

Developments of the RTMB version of the ADMB pollock model

September 2026 Plan Team working paper on the corrected full-age 2024 “PM” model bridge and subsequent RTMB developments

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The eastern Bering Sea walleye pollock assessment has long used a custom AD Model Builder (ADMB) model. This working paper documents its translation to R Template Model Builder (RTMB) and evaluates agreement between the two implementations at a common parameter set. The report presents model fits, fishery and survey selectivity analyses, projections, retrospective results, and SparseNUTS diagnostics. Candidate refinements are evaluated relative to the accepted ADMB assessment model.



RTMB TECHNICAL REPORT

Table of contents

1	Executive Summary	4
2	Purpose and Scope	5
2.1	September 2026 Plan Team review context	5
3	Initial RTMB Developments	6
3.1	Data Inputs	6
3.2	Model Implementation	6
3.2.1	Structure	6
3.2.2	Model assumptions	6
3.2.3	BTS Selectivity Variation and Penalties	6
3.2.4	Fishery Selectivity Specifications	8
3.2.5	Run Definitions	9
4	ADMB Comparison Results	10
5	RTMB Model Results	14
5.1	Fit to Base RTMB-ADMB Run	14
5.1.1	Catch Fit	14
5.1.2	Fits by Fleet	14
5.1.3	Residuals	14
5.1.4	Age Composition Fits	14
5.1.5	OSA Residual Diagnostics	14
5.1.6	Selectivity Curves	21
5.1.7	Selectivity Ridge Plots	21
6	Projections	25
6.1	Seven Tier-3 Scenario Results	25
6.2	Alternative 2 Fixed-Catch Projection	25
6.3	Projection Figures	25
7	Diagnostics	32
7.1	Retrospective Peels	32
7.2	Additional Bridge Diagnostics and Only-BTS Sensitivity	32
8	Summary	38
9	Reproducibility	39
10	Supporting Tables	40
	References	43
	Appendices	44
A-1	Data issues and revisions since the 2024 assessment	44
	FTNIRS age-data	44
	Impact of revised BTS age-data	44
A-2	Evaluation of time-varying BTS availability	47
A-3	SparseNUTS MCMC	49
A-4	Data and output	53
	Downloadable CSV files	53
	Input schedules	60
	Report-object inventory	60
A-5	Length-frequency patterns	60
	Change from 2025 to 2026	60
	A- and B-season distributions	60
	Combined-season distributions	60

B-season distributions by NMFS area	60
A-6 Sex-ratio patterns	60
Pooled fishery patterns by age and length	60
A-season progression	60
Length patterns by age and season	60
Bering Sea summer acoustic survey	67
A-7 Notes	67

1 Executive Summary

The custom ADMB pollock model has been translated into RTMB and evaluated at the same parameter estimates as the ADMB model. The corrected comparison normalizes observed and predicted bottom trawl survey (BTS) age compositions across ages 1–15 and applies the nominal integer sample sizes. The fixed-parameter results isolate differences between implementations from differences caused by estimation. The same corrected specification was used for model-fit summaries, projections, retrospective peels, and sensitivities.

The principal developments are:

- an RTMB implementation of the ADMB population dynamics and likelihood;
- comparisons of state variables, predictions, and likelihood components;
- selectable fishery-selectivity forms, including hierarchical time-varying and two-dimensional autoregressive alternatives;
- RTMB-based retrospective and uncertainty analyses.

The fixed-parameter comparison showed negligible differences between ADMB and RTMB for the tested configuration. Alternative selectivity formulations and diagnostic analyses are presented for review and do not alter current management advice, which remains based on the accepted ADMB assessment model. This document is the primary model-development report for the September 2026 Plan Team meeting. Companion SPoRC and Rceattle analyses provide comparisons with more general modeling frameworks. Among these alternatives, Rceattle is the leading candidate for future operational assessment development, subject to resolution of the remaining diagnostics and the established review process.

2 Purpose and Scope

This document evaluates an RTMB translation of the EBS pollock ADMB assessment model. It follows the assessment-reporting framework used for the FIMS, SPoRC, and Rceattle comparisons and emphasizes agreement with ADMB, model fit, diagnostics, and candidate refinements.

The analyses use a corrected comparison in which observed and predicted BTS age compositions span ages 1–15 and nominal integer sample sizes enter the likelihood. A historical configuration is retained only to quantify the effect of that correction.

2.1 September 2026 Plan Team review context

Three model-development reports are intended to be presented and discussed together. They address different questions and should not be interpreted as three competing operational assessments.

Report	Role in the September 2026 review	Current interpretation
RTMB (this report)	Primary report and detailed reference for the corrected ADMB translation, diagnostics, retrospectives, selectivity alternatives, and projections	Establishes the common implementation baseline and identifies issues requiring further evaluation
SPoRC	Companion comparison using the SPoRC single-region framework	Demonstrates close reproduction of the corrected ADMB candidate and supports continued methods development
Rceattle	Companion comparison using a more general and extensible assessment framework	Leading candidate for future operational assessment development; advancement depends on resolving selectivity identification, retrospective bias, posterior mixing, and completing formal review

The accepted ADMB model continues to provide management advice during this evaluation. The near-term review question is therefore how the three analyses inform future development priorities, with particular attention to whether the remaining Rceattle diagnostics can be satisfactorily resolved.

3 Initial RTMB Developments

3.1 Data Inputs

The RTMB input series include annual fishery catch, fishery age compositions, BTS and ATS age compositions, the BTS biomass index, the ATS survey index, acoustic vessels of opportunity, and fishery CPUE. The input data and bridge ADMB results correspond to the corrected base configuration described above.

The corrected bridge applies one coherent BTS composition likelihood. Observed proportions and multinomial predictions each span ages 1–15 and sum to one. Age-1 selectivity retains its dedicated parameterization, while the ages 2–15 curve retains its existing form. The likelihood uses the nominal sample sizes recorded by `pm.tpl`, with integer truncation preserved because the ADMB data object stores those sample sizes as integers. Separately, the BTS total-numbers quantity used to scale the age composition continues to represent ages 2–15. This quantity is not the fitted BTS survey index, which is defined in biomass.

3.2 Model Implementation

3.2.1 Structure

- **Population:** single EBS pollock stock.
- **Model engine:** RTMB with the negative log-likelihood written in R.
- **Reference model:** ADMB bridge run in `admb/runs/for_rtmb/`.
- **Fleets and indices:** fishery catch, fishery CPUE, BTS, ATS, and AVO.
- **Age compositions:** fishery, BTS, and ATS age-composition likelihoods.
- **Recruitment:** ADMB-port recruitment likelihood and deviations.
- **Natural mortality:** age-specific input vector from the ADMB bridge data.
- **Selectivity:** fishery, BTS, and ATS selectivity blocks ported from the ADMB bridge configuration.

3.2.2 Model assumptions

3.2.3 BTS Selectivity Variation and Penalties

The bottom trawl survey (BTS) selectivity in the RTMB bridge is represented as a time-varying logistic curve for ages 2 and older, with a separate age-1 term. For BTS year (t) and model age (a), the code uses the age midpoint ($x_a = a + 0.5$) and computes

$$\log s_{t,a}^{\text{BTS}} = -\log [1 + \exp \{-\exp(\gamma_t)(x_a - \exp(\alpha_t))\}],$$

Table 3.1: Summary of the EBS pollock RTMB-ADMB input data.

RTMB-ADMB Input Summary

item	value
Years	1964-2024 (61)
Ages	1-15 (15)
Fishery age-composition years	1964-2023 (60)
BTS index years	1982-2024 (42)
ATS index years	1994-2024 (19)
CPUE years	1965-1976 (12)
AVO years	2006-2024 (18)
Saved RTMB output	analysis/output/corrected_full_age_bts/rtmb_base.rds

Table 3.2: BTS age-composition treatment in the corrected ADMB and RTMB bridge. Observed and predicted compositions cover ages 1–15; the total-numbers quantity used for composition scaling retains its ages 2–15 definition.

Corrected BTS Composition Definition

component	corrected_treatment
Observed composition ages	1–15
Predicted composition ages	1–15
Maximum observed row-sum error	4.44e-16
Maximum predicted row-sum error	5.55e-16
Sample-size treatment	Nominal integer values from pm.tpl
BTS total-numbers ages	2–15

Table 3.3: Available observations by fleet and data type.

Data Availability by Fleet

name	type	n_obs	years
ATS	age_comp	19	1994-2024
BTS	age_comp	42	1982-2024
Fishery	age_comp	60	1964-2023
Fishery	catch	61	1964-2024
ATS	index	19	1994-2024
AVO	index	18	2006-2024
BTS	index	42	1982-2024
CPUE	index	12	1965-1976

Table 3.4: ADMB bridge files used by the RTMB implementation.

ADMB Bridge Files

file	role
repo/analysis/output/corrected_full_age_bts/admb_root/runs/full_age_bts/pm.rep	ADMB report used f
repo/analysis/output/corrected_full_age_bts/admb_root/runs/full_age_bts/pm.par	ADMB parameter fil
repo/admb/runs/for_rtmb/pm.tpl	ADMB bridge templ

Table 3.5: Key model assumptions and fixed settings in the current RTMB-ADMB implementation.

RTMB-ADMB Model Assumptions

topic	setting
Bridge source	ADMB bridge run in admb/runs/for_rtmb
Template	Physical bridge pm.tpl copy that intentionally differs from admb/source/pm.tpl
Natural mortality	0.9, 0.45, 0.3, 0.3, 0.3, 0.3, 0.3, 0.3, 0.3, 0.3, 0.3, 0.3, 0.3, 0.3
BTS start year	1982
ATS start year	1994
Recruitment age	1
Age-1 ATS index	1
BTS biology likelihood	1
ATS biology likelihood	1

Table 3.6: BTS selectivity variation and regularization settings in the current RTMB-ADMB configuration.

BTS Selectivity Regularization

item	value
BTS selectivity start year	1982
Terminal year	2024
Number of annual BTS selectivity years	43
Estimated annual slope vector	<code>sel_slp_bts_dev</code>
Estimated annual age-at-50 vector	<code>sel_a50_bts_dev</code>
Estimated annual age-1 vector	<code>sel_age_one_bts_dev</code>
Time-smoothness weight ('selVarbts')	2
Time-smoothness age range	3-14
Age-1 first-difference weight	8
Inactive base BTS terms fixed in config	<code>sel_devs_bts</code> , <code>sel_slp_bts</code> , <code>sel_a50_bts</code> , <code>sel_age_one_bts</code>

where γ_t is the annual log-slope parameter (`sel_slp_bts_dev`) and α_t is the annual log-age-at-50% parameter (`sel_a50_bts_dev`). Thus the realized slope is $\exp(\gamma_t)$, and the realized age-at-50% is $\exp(\alpha_t)$. Age 1 is then overwritten by its own annual log-selectivity term:

$$\log s_{t,1}^{\text{BTS}} = \eta_t,$$

where η_t is `sel_age_one_bts_dev`.

The current RTMB call treats `sel_slp_bts_dev`, `sel_a50_bts_dev`, and `sel_age_one_bts_dev` as estimated annual vectors. The base logistic BTS terms `sel_slp_bts`, `sel_a50_bts`, `sel_age_one_bts`, and `sel_devs_bts` are fixed in `R/config.R`; the time variation is carried by the annual deviation vectors above.

The regularization targets the implied annual log-selectivity curves instead of α_t or γ_t directly. In `selectivity_like_bts()`, an extended matrix $\tilde{\ell}_{t,a}$ is formed by prepending a zero row for the year before the BTS time series. Let $\Delta_t z_t = z_t - z_{t-1}$. The BTS time-variation penalty for ages $a = q_{\min}, \dots, q_{\max} - 1$ is

$$P_{\text{BTS,time}} = \lambda_{\text{BTS}} \sum_{a=q_{\min}}^{q_{\max}-1} \sum_t \left(\Delta_t \tilde{\ell}_{t,a} \right)^2,$$

where λ_{BTS} is `selVarbts`. In this configuration, `q_amin = 3`, `q_amax` defaults to `nages`, and `nages = 15`, so this penalty applies to ages 3 through 14. Age 2 lies below this time-smoothness range, and age 15 lies above the final loop index of `q_amax - 1`.

The age-1 BTS term has a separate first-difference penalty:

$$P_{\text{BTS,age1}} = 8 \sum_t [\Delta_t (\eta_t - \bar{\eta})]^2,$$

where $\bar{\eta}$ is the mean of the age-1 deviation vector. The total BTS selectivity regularization returned by `selectivity_like_bts()` is

$$P_{\text{BTS}} = P_{\text{BTS,time}} + P_{\text{BTS,age1}},$$

with no additional BTS curvature penalty active under the current logistic-deviation parameterization.

3.2.4 Fishery Selectivity Specifications

The base bridge retains the assessment's age coefficients and deviations at configured change years. Two additional fishery-selectivity forms were implemented to evaluate how a more continuous representation of change affects fit, biological patterns, and assessment scale. These runs differ in fishery selectivity while retaining the common data and likelihood framework.

Table 3.7: Configured RTMB-ADMB run definitions.

RTMB-ADMB Run Definitions

run	source	refit_default	output_available	report_el
base	analysis/output/corrected_full_age_bts/rtmb_base.rds	FALSE	TRUE	

Form	Specification	Development status
Base coefficients	Age coefficients with deviations at configured change years; ages 11 and older share the age-11 value	Bridge reference
Time-age varying double logistic	Shared ascending and descending curve with annual random effects at a fixed 30% process CV; the tested formulation evaluates ages through 15 separately	Converged staged development fit
Two-dimensional AR1	Year-by-age latent field with separable AR1 correlation across years and ages; ages 11 and older share the age-11 value	Sensitivity fit

The initial double-logistic experiment estimated 183 annual fixed effects and failed the convergence criteria. A two-stage hierarchical formulation replaced that experiment: stage 1 estimated a shared three-parameter curve, and stage 2 estimated zero-centered annual random effects using the RTMB Laplace approximation. The staged fit passed the optimizer, gradient, positive-Hessian, and finite-standard-error checks recorded in the selectivity analysis.

These alternatives should be evaluated using likelihood components, age-composition residuals, selectivity surfaces, convergence, and effects on spawning biomass. Objective value alone provides an incomplete basis for choosing a selectivity specification. The detailed equations, fitted comparisons, and implementation references remain available in the companion [fishery-selectivity supporting analysis](#), with a [PDF version](#) and [referenceable summary data](#).

3.2.5 Run Definitions

Results are presented for one base RTMB configuration corresponding to the corrected ADMB comparison. Candidate fishery-selectivity formulations are identified separately from this base configuration.

