

Gulf of Alaska Northern Rockfish Model Updates

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1 Introduction

There are four proposed changes/edits to the GOA northern rockfish assessment for 2024.

1. A model change for estimating the survey biomass negative log likelihood from normal to lognormal error.
2. A data change to refine the input sample sizes for survey age composition data.
3. An adjustment to how survey biomass indices are used for generating apportionment in the GOA from the design-based model to VAST-based outputs,
4. A modeling framework change from ADMB to RTMB.

2 Survey Likelihood Change

2.1 Introduction

The model currently estimates the survey biomass negative log likelihood with a normal error structure

$$\mathcal{L} = \lambda \sum_y \frac{(I_y - \hat{I}_y)^2}{2SE(I_y)^2}.$$

We propose adopting the more standard lognormal error structure negative log likelihood error structure to the objective function:

$$\mathcal{L} = \lambda \sum_y \left[\log(\sigma_y) + 0.5 \left(\frac{\log(I_y/\hat{I}_y)}{\sigma_y} \right)^2 \right]$$

where

$$\sigma_y = \sqrt{\log \left(1 + \frac{SE(I_y)^2}{I_y^2} \right)}$$

and I_y are annual survey biomass observations, \hat{I}_y are estimated annual survey biomass, y is year, σ_y is annual survey biomass log standard error estimated using method of moments, and λ is the likelihood weight and $SE(I_y)$ is the annual survey biomass standard error. The lognormal error structure is more appropriate for these data and is more commonly used for assessment models. A comparison will be shown between the SSC accepted 2022 model (Model 22.1, normal error structure) and updated model results (Model 22.1a).

2.2 Results

Changing to a lognormal error structure for the survey biomass likelihood results in an increase in estimated total and female spawning biomass, with an associated increase in B_{40} and **maxABC**, and an increase in the survey biomass likelihood.

Model likelihoods and key parameter estimates are shown in Tables 1 and 2.

Table 1: Model likelihood values. The [Model 22.1](#) is the SSC accepted 2022 model (ADMB), M22.1a updates to a lognormal error structure survey likelihood. *Note that these have different likelihoods and are therefore not directly comparable.*

Likelihood	M22.1	M22.1a
Catch	0.91	0.93
Survey biomass	6.022	1.907
Fishery ages	40.177	40.2879
Survey ages	69.160	69.112
Fishery lengths	67.907	67.854
Recruitment devs	8.640	8.77
F regularity	5.457	5.481
M prior	0.014	0.0069
q prior	0.052	0.00059
Data total	183.4	179.3

Table 2: Parameter estimates and outputs. The M22.1 model is the SSC accepted 2022 model (ADMB), M22.1a updates to a lognormal error structure survey likelihood. *Note that these have different likelihoods and are therefore not directly comparable.*

Parameter	M22.1	M22.1a
M	0.0595	0.0596
q	0.865	0.985
avg rec	3.504	3.530
F40	0.061	0.0614
total biomass	95,559	101,263
spawning biomass	39,463	41,972
B100	82,350	85,217
B40	32,940	34,087
ABC	4,972	5,291

3 Survey Age Composition Input Sample Size (ISS)

3.1 Introduction

Survey age composition input sample sizes (ISS, see Hulson and Williams 2024a) are now available via the (afscISS R package on github, Hulson and Williams 2024b). These sample sizes are corrected for growth variability and aging error and should more accurately reflect the annual sample sizes than the currently used ‘hybrid method’. The hybrid method is the

$\sqrt{no.hauls * no.samples}$ scaled to a max of 100. The data input changes will be shown using the updated Model 22.1a described above.

3.2 Results

Updating the survey input sample size (ISS) results in a slight increase in estimated total and female spawning biomass, and associated management parameters. Model likelihoods and key parameter estimates are shown in Tables 3 and 4.

Table 3: Model likelihood values. The M22.1 model is the SSC accepted 2022 model (ADMB), M22.1a updates to a lognormal error structure survey likelihood, M22.1b uses adjusted ISS values.

