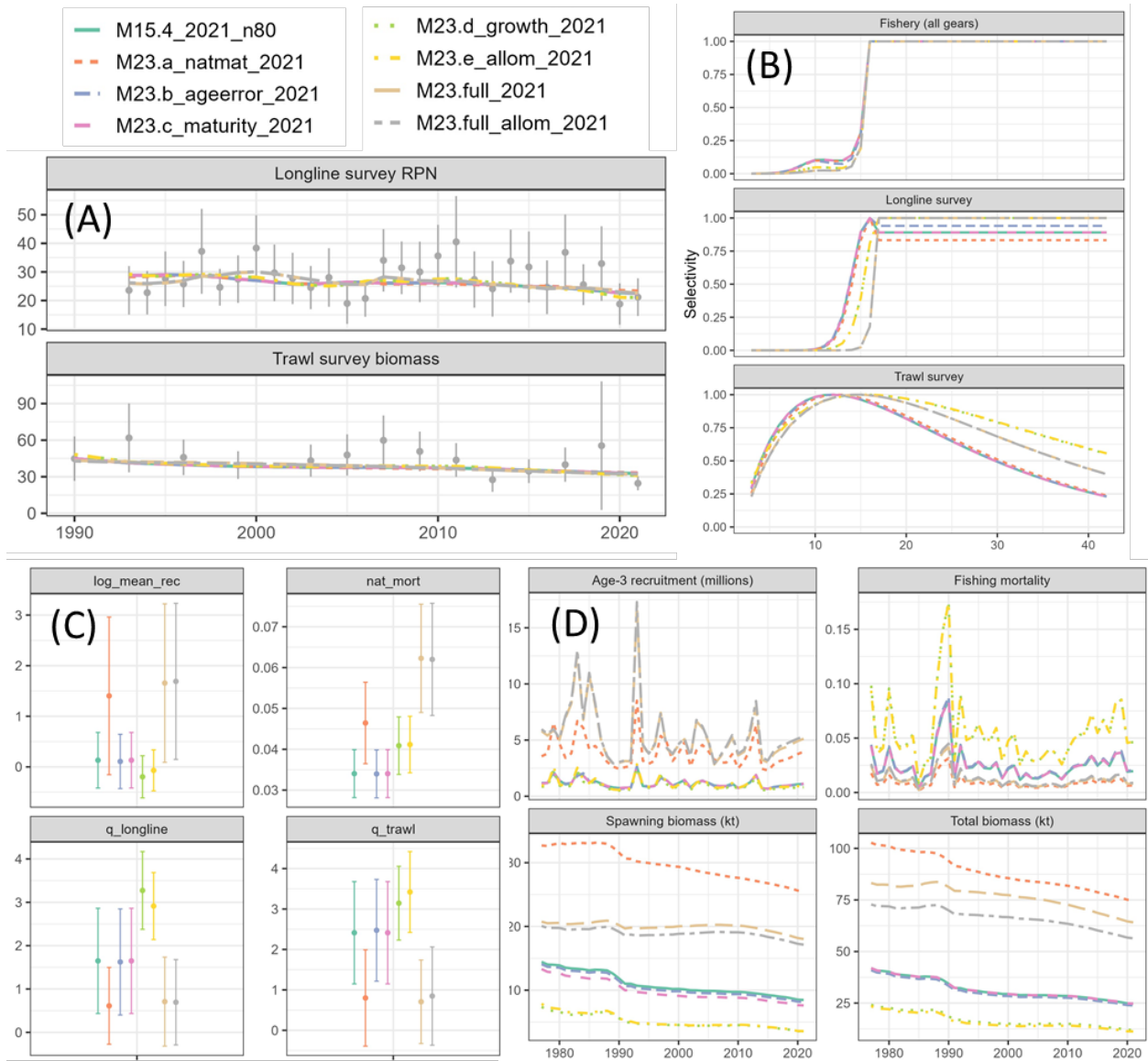Figure 7. A comparison of weight-at-age trajectories.
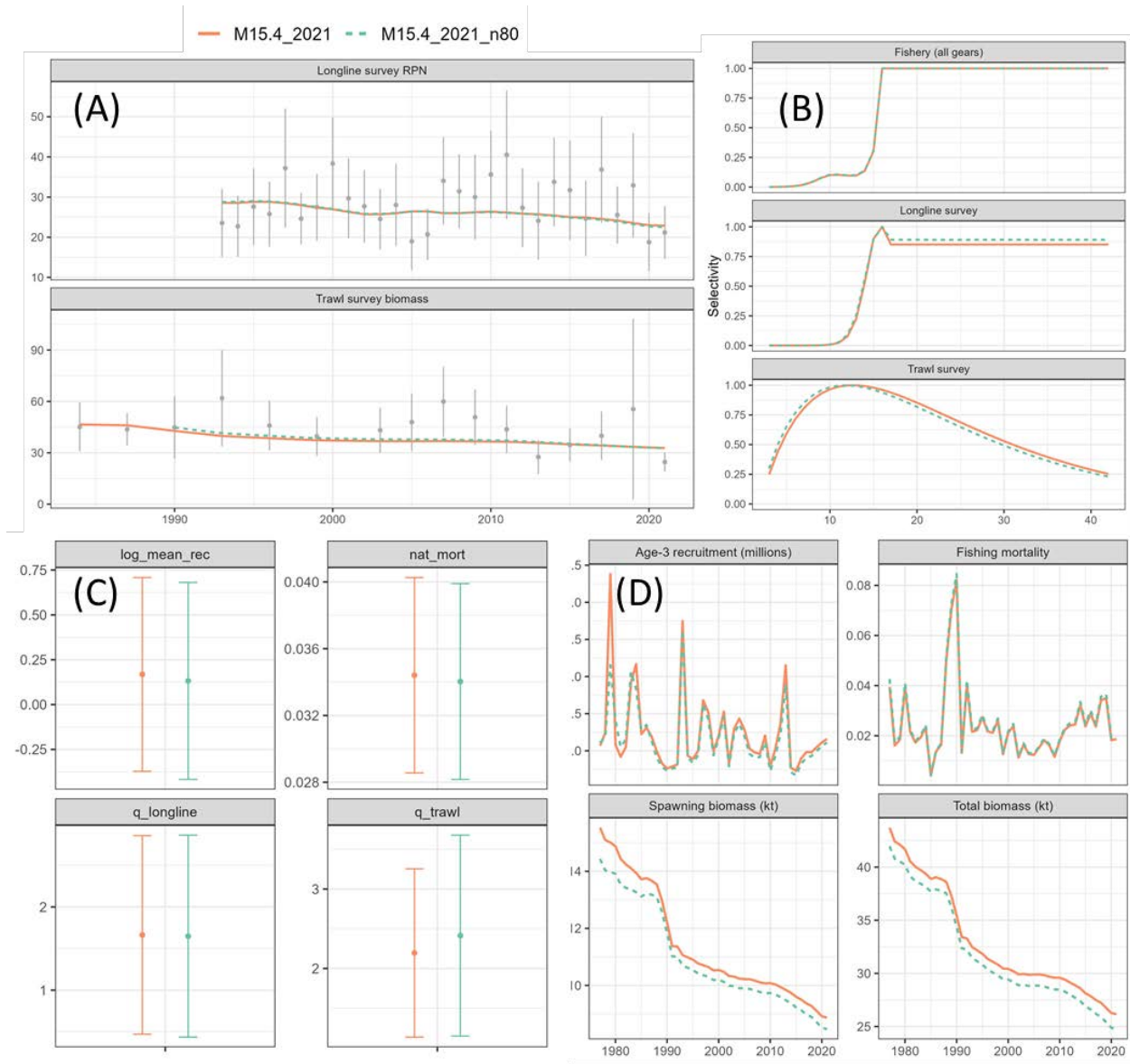
Figure 8. Model comparison summary with (A) fits to the indices of abundance, (B) estimated selectivity-at-age, (C) model parameter estimates with asymptotic 95% confidence intervals (log_mean_rec=average recruitment on the natural log-scale, nat_mat=natural mortality, q_longline=longline survey catchability, q_trawl=bottom trawl survey catchability), and (D) derived estimates of recruitment (age-3 individuals in millions), fully-selected fishing mortality, spawning biomass (kt), and total biomass (kt). M15.4_2021 is the based model, and M15.4_2021_n80 is the base model with 1980s trawl survey data removed