The base output writer follows this pattern.

```
source("R/config.R")
data$return_nll_only <- 0
rtmb_result <- rpm(parms)
saveRDS(
  list(report = rtmb_result$rtmb, metadata = list(model = "rtmb_ebswp")),
  "analysis/output/corrected_full_age_bts/rtmb_base.rds"
)
```

4 ADMB Comparison Results

This fixed-parameter comparison follows the bridge method demonstrated in the September 2025 [EBS pollock development report](#). The corrected ADMB model’s maximum-likelihood parameter estimates are injected into RTMB, and both implementations are evaluated at that identical parameter point. This isolates code translation from optimization behavior and later model alternatives.

The OSA diagnostics, Only-BTS sensitivity, retrospectives, and projections use the same corrected base configuration. The SparseNUTS appendix instead evaluates the hierarchical Form-2 selectivity model and is identified separately throughout.

The total negative log-likelihoods differ by 0.000378912. The maximum difference among key outputs is 0.000487392%, and the largest absolute RTMB gradient at the ADMB estimates is 9.484023e-06. These values satisfy the prespecified corrected-comparison tolerances.

outer mgc: 9.484023e-06

Table 4.1: Summary of the corrected full-age BTS fixed-parameter ADMB-to-RTMB bridge. The absolute NLL difference is on the negative-log-likelihood scale; the key-output difference is the largest absolute percentage difference among state, prediction, selectivity, composition, and likelihood quantities.

Corrected Full-Age BTS ADMB–RTMB Bridge

measure	value
ADMB total negative log-likelihood	7,075.220000000
RTMB total negative log-likelihood	7,075.220378912
Absolute total NLL difference	0.000378912
Maximum key-output difference (%)	0.000487392
Maximum absolute RTMB gradient	0.000009484

Table 4.2: Effect of replacing the historical RTMB-adjusted BTS composition treatment with the corrected full-age treatment. Percent differences summarize paired annual values from the two RTMB configurations.

Effect of Correcting the BTS Composition Likelihood

Quantity	Median absolute difference (%)	Maximum absolute difference (%)
Spawning biomass	0.1962	1.6248
Recruitment	0.3396	1.8131
Numbers at age	0.5584	5.5940

Table 4.3: Corrected-base lineage for primary downstream analyses. Matching checksums confirm that each product was regenerated from the corrected full-age BTS RTMB bridge output.

Corrected Full-Age Bridge Lineage

analysis	base_md5	matches_authoritative_base
Corrected base bridge	76d088857356dea461eab94758d11881	TRUE
Only-BTS sensitivity	76d088857356dea461eab94758d11881	TRUE
OSA diagnostics	76d088857356dea461eab94758d11881	TRUE
Nine-peel retrospective	76d088857356dea461eab94758d11881	TRUE
Seven-scenario Tier 3 projections	76d088857356dea461eab94758d11881	TRUE
Alternative 2 fixed-catch projections	76d088857356dea461eab94758d11881	TRUE

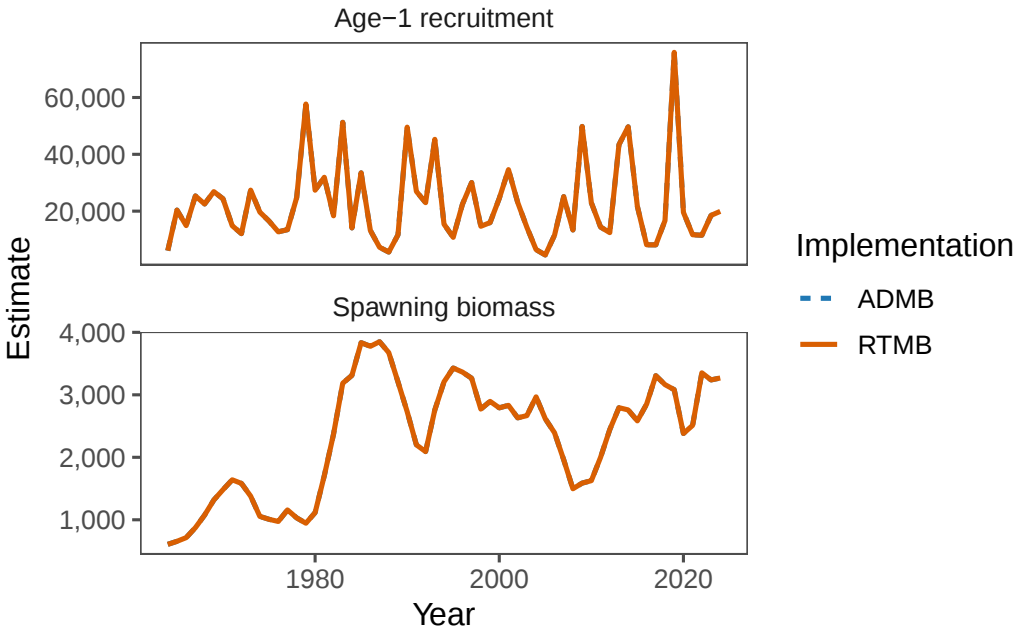


Figure 4.1: Spawning biomass and age-1 recruitment from RTMB and ADMB at the same ADMB maximum-likelihood parameter estimates. The two implementations are visually indistinguishable at the plotted scale. Select the figure to open it in the lightbox.

Table 4.4: Object-by-object comparison of RTMB and ADMB results at the shared ADMB maximum-likelihood parameter point. **Equal** is the result of the numerical comparison at tolerance 1e-5; correlation is shown for compatible nonconstant vectors.

RTMB and ADMB Object Comparison

Quantity	Equal	Elements	Maximum absolute difference	Maximum absolute difference (%)	Correlation
N	TRUE	915	0.0497623	0.0004874	1.0
phat_fsh	TRUE	900	0.0000005	0.0004833	1.0
sel_fsh	TRUE	915	0.0000050	0.0004728	1.0
phat_ats	TRUE	285	0.0048878	0.0004683	1.0
obs_catch	TRUE	61	0.0050000	0.0004579	1.0
F	TRUE	915	0.0000005	0.0004478	1.0
phat_bts	TRUE	630	0.0000005	0.0004441	1.0
sel_ats	TRUE	465	0.0000050	0.0004430	1.0
cpue_like	TRUE	1	0.0000043	0.0004024	1.0
pred_catch	TRUE	61	0.0049850	0.0003898	1.0
sel_bts	TRUE	645	0.0000005	0.0003875	1.0
rec_like	TRUE	7	0.0000390	0.0003826	1.0
pred_avo	TRUE	18	0.0000048	0.0003526	1.0
SSB	TRUE	61	0.0048317	0.0003091	1.0
eb_bts	TRUE	42	0.0277850	0.0002559	1.0
age_like	TRUE	3	0.0003106	0.0001968	1.0
phizero	TRUE	1	0.0000005	0.0001886	1.0
sel_like_dev	TRUE	3	0.0002149	0.0001747	1.0
avgsel_like	TRUE	1	0.0000003	0.0001697	1.0
wt_nll	TRUE	4	0.0041166	0.0001572	1.0
Z	TRUE	915	0.0000005	0.0001522	1.0
Priors	TRUE	4	0.0000286	0.0001421	1.0
sam_fsh	TRUE	60	0.0004988	0.0001344	1.0
eb_ats	TRUE	19	0.0048531	0.0001288	1.0
bts_like	TRUE	1	0.0000406	0.0001275	1.0
pred_cpue	TRUE	12	0.0045251	0.0001233	1.0
ats_age1_like	TRUE	1	0.0000135	0.0001217	1.0
S	TRUE	915	0.0000005	0.0001204	1.0
sel_like	TRUE	3	0.0000137	0.0000938	1.0
wt_like	TRUE	1	0.0048053	0.0000757	1.0
Bzero	TRUE	1	0.0037167	0.0000608	1.0
age_like_offset	TRUE	3	0.0065452	0.0000578	1.0
ats_like	TRUE	1	0.0000024	0.0000255	1.0
cat_like	TRUE	1	0.0000004	0.0000155	1.0
Fpen_like	TRUE	1	0.0000011	0.0000113	1.0
tot_like	TRUE	1	0.0003789	0.0000054	1.0
avo_like	TRUE	1	0.0000004	0.0000040	1.0
steepness	TRUE	1	0.0000000	0.0000031	1.0
M	TRUE	915	0.0000000	0.0000000	1.0
sam_bts	TRUE	42	0.0000000	0.0000000	1.0
sam_ats	TRUE	19	0.0000000	0.0000000	1.0

Table 4.5: Twenty largest RTMB gradients at the ADMB maximum-likelihood parameter estimates. Values close to zero confirm that the injected ADMB solution is also stationary in RTMB.

Largest RTMB Gradients at ADMB Estimates

parameter	gradient	absolute_gradient
sel_age_one_bts_dev	9.4840×10^{-6}	9.4840×10^{-6}
sel_age_one_bts_dev	7.2509×10^{-6}	7.2509×10^{-6}
sel_age_one_bts_dev	-6.4886×10^{-6}	6.4886×10^{-6}
sel_age_one_bts_dev	-5.7878×10^{-6}	5.7878×10^{-6}
sel_devs_ats	5.2185×10^{-6}	5.2185×10^{-6}
sel_devs_ats	-5.0064×10^{-6}	5.0064×10^{-6}
sel_devs_fsh	5.0001×10^{-6}	5.0001×10^{-6}
sel_devs_ats	4.7243×10^{-6}	4.7243×10^{-6}
sel_age_one_bts_dev	4.4816×10^{-6}	4.4816×10^{-6}
sel_devs_ats	4.4574×10^{-6}	4.4574×10^{-6}
sel_devs_ats	-4.4286×10^{-6}	4.4286×10^{-6}
sel_age_one_bts_dev	4.0655×10^{-6}	4.0655×10^{-6}
sel_devs_ats	-3.7469×10^{-6}	3.7469×10^{-6}
sel_devs_ats	-3.6566×10^{-6}	3.6566×10^{-6}
sel_age_one_bts_dev	3.6224×10^{-6}	3.6224×10^{-6}
sel_slp_bts_dev	3.5769×10^{-6}	3.5769×10^{-6}
sel_slp_bts_dev	3.5694×10^{-6}	3.5694×10^{-6}
sel_devs_ats	3.5293×10^{-6}	3.5293×10^{-6}
sel_slp_bts_dev	3.4820×10^{-6}	3.4820×10^{-6}
sel_devs_fsh	-3.4728×10^{-6}	3.4728×10^{-6}

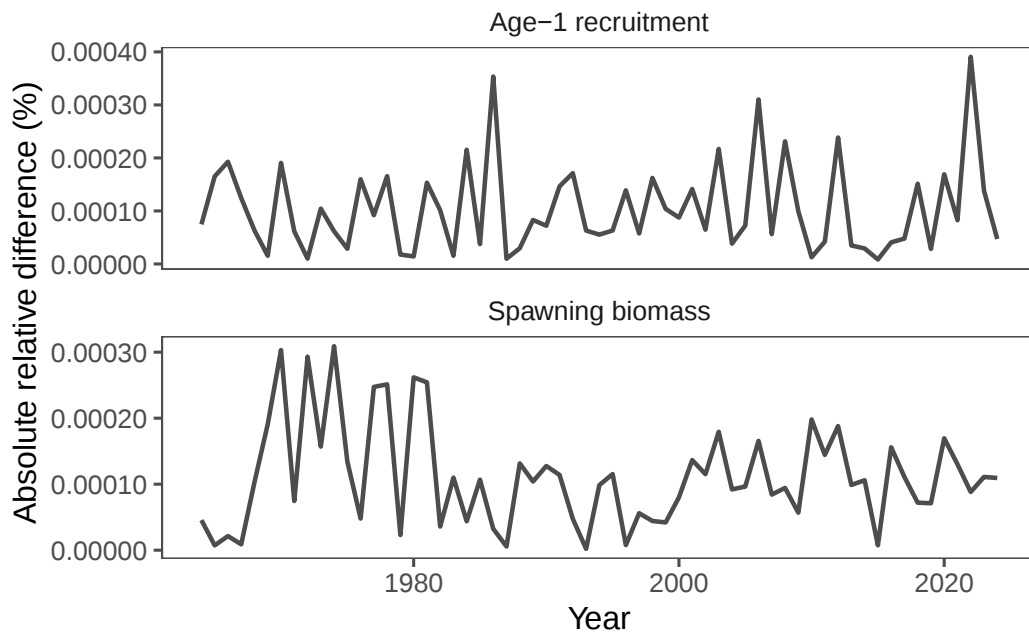


Figure 4.2: Absolute relative differences between RTMB and ADMB spawning biomass and age-1 recruitment at the shared ADMB estimates. Values are percentages; the very small vertical scale is intentional. Select the figure to open it in the lightbox.

5 RTMB Model Results

5.1 Fit to Base RTMB-ADMB Run

The fitted results below are for the base RTMB-ADMB configuration. The spawning biomass trajectory is shown in Figure 5.1. Fishery observed and predicted catch are compared in Figure 5.2, while survey, CPUE, and AVO index fits are summarized in Figure 5.3 and residual patterns in Figure 5.4. Expected age compositions and fleet selectivity curves are shown in Figure 5.5, Figure 5.6, Figure 5.7, and Figure 5.9.

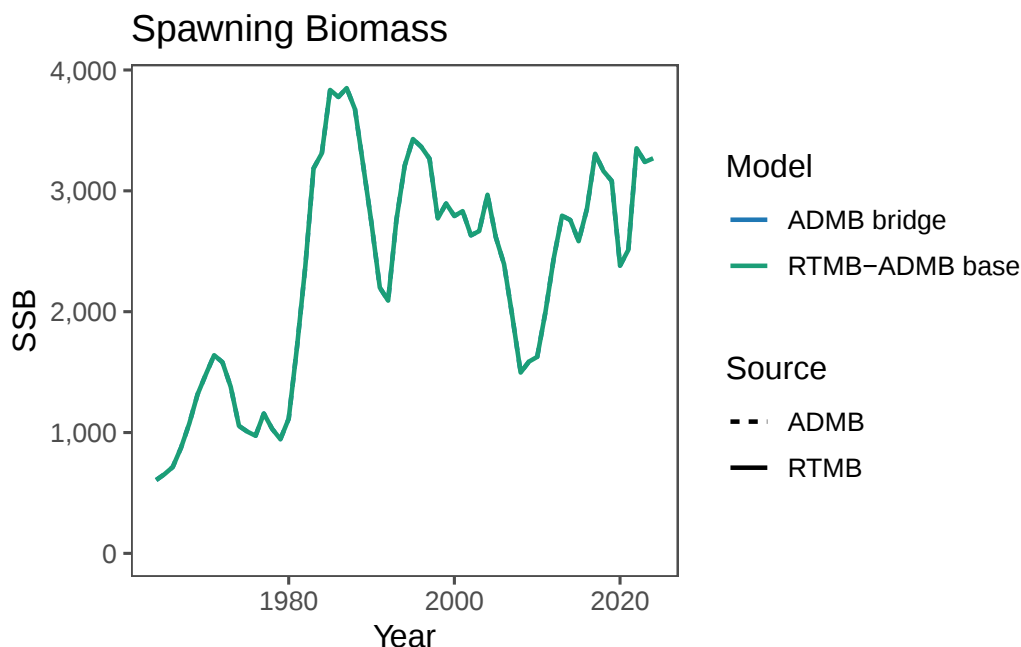


Figure 5.1: Estimated spawning biomass from the saved EBS pollock RTMB-ADMB base model, with the ADMB bridge output overlaid when available.