Likelihood	M22.1	M22.1a	M22.1b
Catch	0.91	0.93	0.109
Survey biomass	6.022	1.907	2.0559
Fishery ages	40.177	40.2879	41.8463
Survey ages	69.160	69.112	83.0683
Fishery lengths	67.907	67.854	70.2137
Recruitment devs	8.640	8.77	9.312
F regularity	5.457	5.481	5.676
M prior	0.014	0.0069	0.012
q prior	0.052	0.00059	0.0063
Data total	183.4	179.3	197.3

Table 4: Parameter estimates and outputs. The M22.1 model is the SSC accepted 2022 model (ADMB), M22.1a updates to a lognormal error structure survey likelihood, M22.1b uses adjusted ISS values.

Parameter	M22.1	M22.1a	M22.1b
M	0.0595	0.0596	0.0595
q	0.865	0.985	0.951
avg rec	3.504	3.530	3.524
F40	0.061	0.061	0.061
total biomass	95,559	101,263	101,794
spawning biomass	39,463	41,972	42,810
B100	82,350	85,217	85,2842
B40	32,940	34,087	34,114
ABC	4,972	5,291	5,343

4 Change to VAST-based Apportionment

4.1 Introduction

Apportionment for GOA northern rockfish has been based upon area estimates from the design-based survey abundance. The assessment uses a model-based (VAST, Thorson *et al.* 2015) index of abundance, which does not always align with the design-based area estimates. For consistency, we propose to change apportionment to be based upon the model-based index of abundance.

The ‘standard’ apportionment scenario has been to use the REMA (Sullivan and Balstad 2022) random effects model to smooth the area apportionments. One issue with the model-based index and REMA analysis is that northern rockfish catch in the eastern GOA has been consistently low or zero Figures 1 and 2. Due to this sparseness both the VAST and REMA models have had convergence issues for the eastern GOA. In order to address this, the eastern GOA is dropped from the estimated index of abundance. There is 1 t allocated for eastern GOA northern rockfish in the ‘Other rockfish’ complex for management purposes.

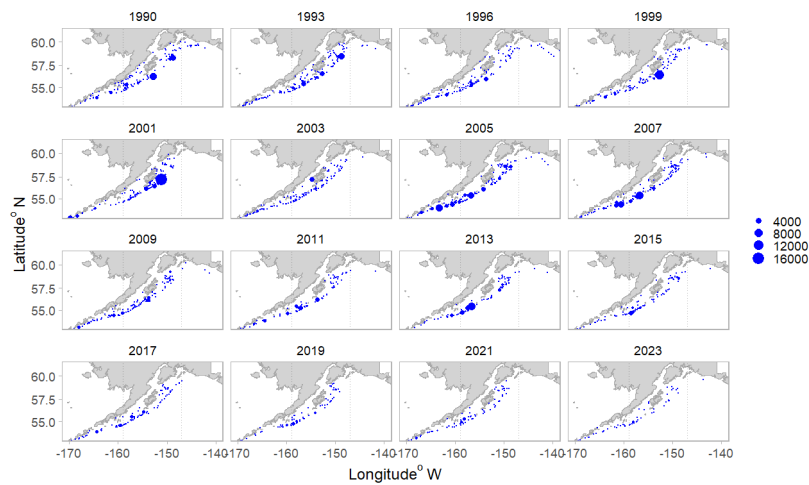


Figure 1: Survey catch (numbers) by year.

An examination of design-based (via REMA), and VAST (without REMA smoothing) will be compared. Apportionment examinations will be presented using survey data through 2023.

4.2 Results

The REMA smoothed design-based and VAST area biomass are on the same scale, though there is greater variability present in the central GOA for the VAST biomass (Figure 3). However, when examined as a proportion, VAST exhibits less variability between regions (Figure 4).

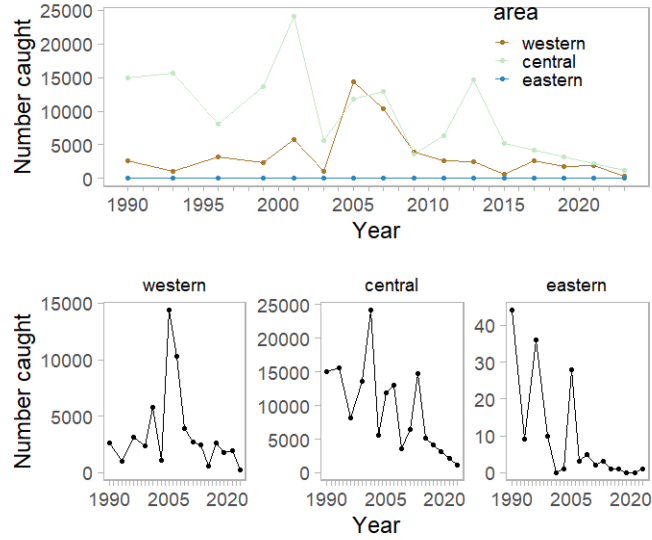


Figure 2: Survey catch (numbers) by year and area. Note the difference y-axis scales