Figure 9. Model comparison summary with (A) fits to the indices of abundance, (B) estimated selectivity-at-age, (C) model parameter estimates with asymptotic 95% confidence intervals (log_mean_rec=average recruitment on the natural log-scale, nat_mat=natural mortality, q_longline=longline survey catchability, q_trawl=bottom trawl survey catchability), and (D) derived estimates of recruitment (age-3 individuals in millions), fully-selected fishing mortality, spawning biomass (kt), and total biomass (kt). M15.4_2021_n80 is the base model with 1980s trawl survey data removed, and M23.full_allom_2021 is the author-preferred model.

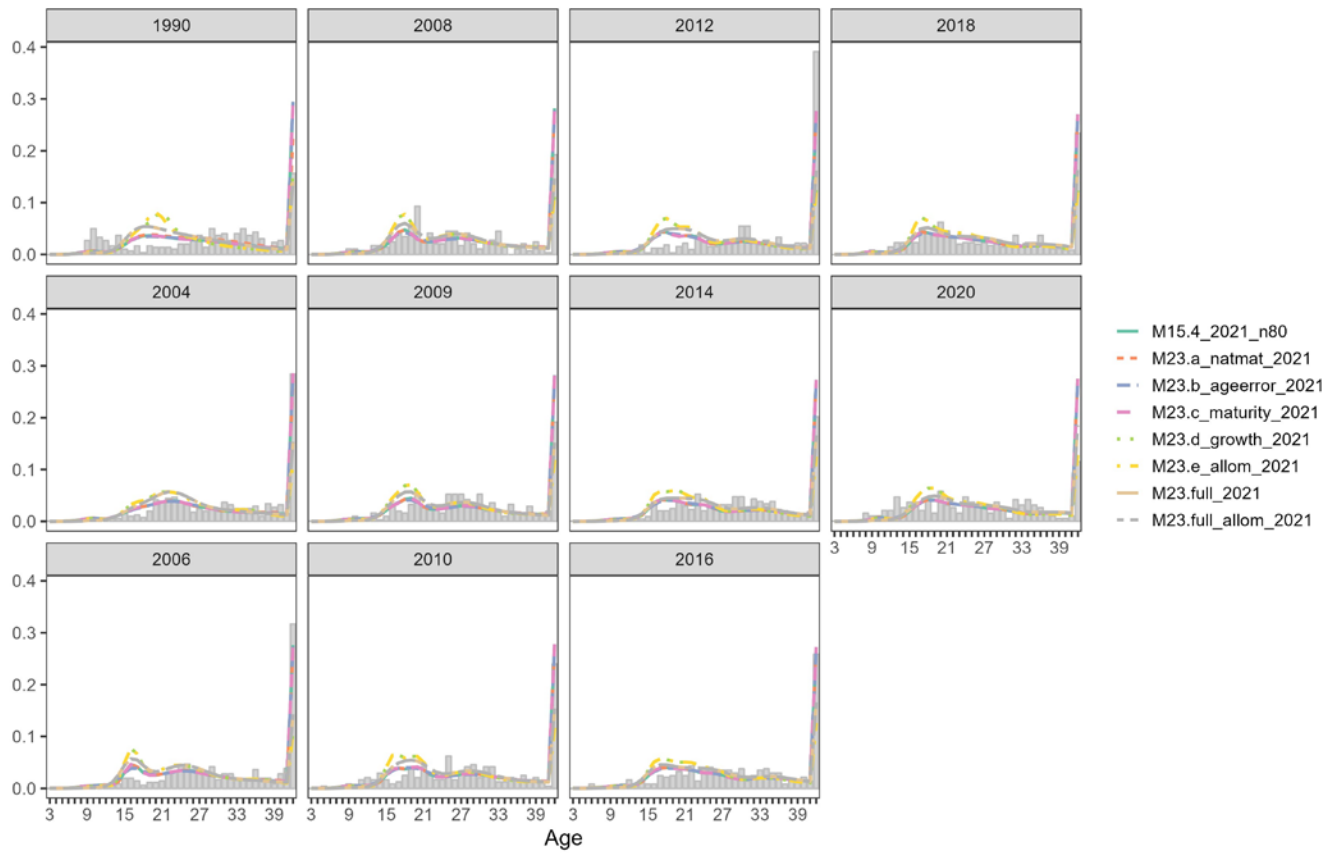Figure 10. Model fits (lines) to the fishery age composition data (bars). Note all fishing gears are combined.
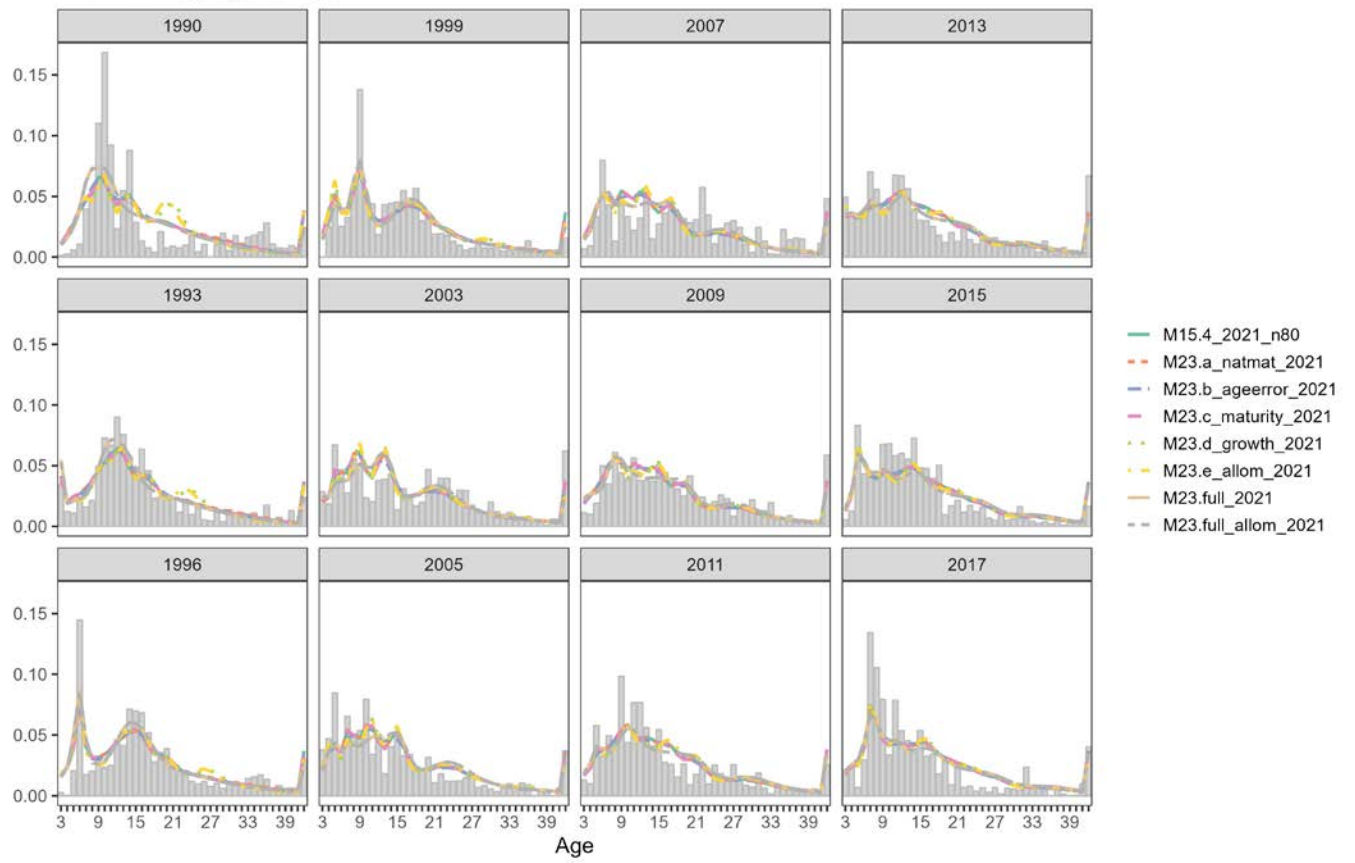
Figure 11. Model fits (lines) to the bottom trawl survey age composition data (bars).
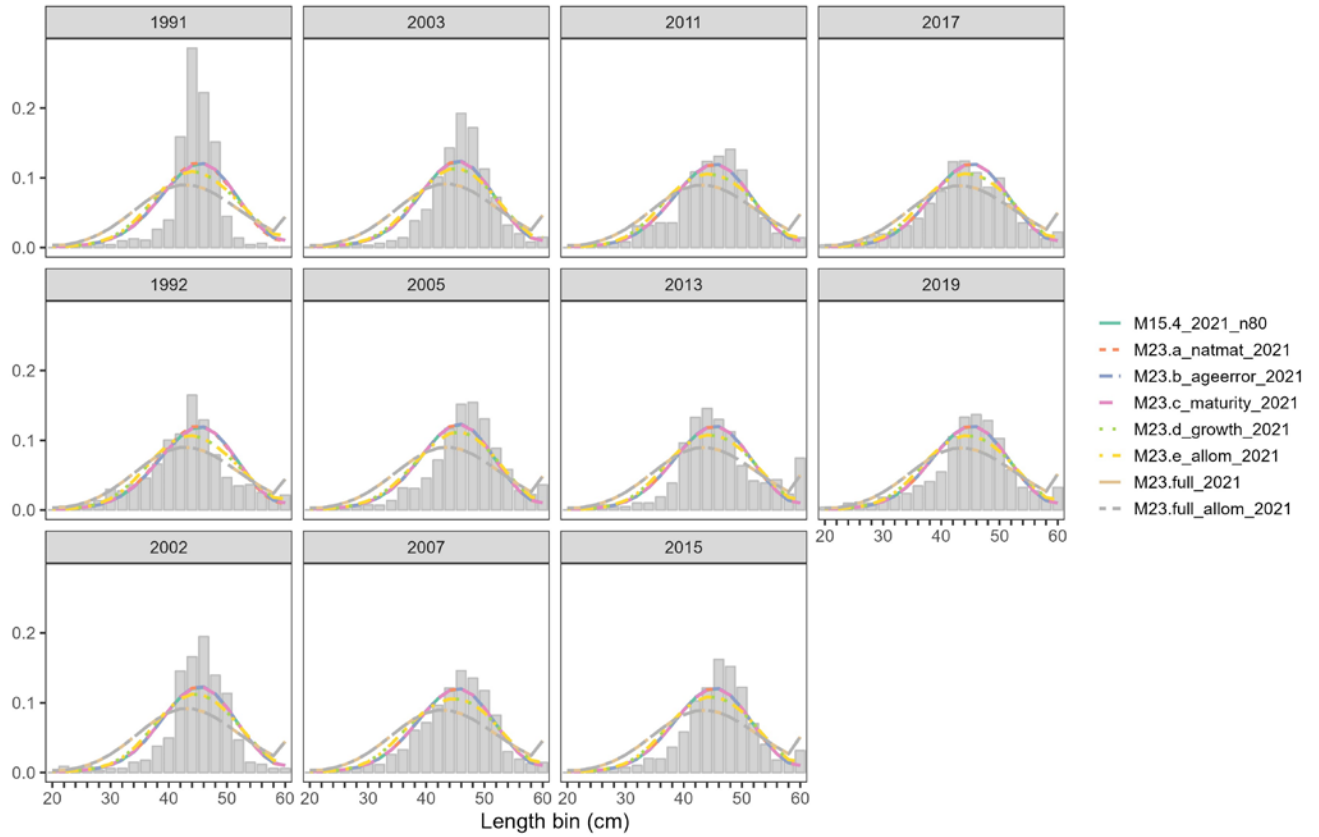
Figure 12. Model fits (lines) to the fishery length composition data (bars). Note all fishing gears are combined.
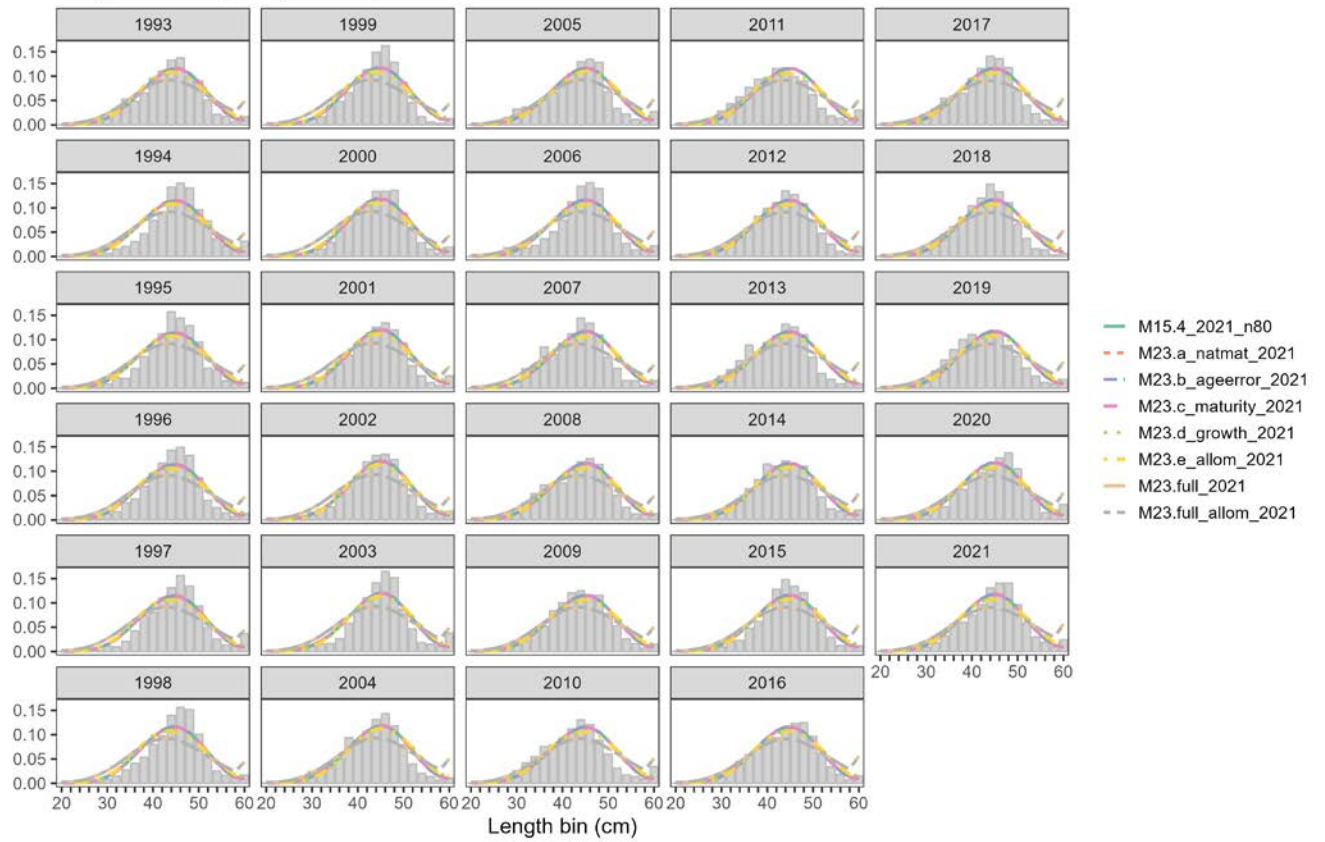
Figure 13. Model fits (lines) to the longline survey length composition data (bars).
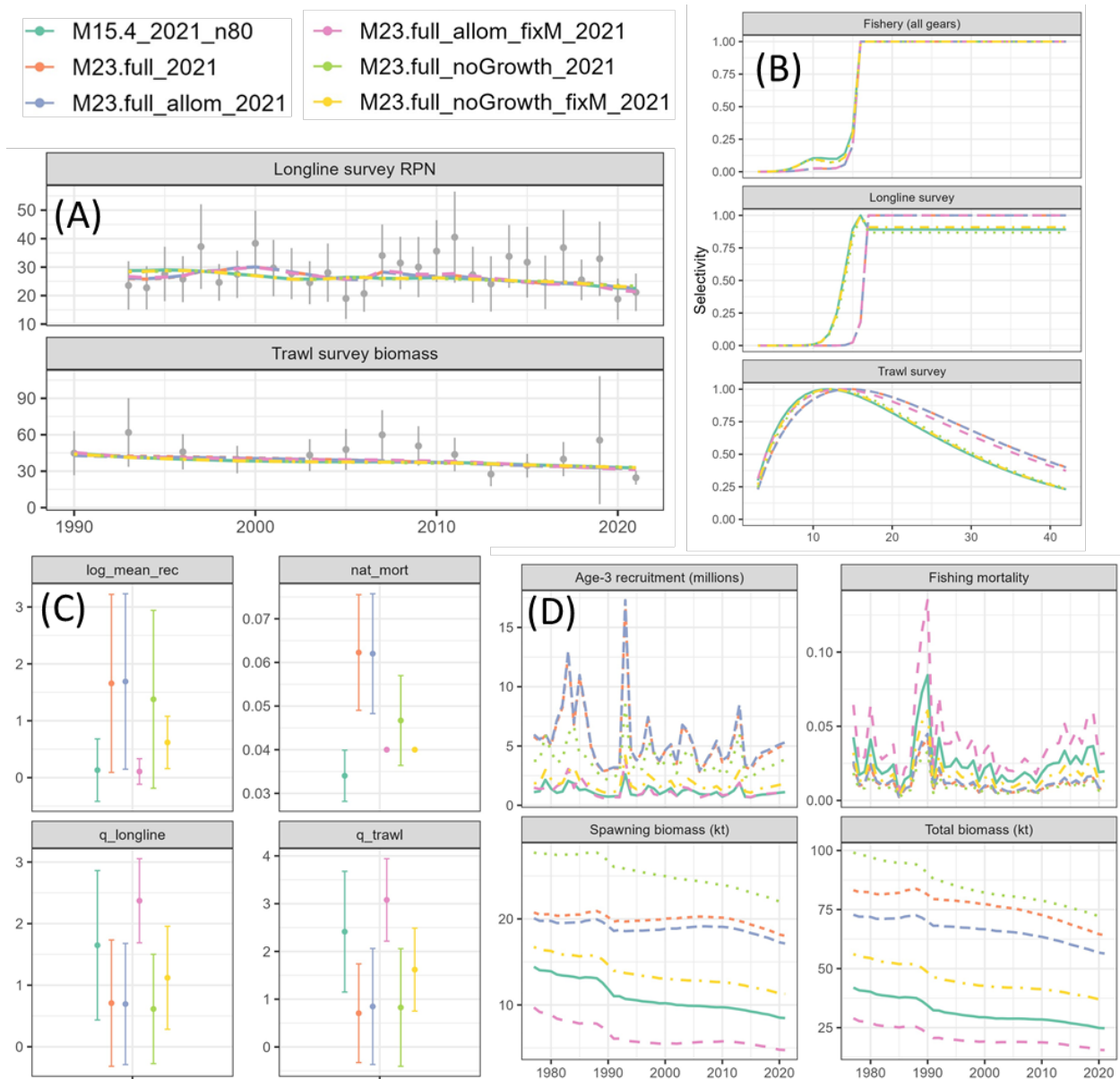
Figure 14. Model comparison summary with (A) fits to the indices of abundance, (B) estimated selectivity-at-age, (C) model parameter estimates with asymptotic 95% confidence intervals (log_mean_rec=average recruitment on the natural log-scale, nat_mat=natural mortality, q_longline=longline survey catchability, q_trawl=bottom trawl survey catchability), and (D) derived estimates of recruitment (age-3 individuals in millions), fully-selected fishing mortality, spawning biomass (kt), and total biomass (kt). M15.4_2021_n80 is the base model with 1980s trawl survey data removed, and M23.full_allom_2021 is the author-preferred model. M23.full_allom_fixM_2021, M23.full_noGrowth _2021, and M23.full_noGrowth_fixM_2021 are sensitivities that either fix *M* and/or do not update the weight-at-age vector or length-age transition matrix.