5.1.1 Catch Fit

5.1.2 Fits by Fleet

5.1.3 Residuals

5.1.4 Age Composition Fits

5.1.5 OSA Residual Diagnostics

The age-composition diagnostics follow the updated [afscOSA guidance](#) incorporated through [afscOSA pull request 10](#). The diagnostics were regenerated from the corrected full-age BTS bridge. In this render, the method is afscOSA 0.0.1 output generated from the corrected full-age BTS RTMB bridge.

The four rows in Figure 5.8 provide a joint interpretation. The aggregate composition first identifies systematic fit patterns, such as selectivity that consistently misses particular ages. The Q-Q plot assesses whether OSA residuals behave approximately as standard normal values and reports the SDNR and lower and upper 2.5% quantiles with their expected intervals. The OSA and Pearson bubble plots then locate temporal, age-specific, or cohort patterns. A statistic outside its interval signals an area for investigation and provides one element of the broader assessment evaluation.

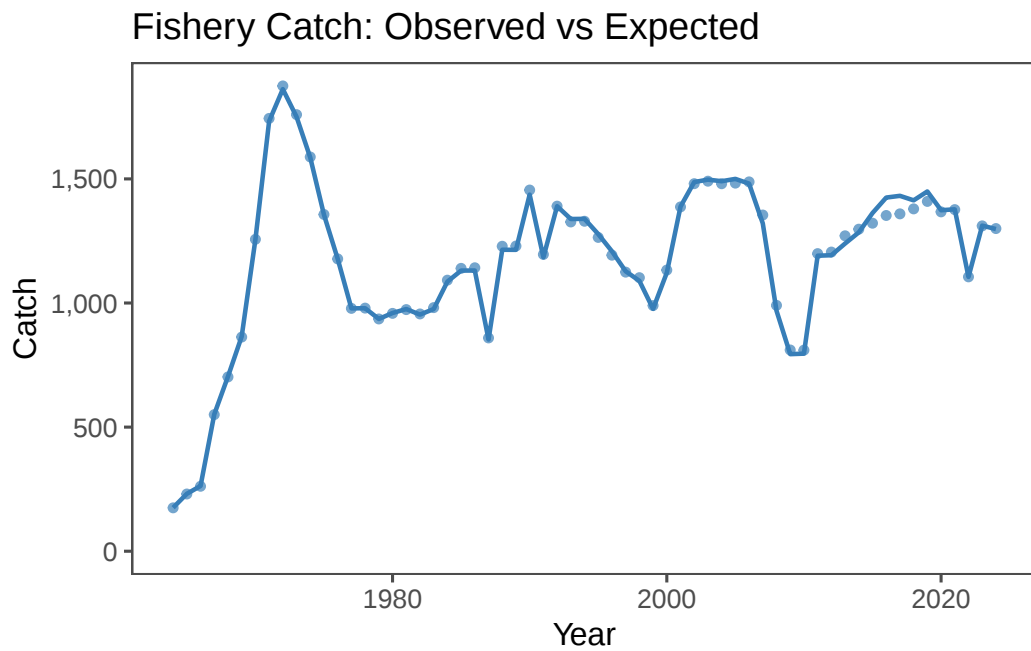


Figure 5.2: Observed fishery catch and predicted catch from the base RTMB-ADMB model.

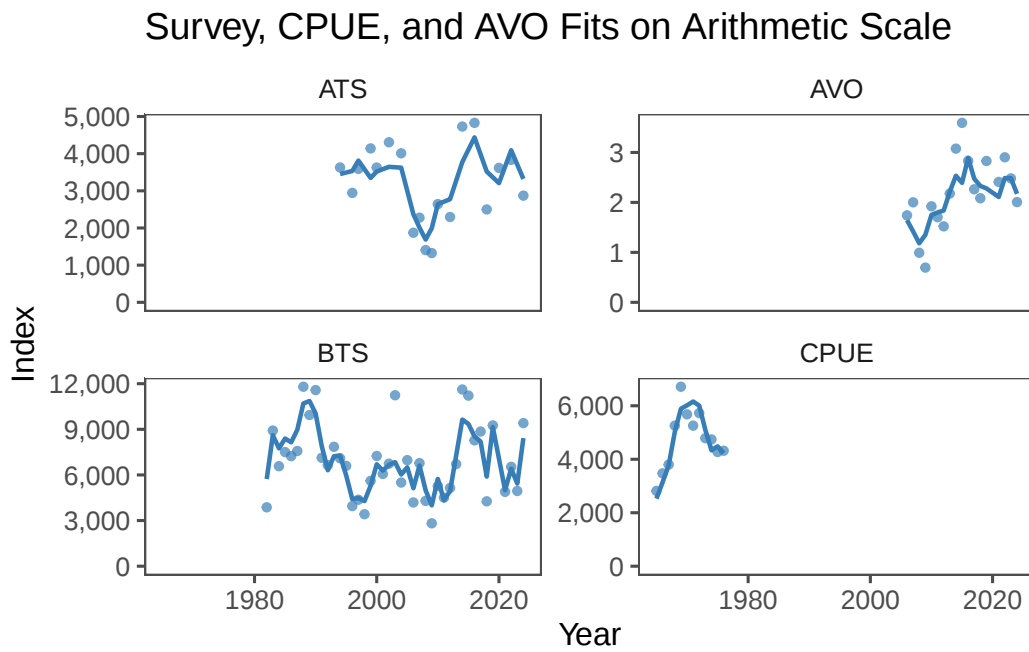


Figure 5.3: Observed and predicted index series from the base RTMB-ADMB model, shown on arithmetic scales with separate facet axes.

Survey, CPUE, and AVO Standardized Residuals

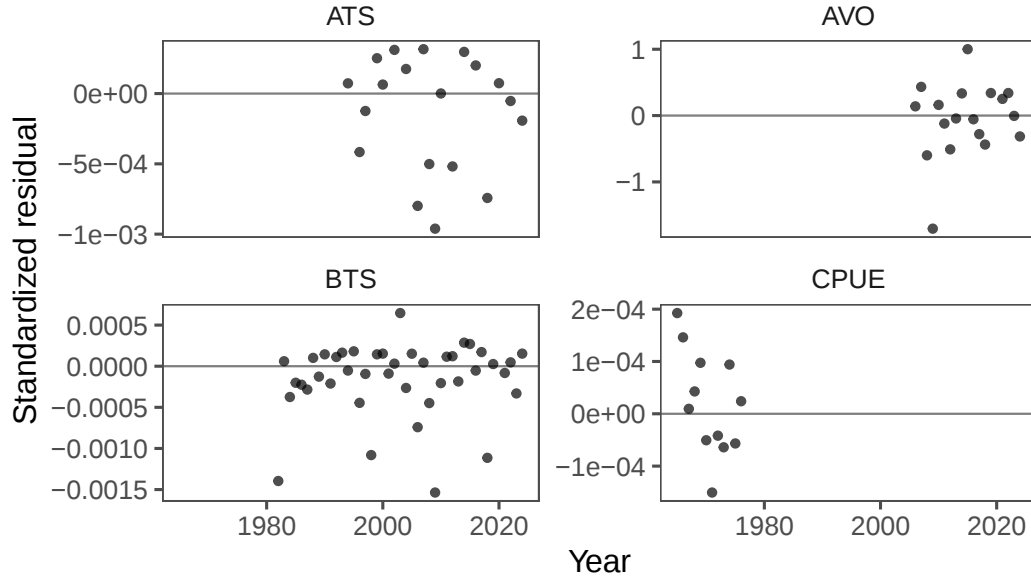


Figure 5.4: Approximate standardized log residuals for RTMB-ADMB index observations. Residuals are divided by the input log standard deviation.

Table 5.1: Source and software checks for the updated OSA diagnostics. The base-model checksum ties these diagnostics to the corrected RTMB object used elsewhere in this report. The ATS 2020 placeholder was excluded because it has zero rounded multinomial observations and supplies zero information to an OSA calculation.

OSA Diagnostic Source Check

item	value
afscOSA version	0.0.1
R version used for OSA calculations	R version 4.6.1 (2026-06-24)
Accepted base-model checksum (MD5)	76d088857356dea461eab94758d11881
OSA input checksum (MD5)	5a49af1db42ab91053cedb80c64504ef
Excluded zero-information composition row	ATS 2020
Fleets	ATS, BTS, Fishery
OSA residuals	1620

Table 5.2: Summary of one-step-ahead residual distributions. Under a correctly specified composition model, OSA residuals are expected to be approximately standard normal: mean near zero, SDNR near one, and 2.5% tail quantiles near -1.96 and 1.96. Formal expected intervals are shown in the Q-Q panels of Figure Figure 5.8; these summaries are diagnostic context rather than model-selection tests.

OSA Residual Distribution Summary

Fleet	OSA residuals	Mean residual	SDNR	Lower 2.5% quantile	Upper 97.5% quantile
ATS	234	0.07	0.81	-1.81	1.66
BTS	588	-0.07	0.98	-2.00	1.75
Fishery	840	-0.06	0.87	-1.92	1.61

Fishery Age Composition Fits

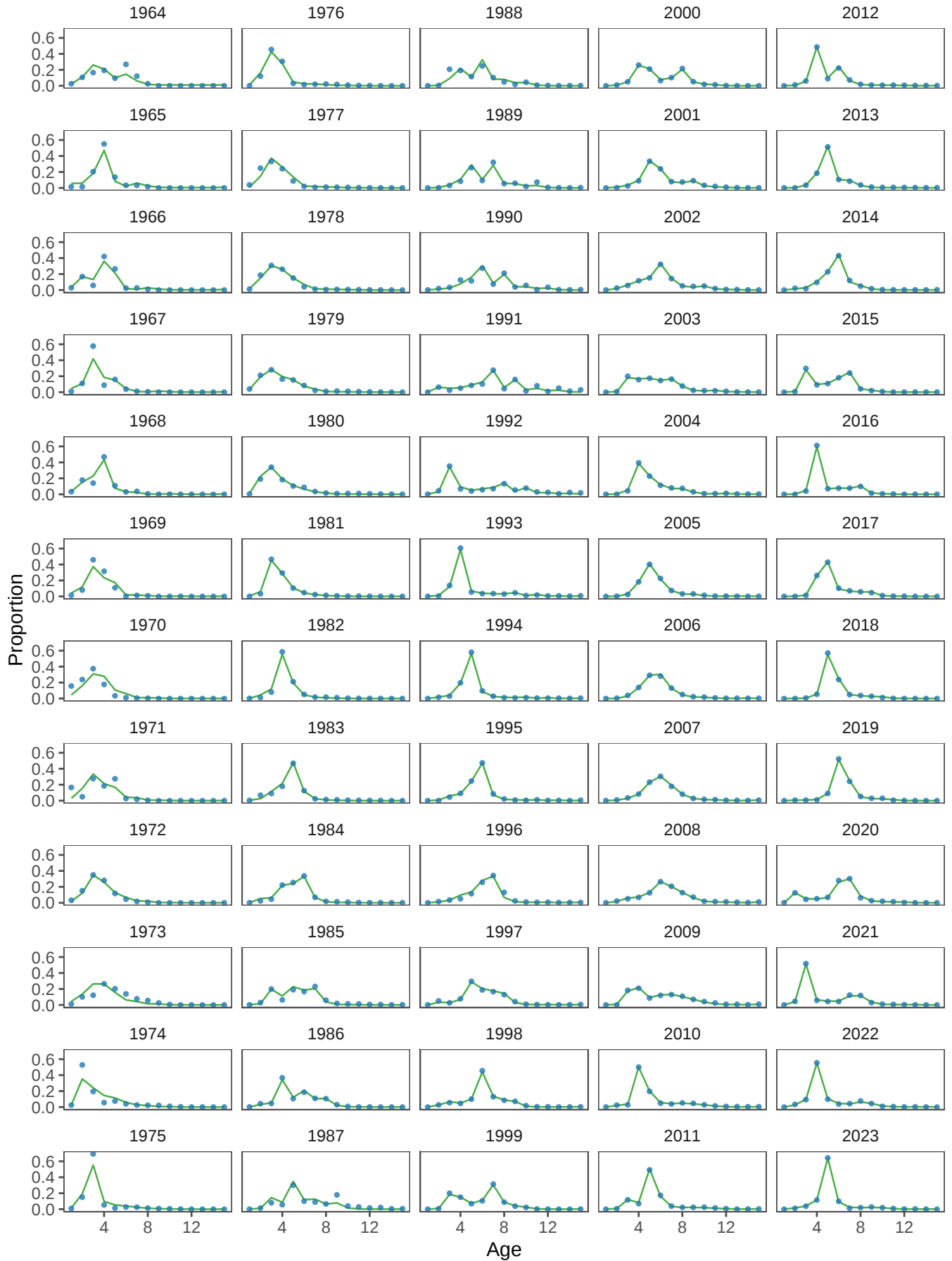


Figure 5.5: Observed and expected fishery age-composition patterns from the base RTMB-ADMB model, faceted by year.