The design-based model w/REMA would place 85.8% of the biomass in the central GOA in 2023, the VAST model w/o REMA would apportion 55.7% (Table 5).

Table 5: Apportionment percent estimates for design-based w/REMA and VAST estimated survey abundance w/o using REMA. The eastern GOA is set at 1t and allocated to the “Other rockfish” complex for all scenarios, and is not shown here.

Year	Area	Design-based w/REMA	VAST - no REMA
2021	Western	44.6	48.0
	Central	55.4	52.0
2022	Western	26.8	48.0
	Central	73.2	52.0
2023	Western	14.2	44.3
	Central	85.8	55.7

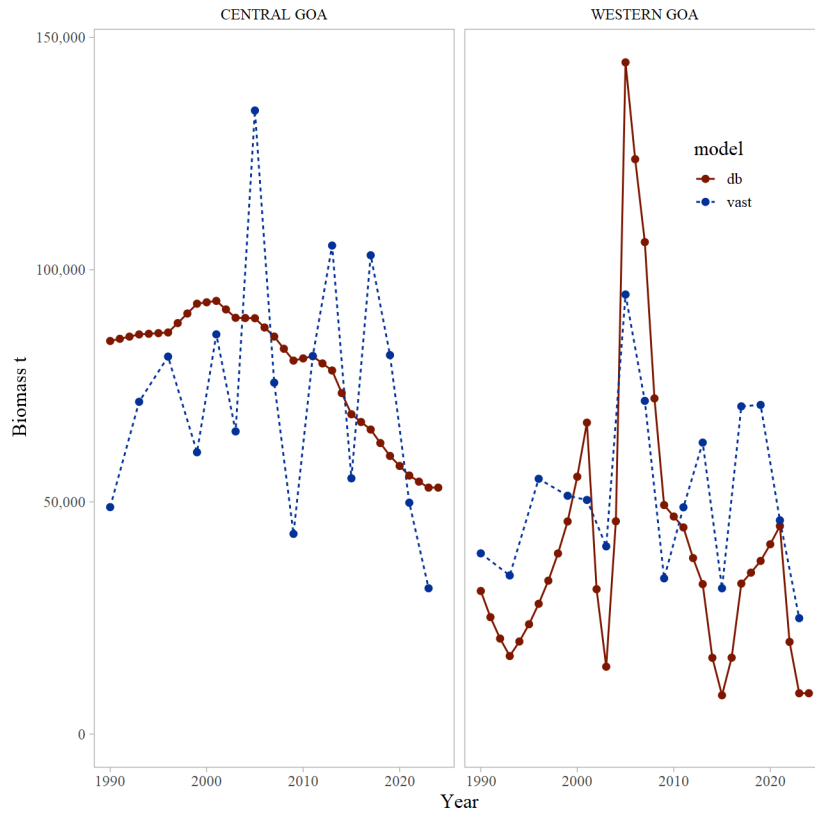


Figure 3: REMA smoothed design-based, and VAST apporportionment biomass by area.