Appendix A. Alternative apportionment methods for the 2023 stock assessment of the Rougheye and Blackspotted rockfish complex in the Gulf of Alaska

Jane Y. Sullivan

September 2023

Executive Summary

The Gulf of Alaska (GOA) rougheye and blackspotted (RE/BS) rockfish complex is assessed on a biennial schedule in odd years and is managed as a Tier 3 stock. The current method for apportioning the GOA-wide Acceptable Biological Catch (ABC) to eastern, central, western GOA management areas (i.e., EGOA, CGOA, WGOA) was first adopted in 2019 (Shotwell et al. 2019) and relies on the two-survey (i.e., bottom trawl and longline surveys) version of the random effects model (REMA; Hulson et al. 2021). Here we recommend several important updates to the underlying REMA model used for apportionment and apportionment methodology:

1) We recommend that REMA model be implemented using the *rema* R library, which was endorsed by the GOA Groundfish Plan Team (GPT) and Scientific and Statistical Committee (SSC) in 2022. The *rema* R library uses Model Builder (TMB; Kristensen et al. 2016) instead of AD Model Builder (ADMB; Fournier et al. 2012). We demonstrate that implementing the base REMA model using *rema* results in nearly identical model results (Figure 1; Table 1).
2) We propose estimating (instead of fixing) the REMA model's area-specific scaling parameters (ϱ). These parameters, which are currently fixed to 1, scale the area-specific longline survey relative population weights (RPW) to biomass. The assumption that $\varrho=1$ means that 1 RPW is equal to 1 mt of biomass, which is invalid because the RPW is an area-weighted catch-per-unit effort index and the units are not meaningful. Moreover, fixing the ϱ parameters in the REMA model results in poor fits to both survey indices (Figure 2).
3) When evaluating REMA models with estimated area-specific ϱ parameters, we considered two alternatives for modeling process error variation. The first model was identical to structure of the current base model and estimated a single, shared process error. The second model estimated separate, area-specific process error parameters. We found that results were nearly identical between the two models (Tables 1-2; Figure 2), and we recommend the simpler model with a single process error, which had the lowest Akaike Information Criterion (AIC; Table 2).
4) We present alternatives that remove the 1984 and 1987 bottom trawl survey biomass estimates based on recommendations from the GOA GPT and SSC in 2022 (Figure 3).
5) Instead of using the proportion of predicted biomass by area to inform apportionment, we propose using the average of the proportion predicted biomass and proportion predicted RPWs by area. In the case of GOA RE/BS, there is data conflict between the trawl and longline survey indices. Specifically, the longline survey RPWs suggest higher proportions of biomass in the eastern and western GOA compared to the bottom trawl survey biomass (Figure 4). The proposed alternative approach has the benefit of utilizing information from the RPWs to inform relative scale of biomass among regions, thus striking a balance between the conflicting survey indices.

For the 2023 assessment, the author-recommended REMA model estimates area-specific ϱ, has a single, shared process error, and starts in 1990. The author recommends the new apportionment method that averages proportions of predicted RPW and biomass by area.

Summary of Methods

Changes in the input data:

The inputs to the REMA model include management area-specific (i.e., EGOA, CGOA, WGOA) design-based bottom trawl survey biomass estimates and longline survey RPWs with associated coefficients of variation (CV). Based on a recommendation from the GOA GPT (September 2022) and SSC (October 2022), we present alternative model results that exclude the 1984 and 1987 bottom trawl surveys and begins in 1990. Otherwise all data presented in this document is identical to the data used in the 2021 assessment.

Changes in the apportionment methodology:

We present the current ADMB REMA model for apportionment, along with the bridge to the TMB model fit in the *rema* R library and an alternative model that estimate area-specific scaling parameters (ϱ) and eliminate the 1984 and 1987 bottom trawl surveys. Detailed REMA model methods are available in Sullivan et al. (2022) and Hulson et al. (2021).

W**e propose an alternative method for apportionment that bases apportionment on the mean proportions of predicted biomass and predicted RPW by area** ("Biomass + RPW"). This approach is contrasted with the standard method of basing apportionment on the proportion of predicted biomass by area ("Biomass").

The two-survey random effects model presented use the following naming conventions:

Apportionment Model	Software	Process error (PE)	Scaling parameters (ϱ)	Model years
M19	ADMB (bespoke model)	Single, shared PE	Area-specific ϱ fixed at 1	1984-2023
M19_update	TMB (*rema* R library)	Single, shared PE	Area-specific ϱ fixed at 1	1984-2023
M23A	TMB (*rema* R library)	Single, shared PE	Area-specific ϱ estimated	1984-2023
M23B	TMB (*rema* R library)	Area-specific PE	Area-specific ϱ estimated	1984-2023
M23A_start1990	TMB (*rema* R library)	Single, shared PE	Area-specific ϱ estimated	1990-2023

Summary of Results

The alternative REMA models and apportionment methods ("Biomass" = standard method based on proportion of predicted biomass by area; "Biomass + RPW" = proposed method for GOA RE/BS based on the = mean proportions of predicted biomass and predicted RPW by area) result in the following apportionment percentages by management area for 2022 and 2023 (author-recommended model and apportionment method in bold):

REMA model names	Apportionment Method	WGOA	CGOA	EGOA
M19	Biomass	23.3%	29.9%	46.8%

M19	Biomass + RPW	23.3%	29.9%	46.8%
M19_update	Biomass	23.3%	29.9%	46.8%
M19_update	Biomass + RPW	23.3%	29.9%	46.8%
M23A	Biomass	14.3%	50.1%	35.6%
M23A	Biomass + RPW	24.4%	32.3%	43.3%
M23B	Biomass	14.1%	51.2%	34.7%
M23B	Biomass + RPW	24.4%	33.1%	42.6%
M23A_start1990	Biomass	13.0%	51.7%	35.3%
M23A_start1990	**Biomass + RPW**	**22.9%**	**33.3%**	**43.8%**

Key results:
- M19 and M19_update results are identical (Figure 1), despite a known error in the ADMB version of the REMA model (note that this error is specific to the two-survey template file; Sullivan et al. 2022). Notably, this error only impacts results for models that estimate the scaling coefficients. Therefore, while technically this error is present in the ADMB model, it does not affect the validity of results in M19, which is why M19 and M19_update results are identical.
- M19 and M19_update apportionment ratios are identical for both apportionment methods ("Biomass" and "Biomass + RPWs"). This is attributable to the fixed ϱ assumption in this model that puts biomass and RPW predictions on the same scale. This assumption also results in terrible fits to the underlying data due to discrepancies between the bottom trawl survey biomass estimates and longline survey RPWs.
- M23A and M23B, which estimate area-specific ϱ parameters, fit the data significantly better than M19 and M19_update (Figure 2). Estimates of process error are considerably higher for M19 and M19_update (Table 1), which is attributable to the model's attempt to fit the data despite the fixed ϱ assumption. There are negligible differences between M23A and M23B fits to the data, and the simpler model M23A has the lowest AIC value (Table 2). Estimates of area-specific ϱ in M23A are 3.09, 0.37, and 1.83 for WGOA, CGOA, and EGOA, respectively, highlighting that fixing ϱ in M19 and M19_update is a flawed assumption.
- The removal of 1984 and 1987 bottom trawl surveys in M23A_start1990 results in a small reduction in the estimate of process error variance relative to M23A (Table 1), thus the predicted biomass and RPWs are slightly smoother for this model (Figure 3). These model results with the shortened time series are satisfactory to the author, making the M23A_start1990 the author-preferred model for 2023.
- The M23A_start1990, M23A, and M23B apportionment ratios are highly sensitive to the apportionment method used. When apportionment is based on the proportion of predicted biomass by area ("Biomass"), resultant ratios are lower in the WGOA and EGOA and higher in the CGOA (Figure 4). Averaging the proportions of predicted biomass and RPWs ("Biomass + "RPWs") results in more even apportionment ratios among area. These results are attributable to the mismatch in relative biomass or RPWs by area between the two surveys.