BTS Age Composition Fits

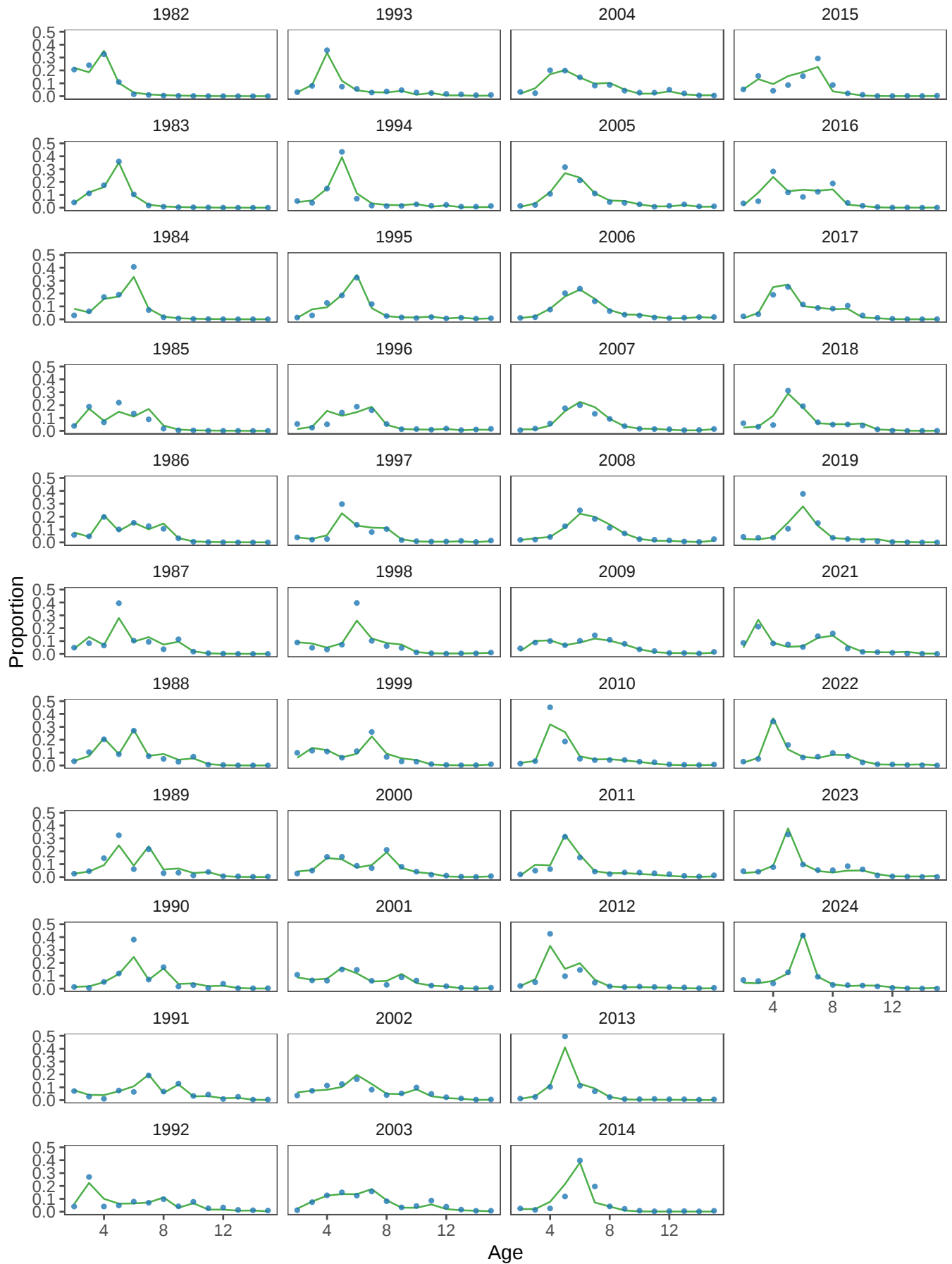


Figure 5.6: Observed and expected BTS age-composition patterns from the base RTMB-ADMB model, faceted by year.

ATS Age Composition Fits

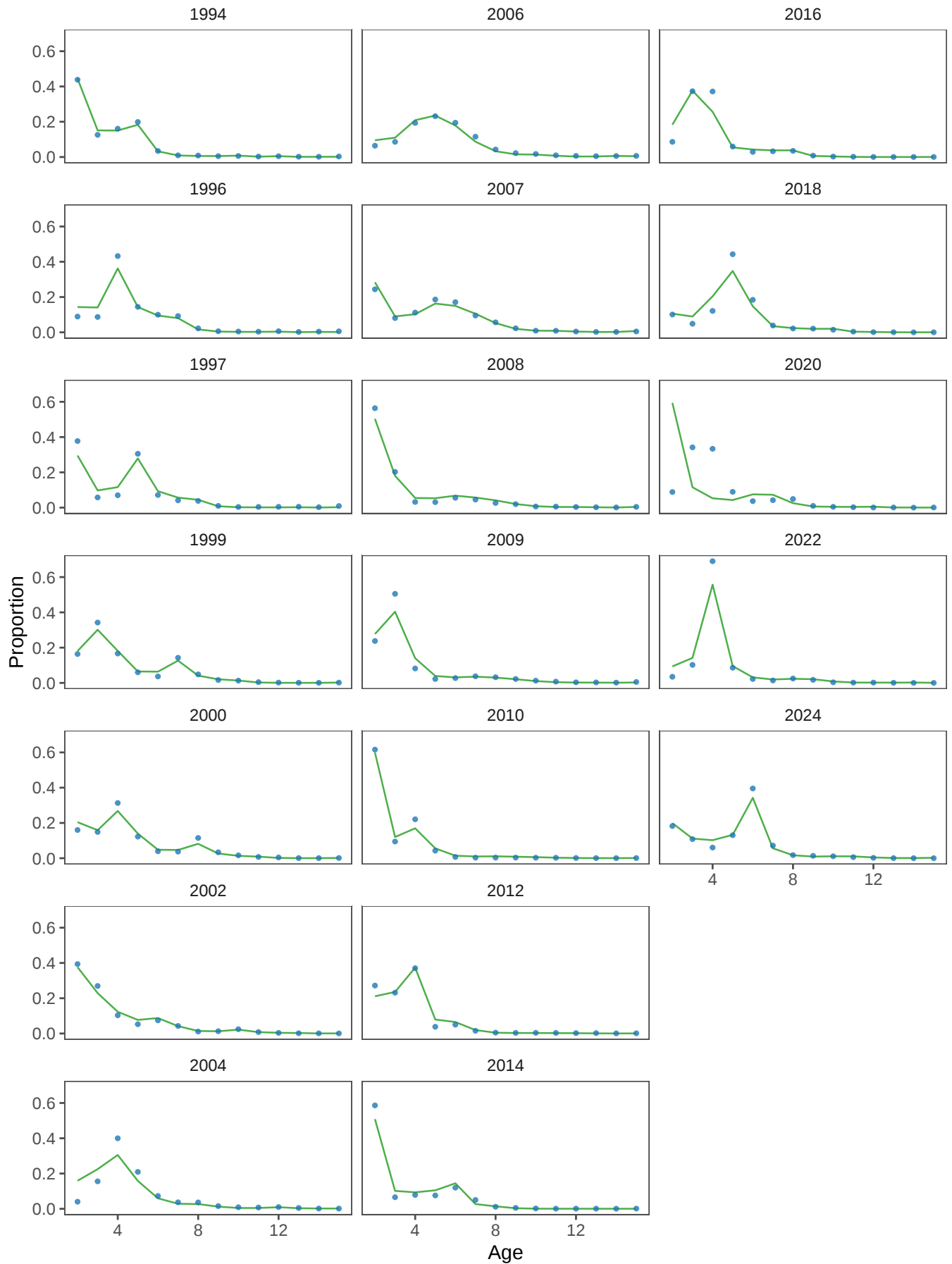


Figure 5.7: Observed and expected ATS age-composition patterns from the base RTMB-ADMB model, faceted by year.

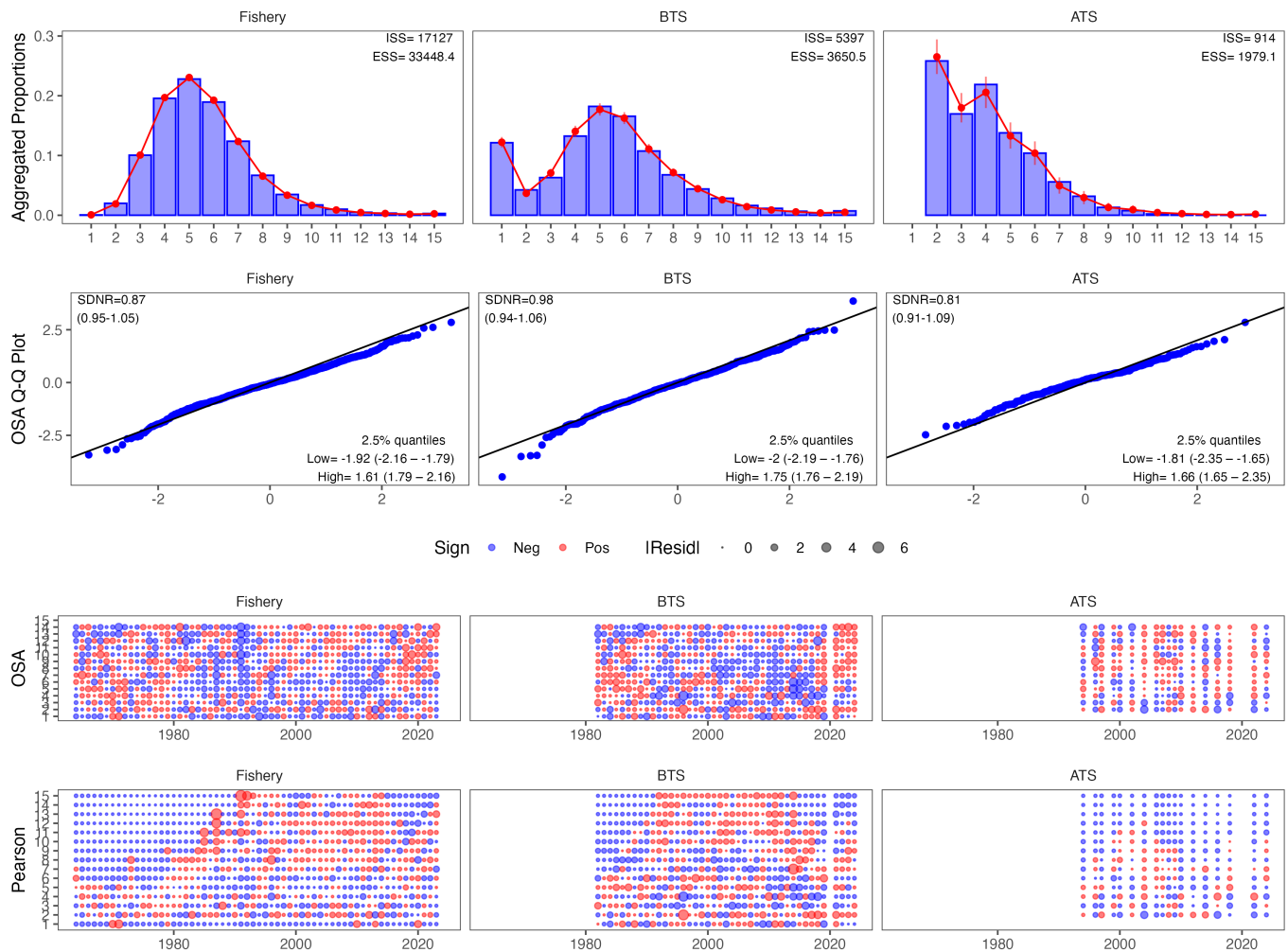


Figure 5.8: Age-composition diagnostics produced with afscOSA for the fishery, bottom trawl survey (BTS), and acoustic-trawl survey (ATS). Top row: observed aggregate proportions (blue bars), expected proportions (red points and line), and 95% conditional intervals for data expected from the fitted model (red vertical lines). ISS and ESS are the aggregate input and effective sample sizes. Second row: OSA residual Q-Q plots with SDNR and 2.5% tail quantiles; parentheses give their expected 95% intervals. Third and fourth rows: OSA and Pearson residual bubbles by year and age, with red positive and blue negative residuals and bubble area increasing with absolute magnitude. Bubble sizes are standardized across fleets; two Pearson residuals greater than 6 were truncated to 6 for display only. Joint interpretation of all panels supports the broader model evaluation.

The aggregate panels show generally close observed and expected patterns, with localized departures that deserve attention. The BTS SDNR lies within its displayed expected interval. Fishery and ATS have narrower OSA residual distributions than standard normal expectations; this can reflect composition weighting, residual dependence, or other model structure and should be considered alongside the aggregate and bubble patterns. The fishery upper tail is also lighter than expected, while the other tail estimates are close to or within their displayed intervals. These results identify focused follow-up work and provide one component of model evaluation.

5.1.6 Selectivity Curves

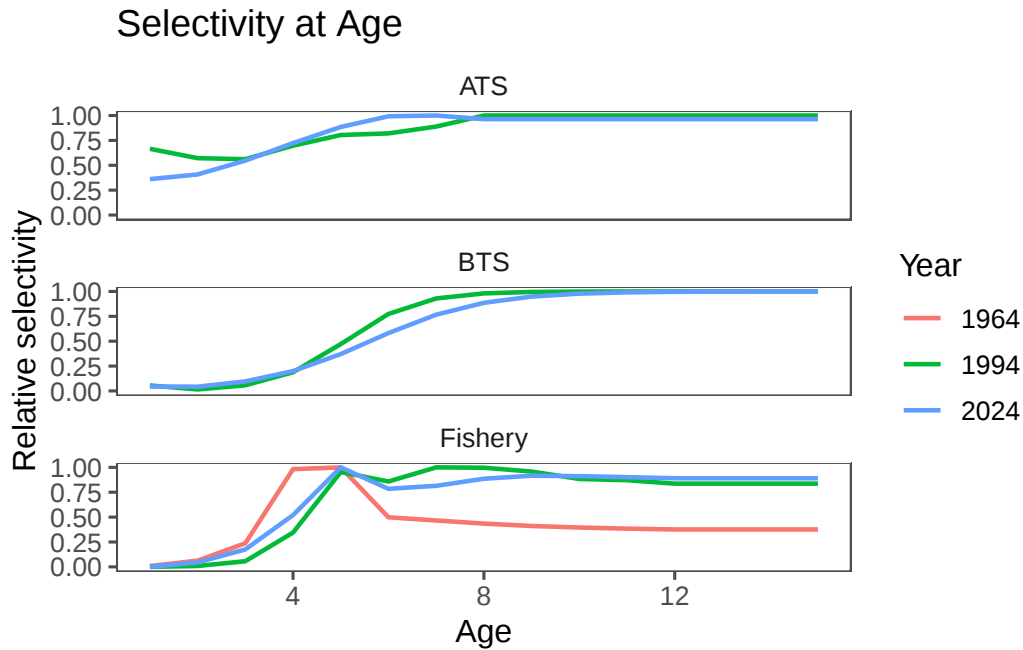


Figure 5.9: Estimated RTMB-ADMB selectivity-at-age curves by fleet in selected years.

The selected-year curves illustrate differences in both shape and temporal change among fleets. Fishery selectivity changes from a pronounced peak near ages 4–5 in the earliest year to a broader pattern that retains relatively high selectivity across older ages in 1994 and 2024. BTS selectivity is low at young ages and increases toward full selection at older ages; the 1994 curve rises more rapidly across the intermediate ages than the 2024 curve. ATS selectivity also increases toward an older-age plateau, with the largest differences between the selected years occurring among the youngest ages. These curves are normalized within fleet and year, so they describe relative age patterns rather than absolute catchability. [Appendix A-2](#) evaluates the consequence of the fitted annual BTS selectivity patterns by holding numbers and weight at age fixed and translating selectivity changes into a relative vulnerable-biomass index.