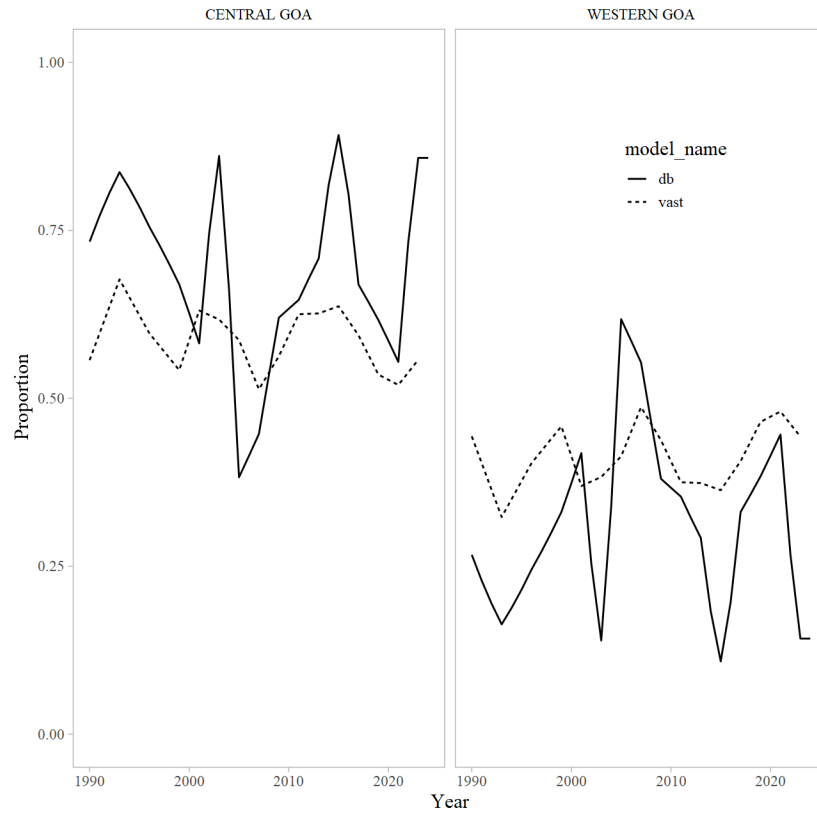


Figure 4: REMA smoothed design-based, and VAST apportionment proportions by area.

5 Bridging from ADMB to RTMB (Model RTMB)

5.1 Introduction

The ADMB program is in the process of an ‘orderly shutdown of development’ (see: [ADMB](#)) and TMB (Template Model Builder) is a viable alternative for fishery stock assessment development. TMB is widely seen as the successor to ADMB, though there are some noted differences (e.g., TMB has no native phasing, so all parameters are estimated simultaneously). RTMB allows for accessing most of the utility found in TMB but the models can be written entirely in R rather than C++ (Kristensen 2024).

To compare model outputs the last full model accepted by the SSC for northern rockfish with the model and data corrections described above [Model 22.1b](#) was converted to RTMB code ([Model 24](#)). [Model 22.1b](#) has historically had a tight prior on M (mean 0.06, CV 0.05), and fixed σ^r at 1.5.

[Model 22.1b](#) parameters outputs were used as fixed parameter inputs for [Model 24](#) for an initial comparison. Additionally, [Model 24](#) was run using the same parameter inputs and bounds (not fixed) as [Model 22.1b](#), these results are presented as model [Model 24.a](#) for reporting purposes.

5.2 Results

When holding all parameters the same between the two models the same output values (total biomass, spawning biomass, etc.) are produced and the likelihoods are generally the same or within a few decimal points [Tables 6](#) and [7](#) ([Model 22.1b](#) and [Model 24](#)). That is, the RTMB model is effectively recreating the ADMB model [Figures 5 - 7](#). There is no discernible differences between model selectivities, biomass estimates and composition data, the percent differences between models are $< 0.0005\%$.

When the [Model 24.a](#) model was initially run, it returned nonsensical results with q estimated at its upper bound (1.5), $\log M$ estimated at its lower bound (0.001) and a non-positive definite Hessian matrix. To address this M was fixed at 0.06 (see Heifetz and Clausen 1991). This stabilizes the model and it produces similar results to the [Model 24](#) model. However, when exploring the posterior distribution using MCMC (Monnahan 2018) (setup with 5 chains, 1,000 iterations, with 250 warmup) there were a substantial number of divergences (2,629) with a minimum effective sample size of 10.4 and a mean \hat{R} of 2.15. Further examination indicated very poor marginal distributions for a number of parameters [Figure 8](#).

To address these divergences log normal priors were placed on fishery and survey selectivity logistic slope (prior mean $\log(3.8)$, CV 1.0) and intercept parameters (prior mean $\log(7.5)$, CV 1.0). It is probable that the differences in the ADMB and RTMB models’ ability to fit to the data are due to the phases present in the ADMB model, which are not natively available in RTMB.