Recommendation and Rationale

For 2023 the author recommends M23A_start1990, which is implemented in TMB using the *rema* R library, has a single shared process error, area-specific scaling parameters, and eliminates the 1984 and 1987 bottom trawl surveys (starts in 1990). This alternative model is responsive to GOA GPT and SSC

recommendations (implements model in REMA and removes 1980s surveys), provides substantially improved fits to the data (Figures 2 and 3), and is parsimonious compared to other REMA models explored (Table 2). Additionally, the proposed apportionment method that averages the proportions of predicted biomass and RPWs ("Biomass + "RPWs") leverages information from both bottom trawl and longline surveys, which often show different patterns in terms of the stock's scale and trend.

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Hulson, P.J.F., Echave, K.B., Spencer, P.D., and Ianelli, J.N. 2021. Using multiple indices for biomass and apportionment estimation of Alaska groundfish stocks. U.S. Dep. Commer. NOAA Tech. Memo. NMFS-AFSC-414, 28 p.

Kristensen K., A. Nielsen, C. W. Berg, H. Skaug, B. M. Bell. 2016. TMB: automatic differentiation and Laplace approximation. J Stat Softw 70(5):1–21. doi:10.18637/jss.v070.i05
Skaug H. and D. Fournier. 2013. Random effects in AD Model Builder: ADMB-RE User Guide. http://ftp.admb-project.org/admb-11.2pre/admbre-11.2pre.pdf

Shotwell, S.K. and D.H Hanselman. 2019. Assessment of rougheye and blackspotted rockfish stock in the Gulf of Alaska. *In* Stock assessment and fishery evaluation report for the groundfish fisheries of the Gulf of Alaska. North Pacific Fishery Management Council, 605 W. 4th. Avenue, Suite 306, Anchorage, AK 9950-2252.

Sullivan, J., C. Monnahan, P. Hulson, J. Ianelli, J. Thorson, and A. Havron. 2022. REMA: a consensus version of the random effects model for ABC apportionment and Tier 4/5 assessments. Plan Team Report, Joint Groundfish Plan Teams, North Pacific Fishery Management Council. 605 W 4th Ave, Suite 306 Anchorage, AK 99501. Available through the Oct 2022 Joint GPT e-Agenda.

Tables

Table 1. Fixed effects parameter estimates, standard errors (SE), and 95% lower and upper confidence intervals (LCI and UCI, respective) for the models considered in this analysis. Process error (PE) variances are listed first, followed by area-specific scaling parameters (ϱ).

Model Name	Parameter	Estimate	SE	LCI	UCI
M19 and M19_update	Combined PE	0.43	0.06	0.33	0.56
M23A	Combined PE	0.17	0.04	0.11	0.27
M23A_start1990	Combined PE	0.10	0.03	0.06	0.18
M23B	CGOA PE	0.12	0.04	0.06	0.24
M23B	EGOA PE	0.22	0.06	0.13	0.38
M23B	WGOA PE	0.18	0.10	0.06	0.51
M19 and M19_update	CGOA ϱ	Fixed at 1	NA	NA	NA
M19 and M19_update	EGOA ϱ	Fixed at 1	NA	NA	NA
M19 and M19_update	WGOA ϱ	Fixed at 1	NA	NA	NA
M23A	CGOA ϱ	0.37	0.03	0.31	0.43
M23A	EGOA ϱ	1.83	0.14	1.58	2.12
M23A	WGOA ϱ	3.09	0.34	2.49	3.85
M23A_start1990	CGOA ϱ	0.37	0.03	0.31	0.43
M23A_start1990	EGOA ϱ	1.87	0.14	1.62	2.16
M23A_start1990	WGOA ϱ	3.21	0.35	2.58	3.98
M23B	CGOA ϱ	0.37	0.03	0.31	0.43
M23B	EGOA ϱ	1.82	0.14	1.56	2.12
M23B	WGOA ϱ	3.09	0.35	2.48	3.85

Table 2. Model selection results for candidate models that use the two-survey random effects model (REMA) fit to the full time series (1984-2021).

| Model Name	Objective Function	Number of Parameters	AIC	Δ AIC
M23A	79.5	4	167.1	0
M23B	78.6	6	169.3	2.2
M19_update	217.6	1	437.2	270.1