5.1.7 Selectivity Ridge Plots

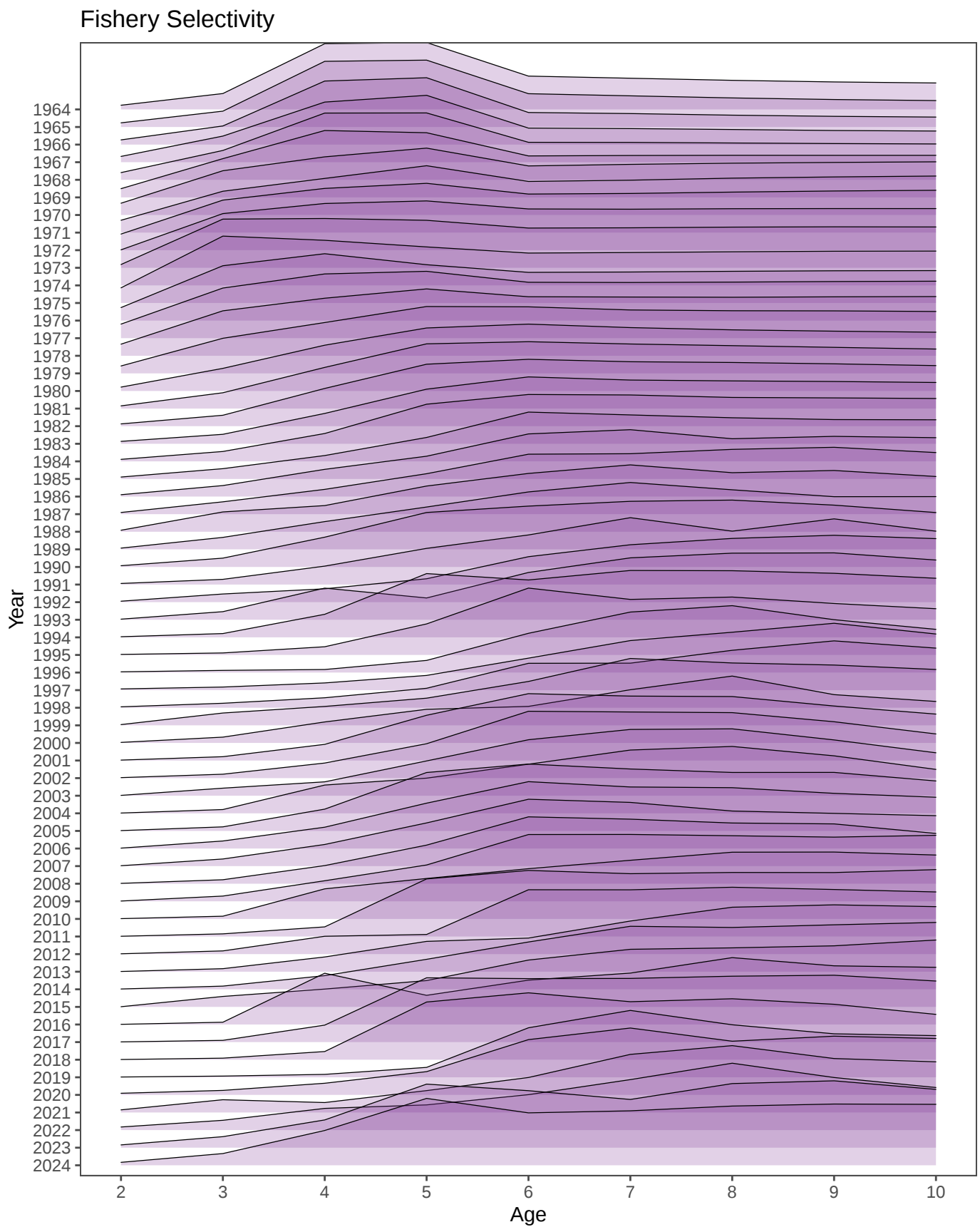


Figure 5.10: Relative fishery selectivity over time from the RTMB-ADMB model. Ridge heights are normalized within year.

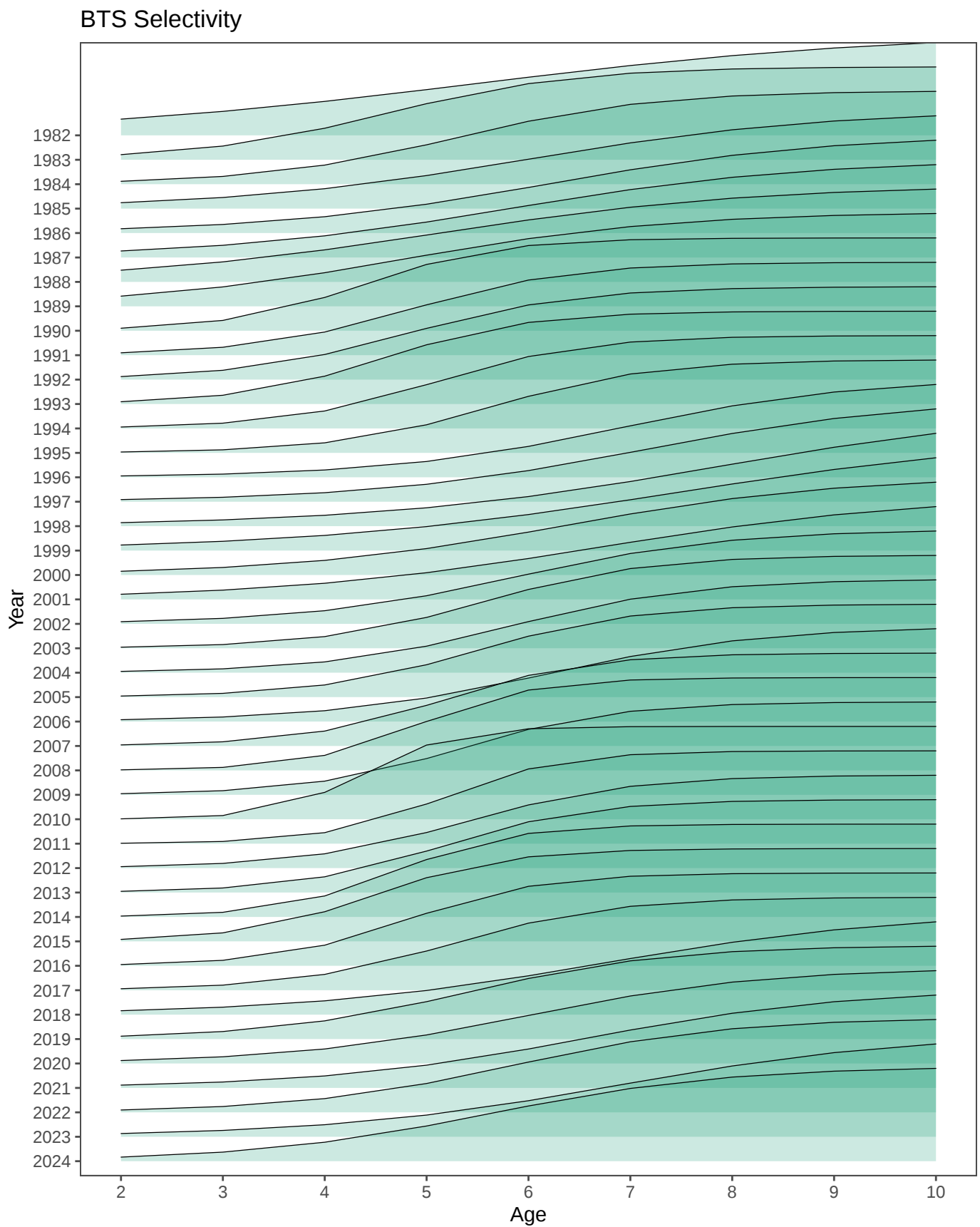


Figure 5.11: Relative BTS selectivity over time from the RTMB-ADMB model. Ridge heights are normalized within year.

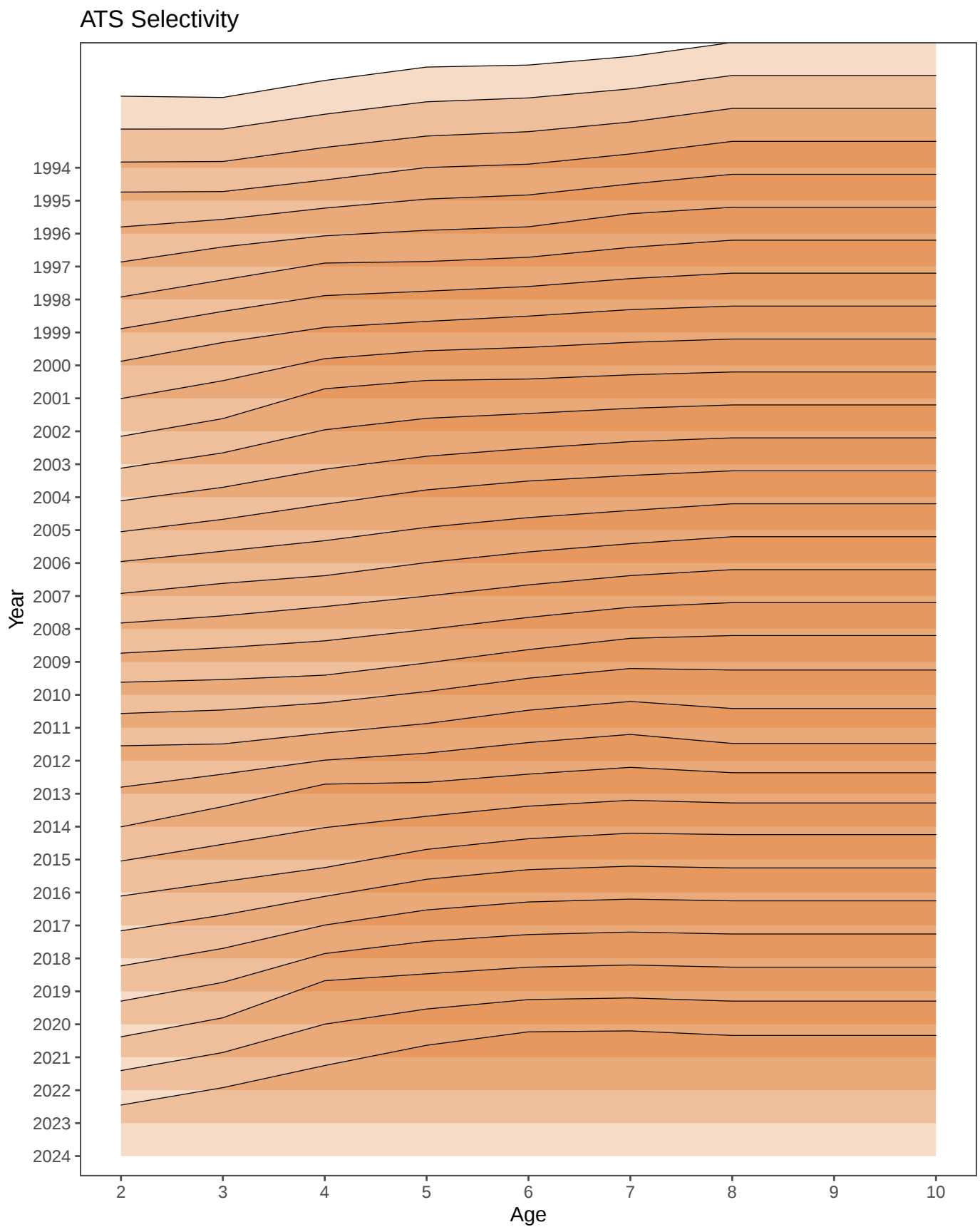


Figure 5.12: Relative ATS selectivity over time from the RTMB-ADMB model. Ridge heights are normalized within year.

6 Projections

The projection analysis is also available as a self-contained attachment: [RTMB EBS pollock: standalone spmR projection attachment](#).

The RTMB estimates were converted to Standard Projection Model inputs and evaluated with **spmR** (Ianelli 2026). The projection configuration matches the ADMB assessment setup, with population quantities supplied by the RTMB model.

6.1 Seven Tier-3 Scenario Results

The projection procedure converted the RTMB fit to standard SPM inputs and evaluated all seven alternatives with the ADMB projection engine in **spmR** (version 0.3.0). The comparison begins with 2027 because catches for 2025 and 2026 are fixed at 1,350 thousand t in every alternative.

6.2 Alternative 2 Fixed-Catch Projection

This additional projection run uses only Alternative 2 and fixes catch at 1,300 thousand t for each year from 2025 through 2032. The projection horizon is set to 2025–2032 so the generated run includes every requested fixed-catch year.

6.3 Projection Figures

The following figures summarize all 1,000 simulations in **spm_detail.csv** for each of the seven Tier 3 alternatives. The lines show simulation medians and the shaded intervals show the central 90% of the simulated outcomes. Figure Figure 6.1 also shows the same 10 reproducibly selected simulation iterations in every alternative: 242, 278, 361, 495, 507, 510, 598, 837, 937, and 989.

The projections use the production ADMB projection engine through **spmR::runSPM()**. This preserves the accepted projection calculations while isolating the effect of using population estimates from the RTMB model.

Table 6.1: Projection input files written for the spmR/SPM workflow.

spmR Projection Input Files

file	role	exists
spm.dat	SPM setup file	TRUE
pm.prj	Species assessment input file generated from RTMB	TRUE
tacpar.dat	SPM TAC parameter file copied from ADMB bridge projection directory	TRUE
spm	SPM executable copied from ADMB bridge projection directory	TRUE

Table 6.2: Key settings in the generated SPM projection setup file.

Generated SPM Setup

item	value
Projection directory	repo/analysis/output/corrected_full_age_bts/spmR_projection
spmR parser	spmR is not installed in the render environment

Table 6.3: Text descriptions of the SPM projection alternatives included in the generated setup file.

SPM Projection Alternatives

Alternative	Name	Description
1	Maximum permissible ABC	Projects catch using the maximum permissible Tier 3 ABC harvest
2	Author-specified ABC	Projects catch using the author-specified adjustment to the Tier 3 ABC
3	Average recent F	Projects catch using the recent average fishing mortality read from
4	Alternative SPR rate	Projects catch using the user-specified Alternative 4 SPR rate. 7
5	No fishing	Projects the stock forward with $F = 0$, so catch is zero after any
6	OFL threshold determination	Projects catch at the OFL harvest rate. This alternative support
7	Status-determination ramp	Applies maximum permissible ABC catch for the first three proj

Table 6.4: Tier-3 projection results for all seven FMP alternatives using inputs generated from the RTMB EBS pollock model. Values are simulation means; catch and biomass quantities are in thousand t. $B/B_{35\%}$ is spawning biomass relative to the Tier-3 $B_{35\%}$ proxy.