With priors placed on the selectivity parameters and M freely estimated (prior mean $\log(0.06)$, CV 0.15), the model converged, has a positive definite Hessian, and produces results similar to the ADMB model (Figure 5). With a minimum effective sample size of 31.1 a mean \hat{R} of 1.013 and no divergences after warmup. The marginal distribution of keys parameters were greatly improved Figure 9. These changes slightly reduce total and spawning biomass Figure 5 and associated biological reference points Table 7.

Table 6: Model likelihood values. Model 22.1b is the SSC accepted 2022 model, with updates to a lognormal error structure survey likelihood and adjusted ISS values. The RTMB Model 24 is based upon parameter outputs from Model 22.1b. Model 24.a is run using uninformed input values and parameter bounds.

Likelihood	Model 22.1b	Model 24	Model 24.1
Catch	0.109	0.109	0.128
Survey biomass	2.0559	2.0559	1.989
Fishery ages	41.8463	41.8431	41.866
Survey ages	83.0683	83.0683	82.970
Fishery lengths	70.214	70.214	70.261
Recruitment devs	9.312	9.312	9.361
F regularity	5.676	5.676	5.647
M prior	0.012	0.012	0.9487
q prior	0.0062	0.0063	-0.1209
a50-fishery prior			-0.923
delta-fishery prior			-1.154
a50-survey prior			-0.935
delta-survey prior			-0.924
Data total	197.3	179.3	197.3

Table 7: Parameter estimates and outputs, italicized values were held constant with Model 22.1b. Model 22.1b is the SSC accepted 2022 model, with updates to a lognormal error structure survey likelihood and adjusted ISS values. The RTMB Model 24 is based upon parameter outputs from Model 22.1b. Model 24.a is run using uninformed input values and parameter bounds.

Parameter	M22.1b	Model 24	Model 24.1
M	0.0595	<i>0.0595</i>	0.0578
q	0.951	<i>0.951</i>	0.986
a50 - fishery	8.167	<i>8.167</i>	8.176
delta - fishery	1.876	<i>1.876</i>	1.914
a50 - survey	9.023	<i>9.023</i>	8.996
delta - survey	4.217	<i>4.217</i>	4.188
avg recruitment	3.5243	<i>3.5243</i>	3.454
F40	0.061	0.061	0.596
B100	85,284	85,284	84,415
B40	34,114	34,114	33,766
2023 total biomass	101,794	101,794	98,737
2023 spawning biomass	42,811	42,811	41,670
2023 OFL	6,376	6,376	6,072
2023 ABC	5,343	5,343	5,087