Figures
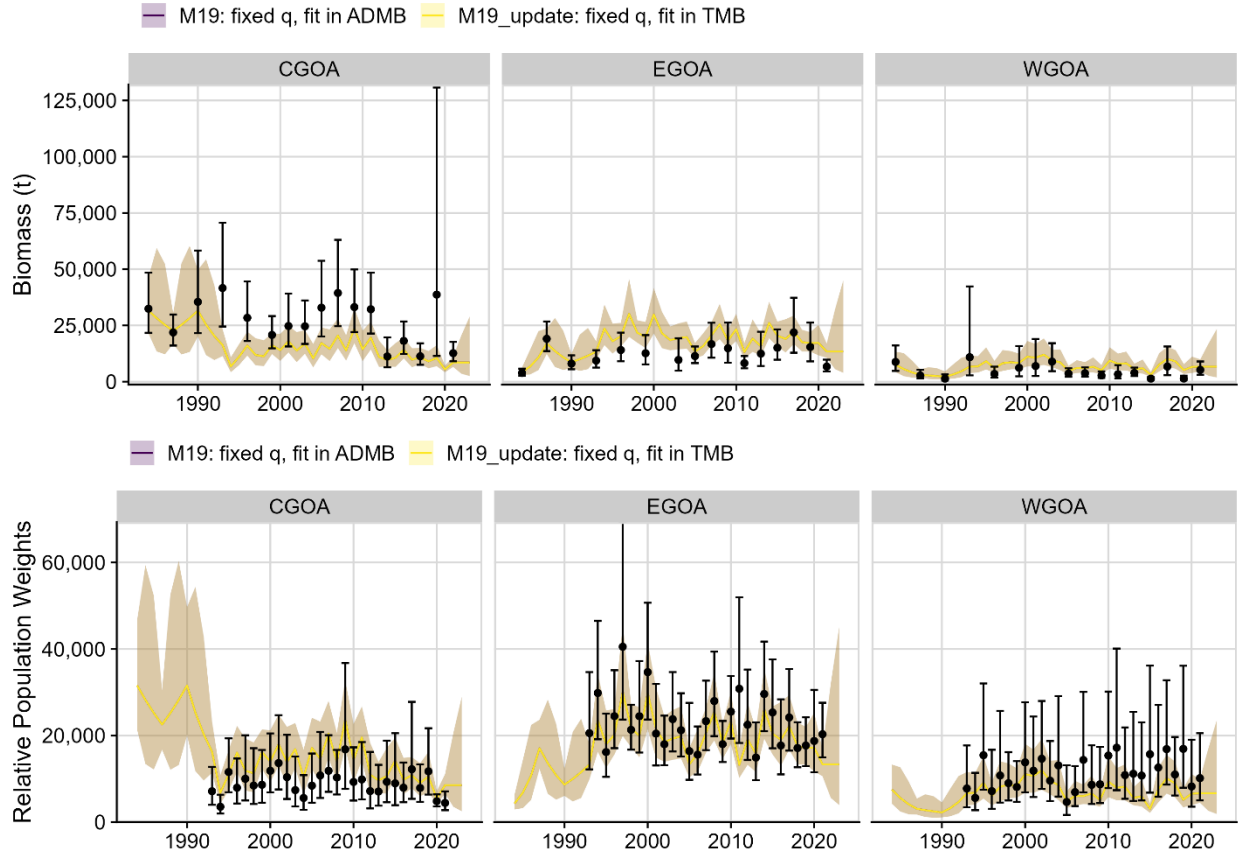
Figure 1. Two-survey random effects (REMA) model fits to the GOA bottom trawl survey (BTS) biomass (top panels) and longline survey (LLS) relative population weights (RPWs; bottom panels) by central, eastern, and western Gulf of Alaska (CGOA, EGOA, WGOA) management area, where the points and error bars are the design-based survey estimates and the lines with shaded regions are the model predictions and 95% confidence intervals from the REMA model. Results are shown for Model 19 (the ADMB version of the base model where the scaling coefficients ǫ [denoted as q in the figure] are fixed at 1) in purple and Model 19_updated (identical to Model 19, fit in TMB).
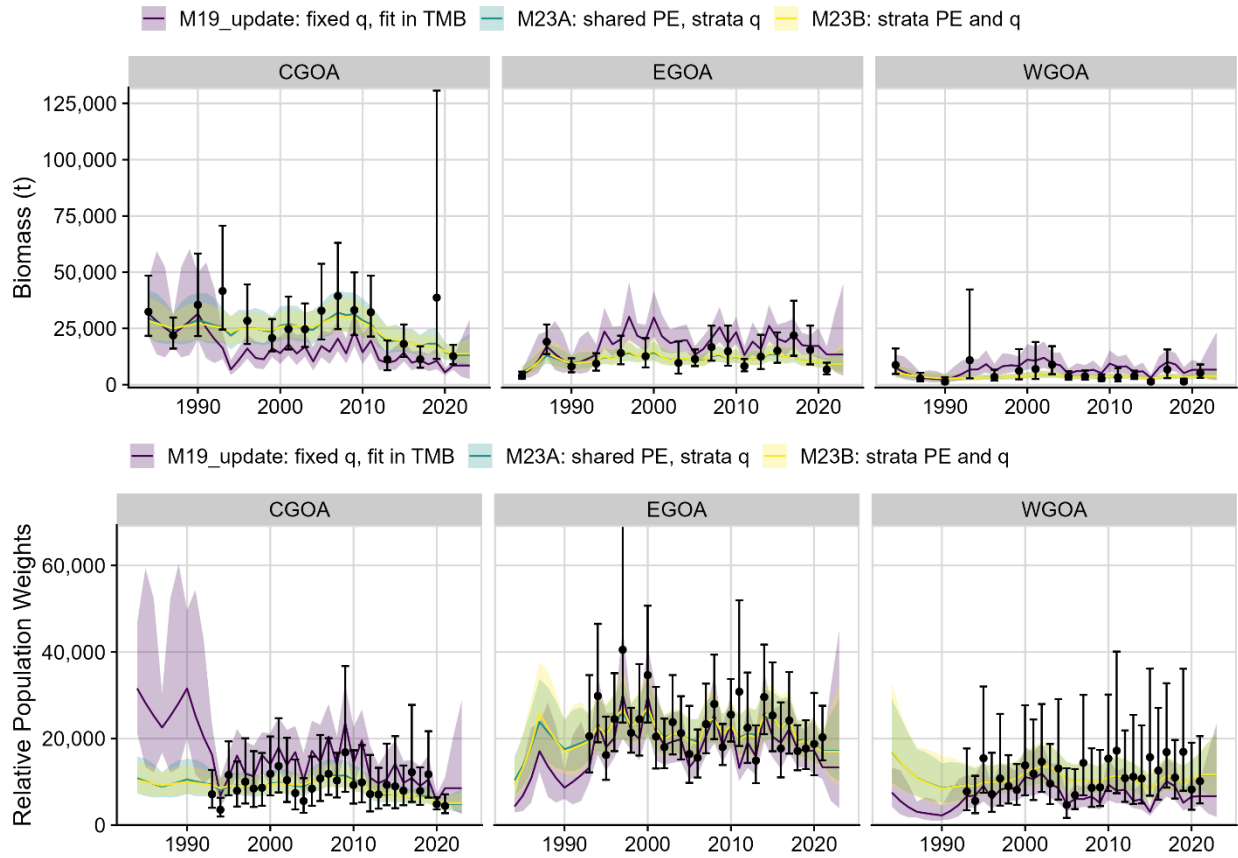
Figure 2. Two-survey random effects (REMA) model fits to the GOA bottom trawl survey (BTS) biomass (top panels) and longline survey (LLS) relative population weights (RPWs; bottom panels) by central, eastern, and western Gulf of Alaska (CGOA, EGOA, WGOA) management area, where the points and error bars are the design-based survey estimates and the lines with shaded regions are the model predictions and 95% confidence intervals from the REMA model. Results are shown for Model 19_updated in purple (identical to the base Model 19 where the scaling coefficients ϱ [denoted as q in the figure] are fixed at 1, fit in TMB), Model 23A in blue (single, shared process error and area-specific ϱ), and Model 23B in yellow (area-specific process error and area-specific ϱ).
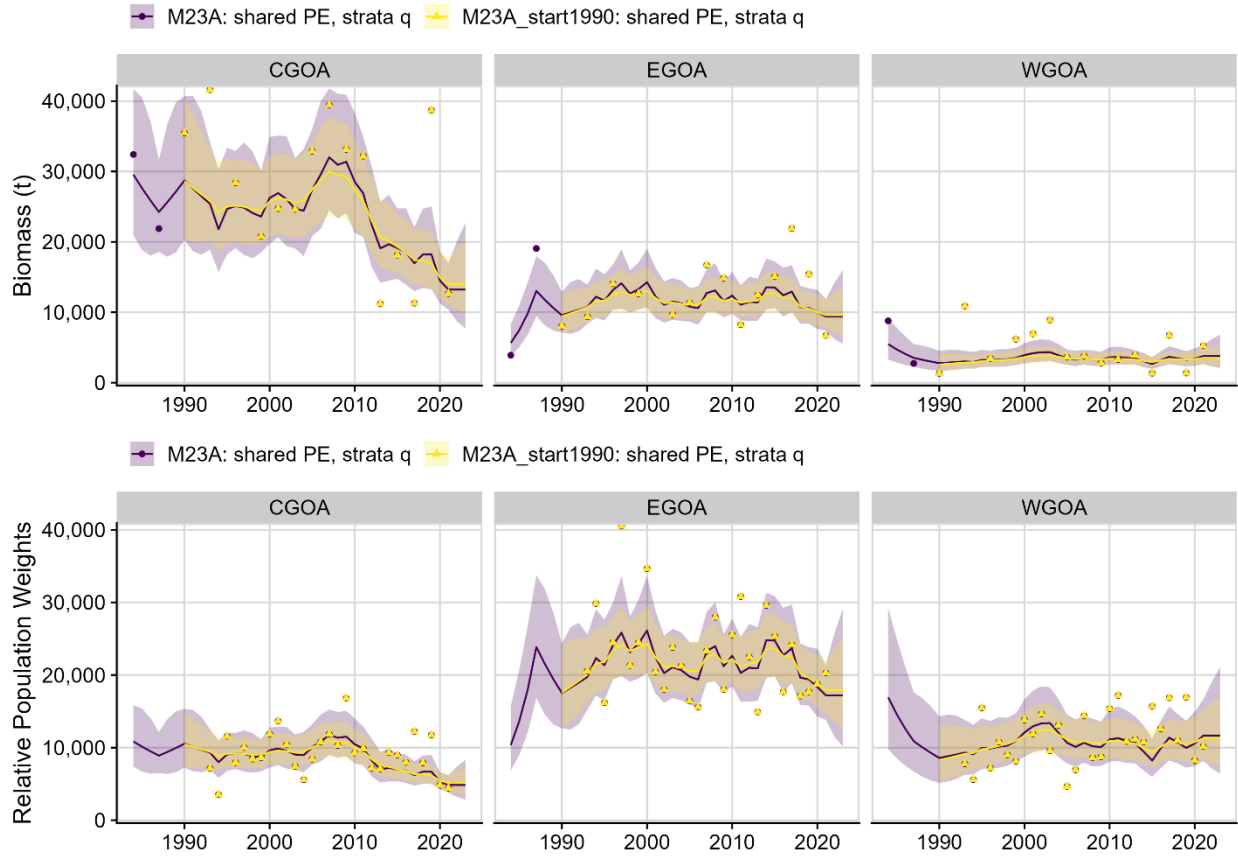