Seven Tier-3 Projection Alternatives

Alternative	Scenario	2027						Catch	ABC
		Catch	ABC	OFL	B	F	$B/B_{35\%}$		
1	Maximum permissible ABC	1,620	1,620	1,947	2,553	0.270	1.22	1,507	1,507
2	Author-specified ABC	1,620	1,620	1,947	2,553	0.270	1.22	1,507	1,507
3	Average recent F	1,353	1,353	1,947	2,587	0.220	1.24	1,347	1,347
4	Alternative SPR rate	783	783	1,947	2,656	0.120	1.27	843	843
5	No fishing	0	0	1,947	2,744	0.000	1.31	0	0
6	OFL threshold determination	1,671	1,671	1,671	2,262	0.310	1.08	1,501	1,501
7	Status-determination ramp	1,537	1,840	1,840	2,417	0.270	1.16	1,692	1,692

Table 6.5: Key age-specific schedules used in the generated SPM projection input files.

Projection Age-Specific Schedules

Age	Spawning wt-at-age	Fishery wt-at-age	Maturity	Selectivity
1	0.085	0.025	0.000	0.000
2	0.196	0.186	0.008	0.063
3	0.322	0.401	0.289	0.250
4	0.534	0.667	0.641	0.743
5	0.621	0.663	0.842	1.426
6	0.707	0.720	0.901	1.118
7	0.822	0.791	0.947	1.162
8	0.946	0.905	0.963	1.263
9	1.051	1.009	0.970	1.307
10	1.113	1.061	1.000	1.300
11	1.178	1.138	1.000	1.286
12	1.290	1.257	1.000	1.271
13	1.332	1.267	1.000	1.271
14	1.367	1.290	1.000	1.271
15	1.415	1.368	1.000	1.271

Table 6.6: Candidate ABC projection given assumed future catches. Catch represents the estimate or expectation. $B/B_{35\%}$ is mean biomass divided by $B_{35\%}$, where $B_{35\%}$ is the proxy for B_{MSY} . ABC is the maximum permissible ABC from the SPM Alternative 2 projection.

Candidate ABC Projection Given Assumed Future Catches

Year	Catch	ABC	OFL	Mean B	$B/B_{35\%}$
2025	1,300	2,029	2,433	3,269	156%
2026	1,300	1,726	2,073	2,870	137%
2027	1,300	1,641	1,971	2,631	126%
2028	1,300	1,632	1,951	2,534	121%
2029	1,300	1,606	1,921	2,553	122%
2030	1,300	1,638	1,962	2,612	125%
2031	1,300	1,668	2,003	2,684	128%
2032	1,300	1,697	2,043	2,751	132%

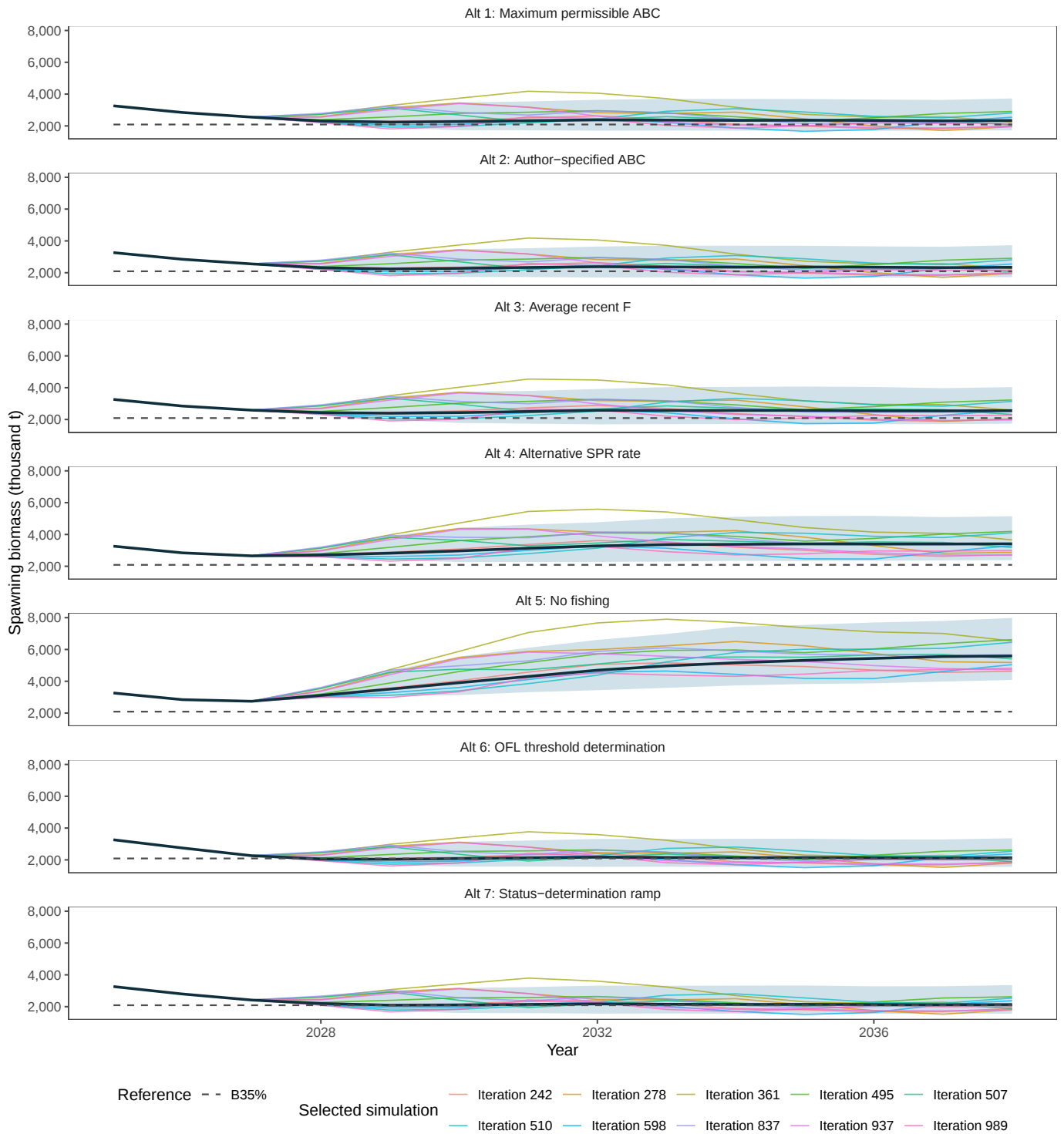


Figure 6.1: Projected spawning biomass under all seven Tier 3 alternatives. The dark line is the simulation median, shaded bands span the 5th to 95th percentiles of the 1,000 SPM simulations, and colored lines show the same 10 randomly selected simulation iterations in every panel. Spawning biomass is in thousand metric tons; the dashed horizontal line marks B35%.

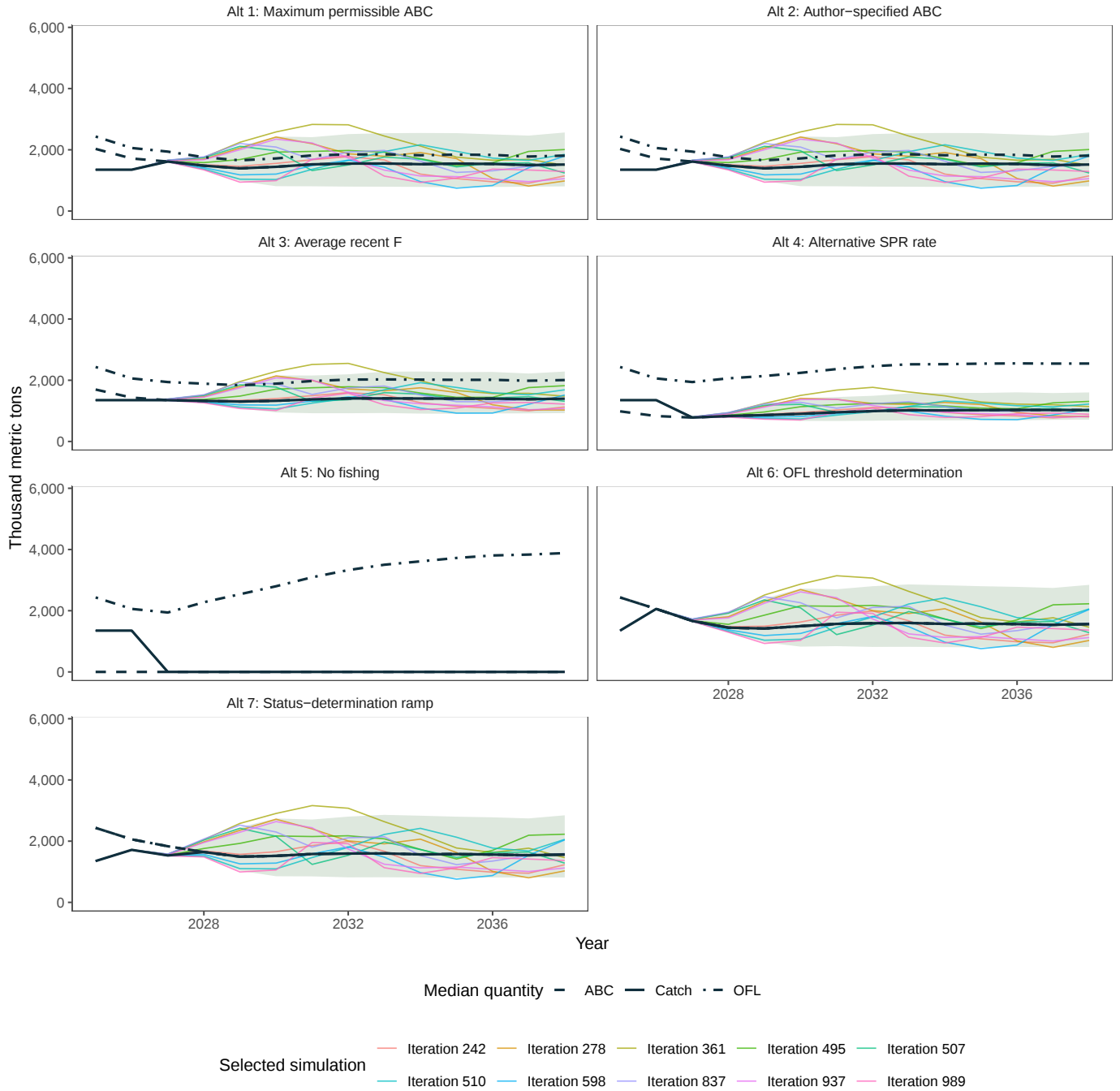


Figure 6.2: Projected catch and calculated ABC and OFL under all seven Tier 3 alternatives. Black lines show simulation medians, with line type distinguishing catch, ABC, and OFL; catch ribbons span the 5th to 95th percentiles of the 1,000 simulations. Colored lines show catch for the same 10 selected simulation iterations used in Figure 15. All quantities are thousand metric tons. ABC and OFL are reference quantities and can differ from realized catch under some alternatives.

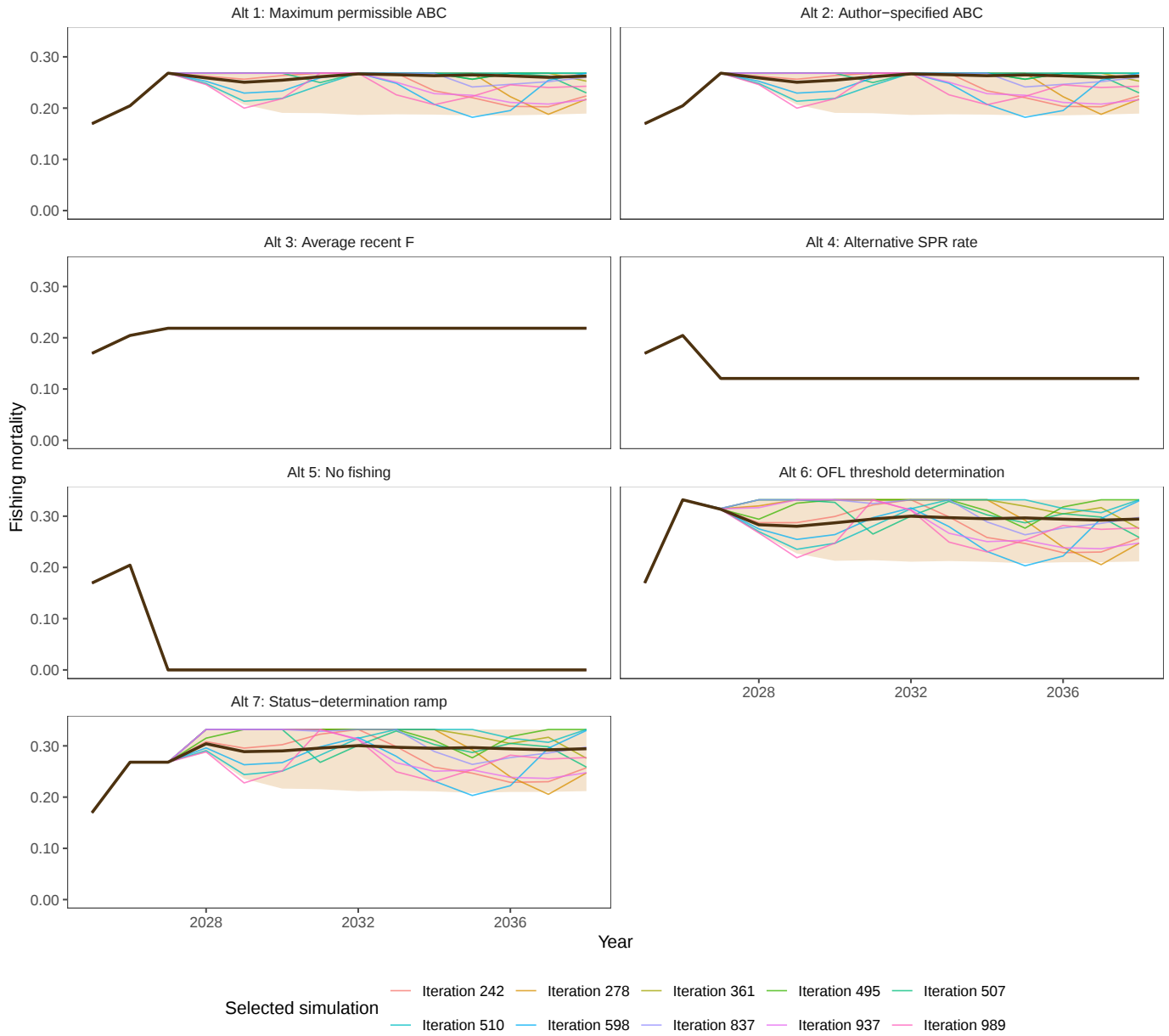


Figure 6.3: Projected fishing mortality under all seven Tier 3 alternatives. The dark line is the simulation median, shaded bands span the 5th to 95th percentiles of the 1,000 simulations, and colored lines show the same 10 selected simulation iterations used in Figures 15 and 16.