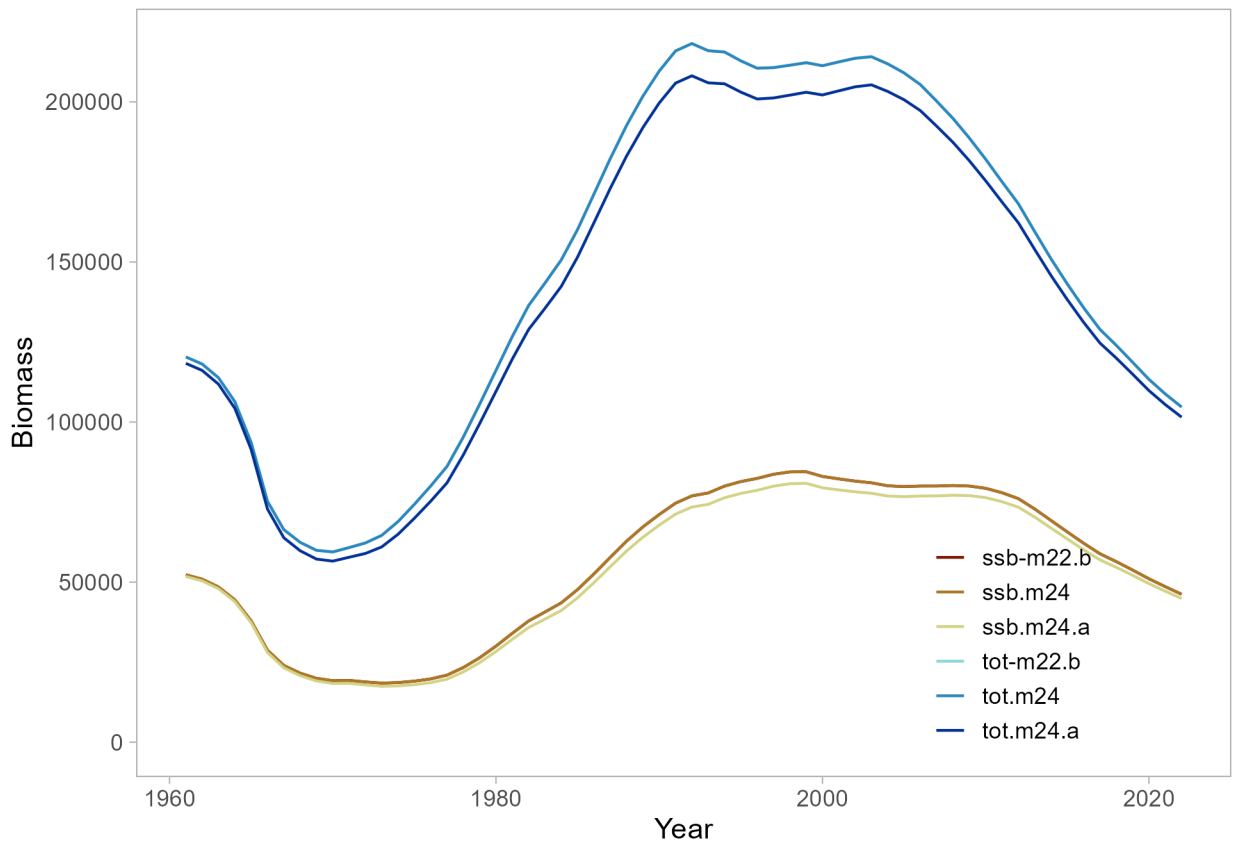


Figure 5: Spawning and total biomass from ADMB Model 22.1b and RTMB Models 24 and 24.a. Model 22.1b and Model 24 overlap and are not distinguishable.