Figure 3. Two-survey random effects (REMA) model fits to the GOA bottom trawl survey (BTS) biomass (top panels) and longline survey (LLS) relative population weights (RPWs; bottom panels) by central, eastern, and western Gulf of Alaska (CGOA, EGOA, WGOA) management area, where the points and error bars are the design-based survey estimates and the lines with shaded regions are the model predictions and 95% confidence intervals from the REMA model. Results are shown for Model 23A in purple (single, shared process error and area-specific ϱ [denoted as q in the figure]) and Model 23A_start1990 in yellow (same as M23A but starts in 1990 instead of 1984).
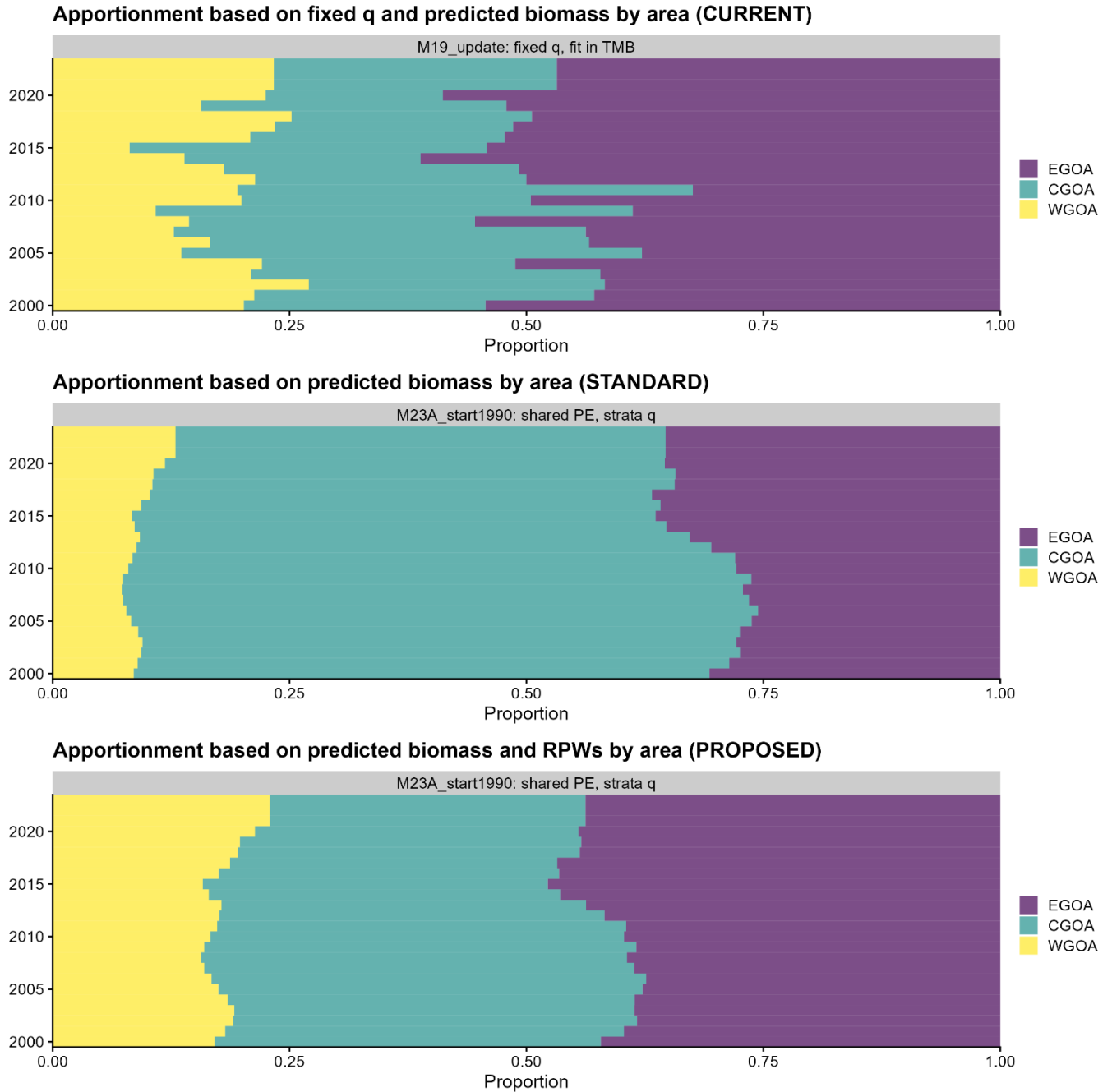
Figure 4. Apportionment results (i.e. the proportion of Acceptable Biological Catch that would be apportioned to each management area) for 2000-2023 based on the alternative method of apportionment and two-survey random effects (REMA) model used. Top panel: results from the updated base model (M19_update) and current apportionment method that assumes fixed scaling coefficients (ϱ; denoted as q in the figure) in the model and is based on proportions of predicted biomass by area. Middle panel: results from the author-recommend model (M23A_start1990) and standard apportionment method based on proportions of predicted biomass by area. Bottom panel: results from the author-recommend model (M23A_start1990) and proposed apportionment method based on the average proportions of predicted biomass and predicted relative population weights (RPWs) by area.