Table 6.7: Mean SPM projection results by alternative and year, read from spm_detail.csv when available. The table initially filters to Alternative 1 and includes all projection years; use the column filters to show other alternatives. $B/B_{35\%}$ is mean biomass divided by $B_{35\%}$, where $B_{35\%}$ is the proxy for B_{MSY} .

SPM Projection Means

Alt	Year	B	Catch	ABC	OFL	F	$B/B_{35\%}$
1	2025	3,263	1,350	2,029	2,433	0.170	156%
1	2026	2,844	1,350	1,715	2,059	0.204	136%
1	2027	2,553	1,620	1,620	1,947	0.268	122%
1	2028	2,360	1,507	1,507	1,795	0.259	113%
1	2029	2,348	1,458	1,458	1,744	0.246	112%
1	2030	2,395	1,504	1,504	1,801	0.244	115%
1	2031	2,439	1,538	1,538	1,843	0.245	117%
1	2032	2,478	1,563	1,563	1,874	0.246	119%
1	2033	2,498	1,581	1,581	1,894	0.246	120%
1	2034	2,489	1,572	1,572	1,883	0.246	119%
1	2035	2,484	1,564	1,564	1,874	0.246	119%
1	2036	2,476	1,562	1,562	1,871	0.246	118%
1	2037	2,472	1,554	1,554	1,861	0.246	118%
1	2038	2,484	1,561	1,561	1,870	0.245	119%

7 Diagnostics

7.1 Retrospective Peels

The retrospective procedure included peel 0 (the full model terminating in 2024) and nine peels terminating in 2023 through 2015. Each peel retained the full model's stream-specific observation lag. Thus, because fishery age compositions ended in 2023 in the full model, they ended in 2022 in the first peel. Terminal-year fishery, BTS, and ATS selectivity was fixed at the corresponding penultimate-year value within each peel. Annual inputs and parameter vectors were truncated to the applicable terminal year, and each fit was initialized from the preceding fitted peel. The established 2020 gap in the BTS biomass index was retained.

The observations underlying Table 7.1 are available as a [machine-readable CSV file](#).

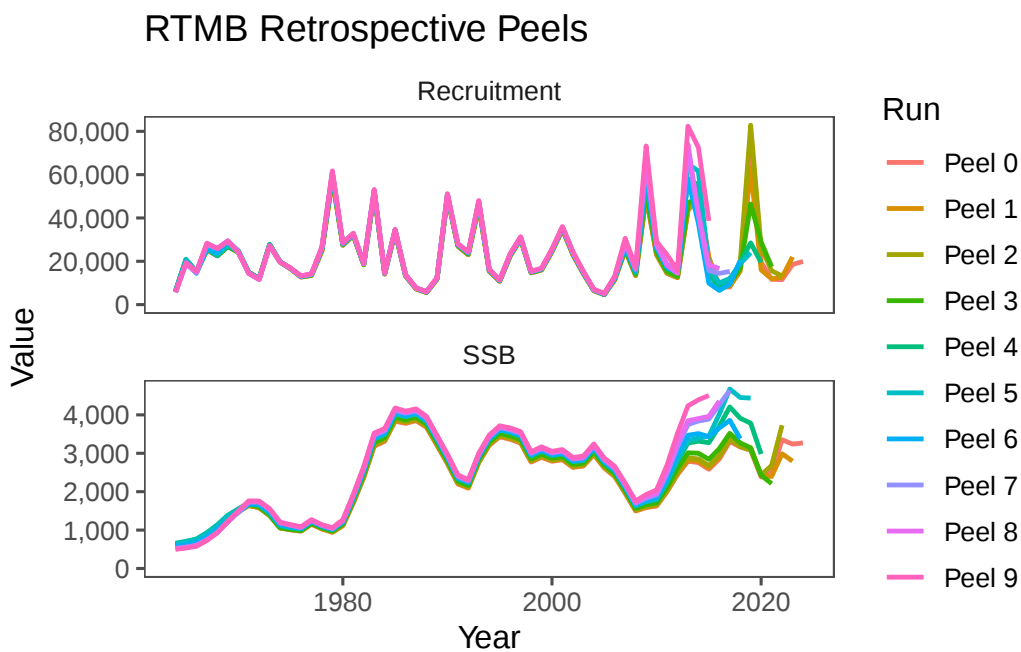


Figure 7.1: RTMB spawning-biomass and recruitment trajectories for the full model and nine retrospective peels. Each trajectory ends in its peel-specific terminal year.

All 9 peels completed and produced trajectory estimates. 9 of the 10 fits ended with convergence code 0. The largest maximum gradient across all fits was 0.0008. Mohn's rho was 0.255 for spawning biomass and 0.342 for recruitment. Positive values indicate that truncated assessments estimate these quantities above their corresponding full-model estimates. The retrospective pattern forms an important component of the stability and uncertainty evaluation.

7.2 Additional Bridge Diagnostics and Only-BTS Sensitivity

The **Only BTS** curve is a separate RTMB sensitivity from the same base configuration with the ATS biomass index, ATS age-1 index, and AVO index likelihood components excluded. BTS, CPUE, catch, composition, recruitment, selectivity, and weight-at-age components remain active. This sensitivity illustrates the influence of the excluded indices and is not an alternative assessment model.

Table 7.1: Maximum observation year retained for each data stream in the full model and nine retrospective peels. Stream-specific lags remain constant across peels.

Retrospective Data-Availability Audit

peel	terminal_year	data_stream	maximum_year
0	2024	ATS	2024
0	2024	AVO	2024
0	2024	BTS	2024
0	2024	CPUE	1976
0	2024	Fishery age composition	2023
1	2023	ATS	2022
1	2023	AVO	2023
1	2023	BTS	2023
1	2023	CPUE	1975
1	2023	Fishery age composition	2022
2	2022	ATS	2022
2	2022	AVO	2022
2	2022	BTS	2022
2	2022	CPUE	1974
2	2022	Fishery age composition	2021
3	2021	ATS	2020
3	2021	AVO	2021
3	2021	BTS	2021
3	2021	CPUE	1973
3	2021	Fishery age composition	2020
4	2020	ATS	2020
4	2020	AVO	2019
4	2020	BTS	2019
4	2020	CPUE	1972
4	2020	Fishery age composition	2019
5	2019	ATS	2018
5	2019	AVO	2019
5	2019	BTS	2019
5	2019	CPUE	1971
5	2019	Fishery age composition	2018
6	2018	ATS	2018
6	2018	AVO	2018
6	2018	BTS	2018
6	2018	CPUE	1970
6	2018	Fishery age composition	2017
7	2017	ATS	2016
7	2017	AVO	2017
7	2017	BTS	2017
7	2017	CPUE	1969
7	2017	Fishery age composition	2016
8	2016	ATS	2016
8	2016	AVO	2016
8	2016	BTS	2016
8	2016	CPUE	1968
8	2016	Fishery age composition	2015
9	2015	ATS	2014
9	2015	AVO	2015
9	2015	BTS	2015
9	2015	CPUE	1967
9	2015	Fishery age composition	2014

Table 7.2: Maximum absolute difference between terminal-year and penultimate-year selectivity by fleet for each retrospective peel. Values at numerical zero verify the terminal-year equality constraint.

Retrospective Terminal-Selectivity Audit

peel	terminal_year	fleet	maximum_absolute_difference
1	2023	ATS	0.0000000000
1	2023	BTS	0.0000000000
1	2023	Fishery	0.0000000000
2	2022	ATS	0.0000000000
2	2022	BTS	0.0000000000
2	2022	Fishery	0.0000000000
3	2021	ATS	0.0000000000
3	2021	BTS	0.0000000000
3	2021	Fishery	0.0000000000
4	2020	ATS	0.0000000000
4	2020	BTS	0.0000000000
4	2020	Fishery	0.0000000000
5	2019	ATS	0.0000000000
5	2019	BTS	0.0000000000
5	2019	Fishery	0.0000000000
6	2018	ATS	0.0000000000
6	2018	BTS	0.0000000000
6	2018	Fishery	0.0000000000
7	2017	ATS	0.0000000000
7	2017	BTS	0.0000000000
7	2017	Fishery	0.0000000000
8	2016	ATS	0.0000000000
8	2016	BTS	0.0000000000
8	2016	Fishery	0.0000000000
9	2015	ATS	0.0000000000
9	2015	BTS	0.0000000000
9	2015	Fishery	0.0000000000

Table 7.3: RTMB retrospective run status for the full model (peel 0) and nine terminal-year peels. A convergence code of 0 indicates normal optimizer completion. Peels with an initial maximum gradient above 0.001 received one tighter restart; optimization passes records whether that restart was used.

RTMB Retrospective Peel Status

peel	terminal_year	status	optimization_passes	objective	max_gradient	error
0	2024	converged	1	7,075.220	0.000	
1	2023	converged	2	6,214.942	0.000	
2	2022	converged	2	4,512.666	0.000	
3	2021	converged	1	2,644.427	0.001	
4	2020	converged	1	1,078.294	0.001	
5	2019	converged	1	42.781	0.000	
6	2018	converged	1	-1,140.010	0.001	
7	2017	optimizer code 1	2	-2,622.080	0.000	
8	2016	converged	1	-4,251.361	0.001	
9	2015	converged	2	-6,396.163	0.000	

Table 7.4: Mohn's rho for spawning biomass and recruitment across nine retrospective peels. For each peel, the terminal-year estimate is compared with the estimate for the same year from the full model; rho is the mean relative difference. Positive values indicate that the truncated assessments estimate the quantity above the corresponding full-model estimate.

Nine-Peel Retrospective Summary

Quantity	Mohn's rho	Peels
Spawning biomass	0.255	9
Recruitment	0.342	9

Table 7.5: Status for the Only BTS RTMB sensitivity model used in the bridge-comparison plot.

Only BTS Sensitivity Run

item	value
Only BTS output	repo/analysis/output/corrected_full_age_bts/only_bts.rds
Excluded likelihoods	ATS index, ATS age-1 index, AVO index
Convergence	0
Objective	7042.290
Maximum gradient	0.000531

Table 7.6: Maximum absolute percent difference between the RTMB-ADMB base model and the ADMB bridge report for shared quantities.

RTMB vs ADMB Bridge Comparison

variable	equal	length	max_abs_diff	max_abs_pct_diff	cor
N	TRUE	915	0.049762	0.000487	1.000000
phat_fsh	TRUE	900	0.000000	0.000483	1.000000
sel_fsh	FALSE	915	0.000005	0.000473	1.000000
phat_ats	TRUE	285	0.004888	0.000468	1.000000
obs_catch	FALSE	61	0.005000	0.000458	1.000000
F	TRUE	915	0.000000	0.000448	1.000000
phat_bts	FALSE	630	0.000000	0.000444	1.000000
sel_ats	FALSE	465	0.000005	0.000443	1.000000
cpue_like	FALSE	1	0.000004	0.000402	NA
pred_catch	FALSE	61	0.004985	0.000390	1.000000
sel_bts	TRUE	645	0.000000	0.000387	1.000000
rec_like	FALSE	7	0.000039	0.000383	1.000000
pred_avo	TRUE	18	0.000005	0.000353	1.000000
SSB	FALSE	61	0.004832	0.000309	1.000000
eb_bts	TRUE	42	0.027785	0.000256	1.000000
age_like	FALSE	3	0.000311	0.000197	1.000000
phizero	FALSE	1	0.000000	0.000189	NA
sel_like_dev	FALSE	3	0.000215	0.000175	1.000000
avgsel_like	FALSE	1	0.000000	0.000170	NA
wt_nll	TRUE	4	0.004117	0.000157	1.000000
Z	TRUE	915	0.000000	0.000152	1.000000
Priors	FALSE	4	0.000029	0.000142	1.000000
sam_fsh	TRUE	60	0.000499	0.000134	1.000000
eb_ats	TRUE	19	0.004853	0.000129	1.000000
bts_like	FALSE	1	0.000041	0.000127	NA
pred_cpue	TRUE	12	0.004525	0.000123	1.000000
ats_age1_like	FALSE	1	0.000014	0.000122	NA
S	TRUE	915	0.000000	0.000120	1.000000
sel_like	TRUE	3	0.000014	0.000094	1.000000
wt_like	TRUE	1	0.004805	0.000076	NA
Bzero	TRUE	1	0.003717	0.000061	NA
age_like_offset	TRUE	3	0.006545	0.000058	1.000000
ats_like	TRUE	1	0.000002	0.000025	NA
cat_like	TRUE	1	0.000000	0.000016	NA
Fpen_like	TRUE	1	0.000001	0.000011	NA
tot_like	TRUE	1	0.000379	0.000005	NA
avo_like	TRUE	1	0.000000	0.000004	NA
steepness	TRUE	1	0.000000	0.000003	NA
M	TRUE	915	0.000000	0.000000	1.000000
sam_bts	TRUE	42	0.000000	0.000000	1.000000
sam_ats	TRUE	19	0.000000	0.000000	1.000000
C	NA	NA	NA	NA	NA

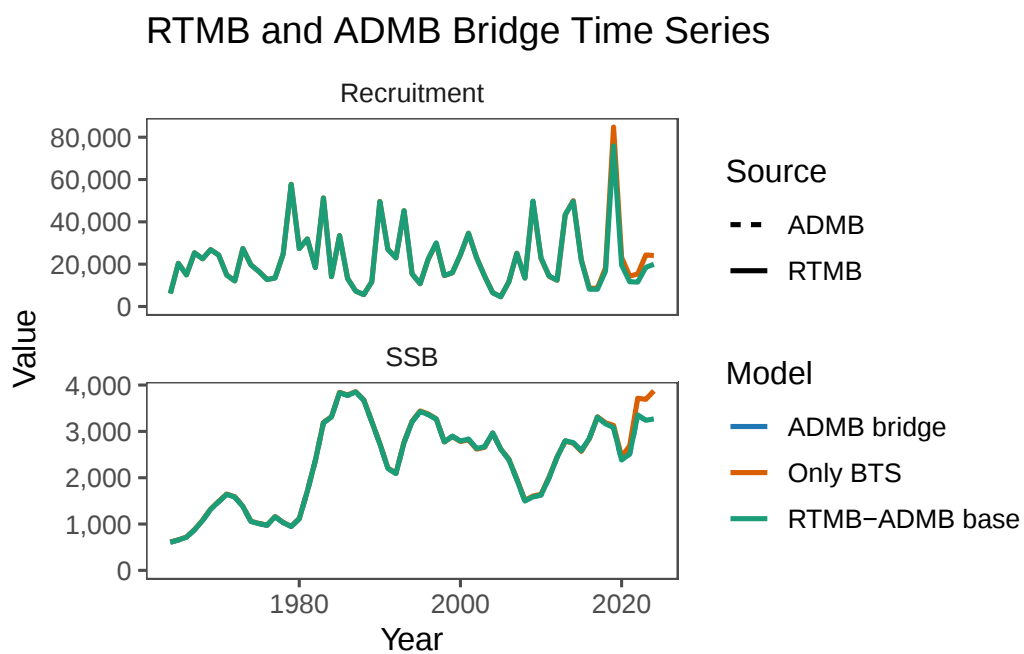


Figure 7.2: Shared RTMB and ADMB bridge time series for spawning biomass and recruitment, including the Only BTS RTMB sensitivity model with ATS and AVO survey index likelihoods excluded.