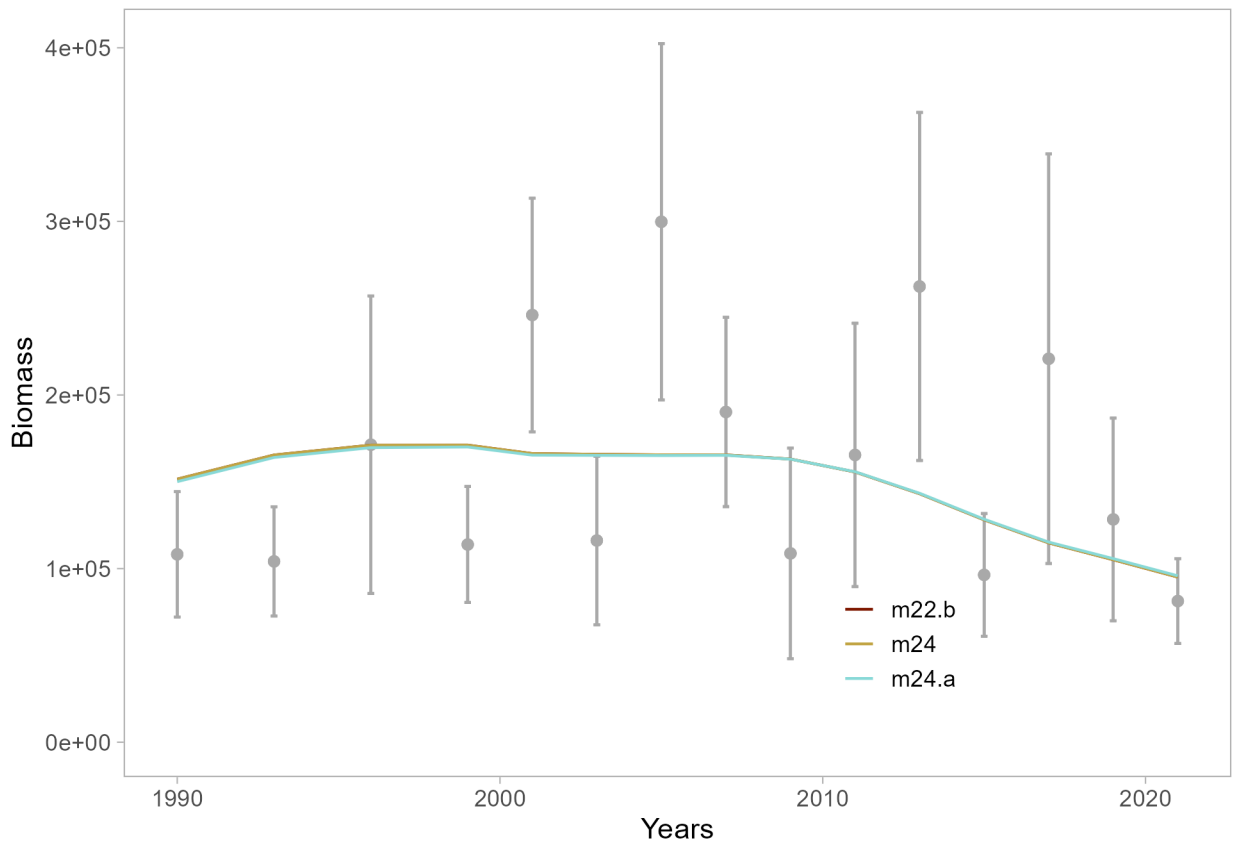


Figure 6: Survey biomass from ADMB Model 22.1b and RTMB Models 24 and 24.a. Model 22.1b and Model 24 overlap and are not distinguishable.

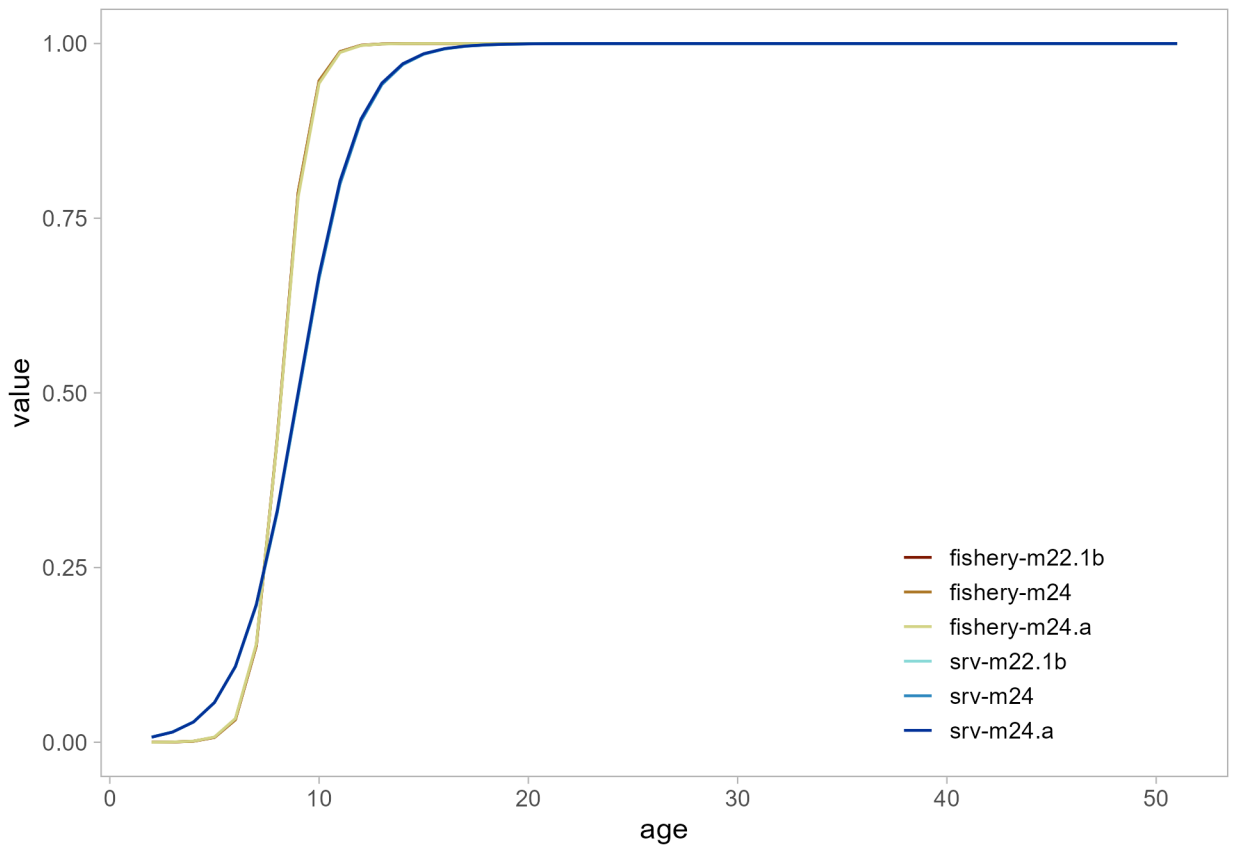


Figure 7: Fishery and survey selectivity from ADMB Model 22.1b and RTMB Models 24 and 24.a. Model 22.1b and Model 24 overlap and are not distinguishable.

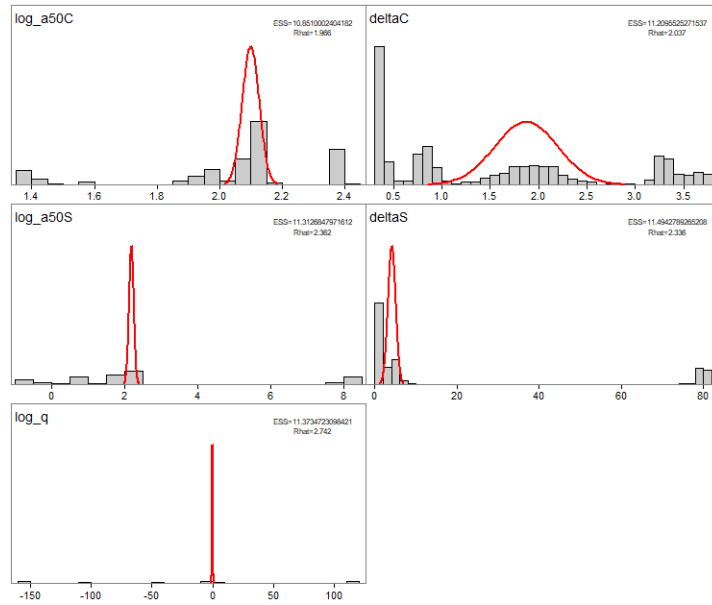


Figure 8: Marginal posterior histogram vs the asymptotic normal (red lines) from the inverse Hessian from the first attempt at fitting Model 24.a.

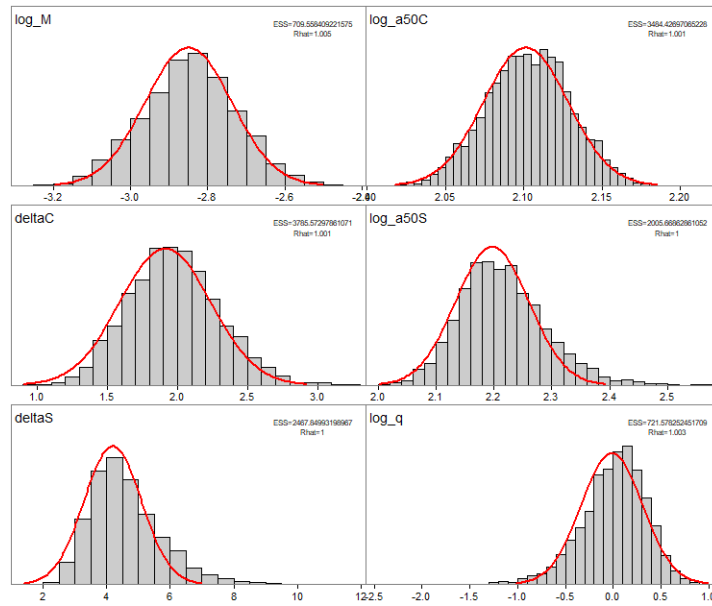


Figure 9: Marginal posterior histogram vs the asymptotic normal (red lines) from the inverse Hessian from the second attempt at fitting Model 24.a with priors on selectivity.

References

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