8 Summary

The RTMB implementation reproduces the corrected full-age BTS ADMB bridge at the shared ADMB maximum-likelihood estimates. Observed and predicted BTS compositions each span ages 1–15 and sum to one, nominal integer sample sizes enter the multinomial likelihood, and the BTS total-numbers quantity used for composition scaling retains its ages 2–15 definition. The fitted BTS survey index is a biomass index. Comparison with the historical configuration shows the effect of correcting the BTS likelihood treatment.

The OSA diagnostics, Only-BTS sensitivity, nine retrospective peels, and SPM projections use the same corrected base specification. The retrospective procedure preserves stream-specific data lags and fixes terminal-year selectivity at the penultimate-year curve. Positive Mohn’s rho values identify a stability concern requiring continued evaluation. Candidate refinements require simulation testing and review before operational use. Current management advice remains based on the accepted ADMB assessment model; the hierarchical Form-2 SparseNUTS results characterize a separate candidate selectivity formulation.

9 Reproducibility

Table 9.1: Files and commands supporting reproducibility of the RTMB-ADMB results.

Reproducibility Checklist

item	value
Working directory	repo
Complete corrected rebuild command	Rscript R/rebuild_corrected_full_age_bts_products.R
Render command	quarto render reporting/ebs_pollock_rtmb_ebswp_assessment.qmd
Default SparseNUTS command	quarto render -P run_sparsenuts:true
RTMB report object	repo/analysis/output/corrected_full_age_bts/rtmb_base.rds
Default SparseNUTS output	repo/analysis/output/sparsenuts/fishery_sel_forms/rtmb_ebswp_sp
ADMB bridge run	repo/analysis/output/corrected_full_age_bts/admb_root/runs/full
RTMB source	repo

10 Supporting Tables

Table 10.1: Key terminal-year values from the saved base RTMB-ADMB model.

Terminal-Year RTMB-ADMB Estimates

metric	year	value
Total biomass	2024	12,278.783
Spawning biomass	2024	3,269.154
Recruitment	2024	19,925.191
Mean F	2024	0.162
Total F	2024	2.437

Table 10.2: Index catchability and stock-recruitment scalars reported by the RTMB-ADMB model.

Reported Scalar Quantities

quantity	value
Bzero	6,116.336283
phizero	0.252161
steepness	0.618428

Table 10.3: Initial and terminal estimated numbers-at-age from the base RTMB-ADMB model.

Numbers at Age

year	age	numbers
1964	1	6,093.775
1964	2	3,036.497
1964	3	1,837.634
1964	4	387.752
1964	5	180.120
1964	6	503.029
1964	7	228.638
1964	8	71.914
1964	9	45.122
1964	10	45.575
1964	11	45.870
1964	12	46.048
1964	13	45.959
1964	14	45.885
1964	15	45.810
2024	1	19,925.191
2024	2	7,521.843
2024	3	2,957.476
2024	4	2,134.256
2024	5	2,391.492
2024	6	5,374.219
2024	7	878.685
2024	8	275.063
2024	9	152.880
2024	10	180.893
2024	11	171.256
2024	12	71.879
2024	13	18.389
2024	14	14.818
2024	15	38.813

Table 10.4: Estimated terminal-year fishery F-at-age from the base RTMB-ADMB model.

Terminal-Year Fishery F at Age

year	age	f_at_age
2024	1	0.000034
2024	2	0.010239
2024	3	0.040608
2024	4	0.120608
2024	5	0.231670
2024	6	0.181642
2024	7	0.188690
2024	8	0.205179
2024	9	0.212236
2024	10	0.211192
2024	11	0.208872
2024	12	0.206389
2024	13	0.206389
2024	14	0.206389
2024	15	0.206389

References

- Ianelli, Jim. 2026. *spmR: Standard Projection Model*. <http://afsc-assessments.github.io/spmR/>.
- Thorson, James T., Sean C. Anderson, Pamela Goddard, and Christopher N. Rooper. 2025. “tinyVAST: R Package with an Expressive Interface to Specify Lagged and Simultaneous Effects in Multivariate Spatio-Temporal Models.” *Global Ecology and Biogeography* 34: e70035. <https://doi.org/10.1111/geb.70035>.
- Thorson, James T., and Melissa A. Haltuch. 2019. “Spatio-Temporal Analysis of Compositional Data: Increased Precision and Improved Workflow Using Model-Based Inputs to Stock Assessment.” *Canadian Journal of Fisheries and Aquatic Sciences* 76 (3): 401–14. <https://doi.org/10.1139/cjfas-2018-0015>.

Appendices

A-1 Data issues and revisions since the 2024 assessment

This appendix documents two distinct age-data issues considered after the 2024 assessment: the method used to assign ages to individual otoliths and the spatio-temporal method used to expand BTS age samples into annual proportions at age. The first concerns traditional microscope ages (TMA) versus ages predicted by Fourier-transform near-infrared spectroscopy (FT-NIRS). The second concerns replacement of the prior BTS age-composition estimator with a tinyVAST implementation. These changes occur at different stages of the data workflow and should be evaluated separately.

FTNIRS age-data

TMA assigns age by preparing an otolith and visually counting annual growth zones under a microscope. FT-NIRS instead measures the wavelengths and amount of near-infrared light absorbed by an otolith and predicts age from its spectral and chemical signal using a calibration model. FT-NIRS can process otoliths substantially faster, but its predicted ages are methodologically different from direct microscope readings ([NOAA Fisheries age-method overview](#)).

The 2025 CIE discussion paper compared the two methods using pollock data. For the same design-based BTS abundance-at-age inputs, TMA estimates showed a high degree of cohort consistency, whereas FT-NIRS estimates showed lower cohort consistency; the assessment authors described the consequence of that difference as unresolved. The comparison also identified differences between TMA- and FT-NIRS-based proportions at age for the fishery, BTS, and ATS. Model tests therefore treated FT-NIRS ages as a separate data source and considered both global and fleet-specific FT-NIRS age-error matrices. See the official [FT-NIRS data consistency comparisons](#) for the cohort plots, composition comparisons, data coverage, and alternative age-error treatments.

The FT-NIRS issue concerns age assignment and associated ageing error. The BTS bridge below concerns the subsequent expansion of age observations across space and time. Consequently, the controlled BTS bridge should not be interpreted as a test of TMA against FT-NIRS.

Impact of revised BTS age-data

This appendix isolates the effect of replacing the original bottom-trawl survey (BTS) proportions at age in `BTSProp.csv` with the revised proportions in `tinyVAST_props_new.csv`. Both ADMB runs use the complete 2025 input set and the same model specification, executable, starting parameter file, and tinyVAST 2025 BTS age observation. The sensitivity restores the original 1982-2024 BTS proportions while holding the 2025 tinyVAST row constant. The comparison therefore addresses the historical estimator change.

The 2024 assessment used the previous spatio-temporal expansion of BTS age samples. The revised series uses an improved implementation in `tinyVAST`, a multivariate spatio-temporal generalized linear mixed-model framework that can model age groups jointly, share information across locations and years, and area-expand predictions to annual abundance and proportions at age ([Thorson and Haltuch 2019](#); [Thorson et al. 2025](#)). The [tinyVAST age-composition expansion example](#) documents this workflow for EBS pollock age data. This methodological update changes the estimated BTS proportions at age supplied to the assessment; the controlled runs below quantify the resulting assessment-model effect while holding the other inputs and model configuration fixed.

The source-data comparison uses the `both` region from `BTSProp.csv` as the original series and `tinyVAST_props_new.csv` as the revised series (Figure 10.1). Across the 42 matched survey years, relative changes range from -11.9% to +54.8%; the largest absolute change is 1.58 percentage points. The calculation uses the original proportion as the denominator and describes the input revision rather than its influence on model results. The revised 2025 row is excluded because the original file ends in 2024.

Both runs reached maximum absolute gradients below 0.001. The likelihood components in Table 10.6 document the fits and support a structured contrast between scenarios with different observed BTS age values.

The revision changes terminal spawning biomass by -0.415%. The largest spawning-biomass difference is 0.881% in 1985. Terminal age-1 recruitment changes by -2.015%, which is the largest recruitment difference in the series. Terminal predicted catch changes by +0.016%.

Table 10.5: Controlled input contrast for the revised BTS age-data bridge. The 2025 BTS age observation and all non-BTS-age inputs are identical between runs.

BTS Age-Data Contrast

metric	value
Historical BTS years replaced	42
First replaced year	1982
Last replaced year	2024
2025 BTS age row held constant	Yes
Maximum absolute proportion-at-age difference	0.015778407

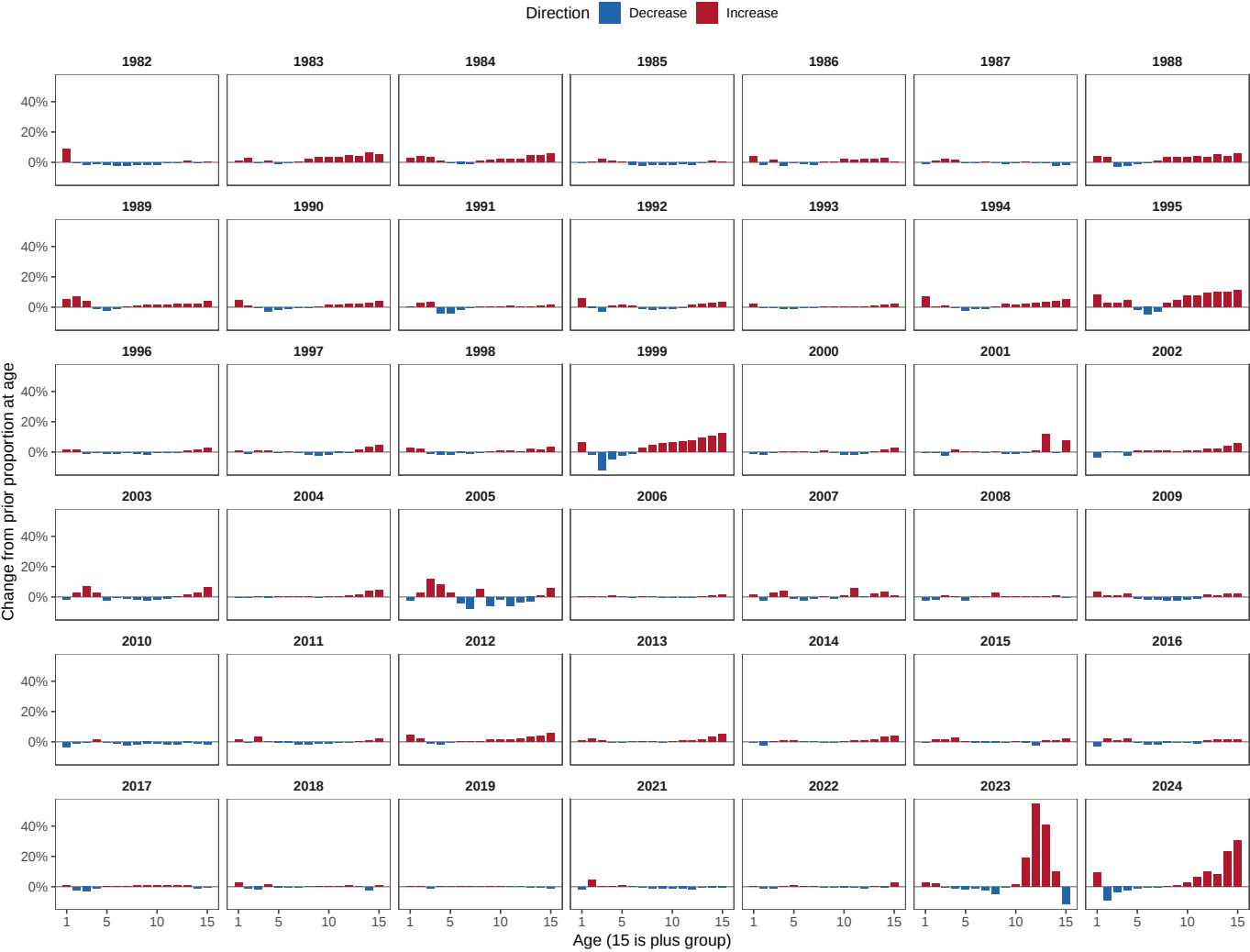


Figure 10.1: Percent change in BTS proportions at age from the original BTSProp.csv series to the revised tinyVAST_props_new.csv series for each matched historical survey year. Positive bars indicate a larger tinyVAST proportion and negative bars indicate a smaller tinyVAST proportion. Age 15 is the plus group; no BTS survey occurred in 2020.

Table 10.6: ADMB fit diagnostics for the matched 2025 model with tinyVAST BTS proportions and with original BTSProp proportions for 1982-2024. Negative-log-likelihood values diagnose each data version; cross-data model selection requires a common observation set and likelihood definition.

BTS Age-Data Bridge Diagnostics

Data version	Total NLL	BTS index NLL	BTS age NLL	Maximum gradient
Current tinyVAST BTS ages	7,062.470	32.673	211.608	4.97×10^{-4}
Prior BTSProp ages for 1982-2024	7,061.360	32.856	210.849	2.07×10^{-4}

Table 10.7: Relative effects of replacing the original historical BTS proportions with tinyVAST proportions. Percent differences are tinyVAST minus original, divided by the absolute original estimate.

Effects of tinyVAST Historical BTS Proportions

Quantity	Terminal year	Terminal difference (%)	Maximum absolute difference (%)	Year of ma
Predicted catch	2025	0.016	0.050	
Age-1 recruitment	2025	-2.015	3.851	
Spawning biomass	2025	-0.415	0.881	

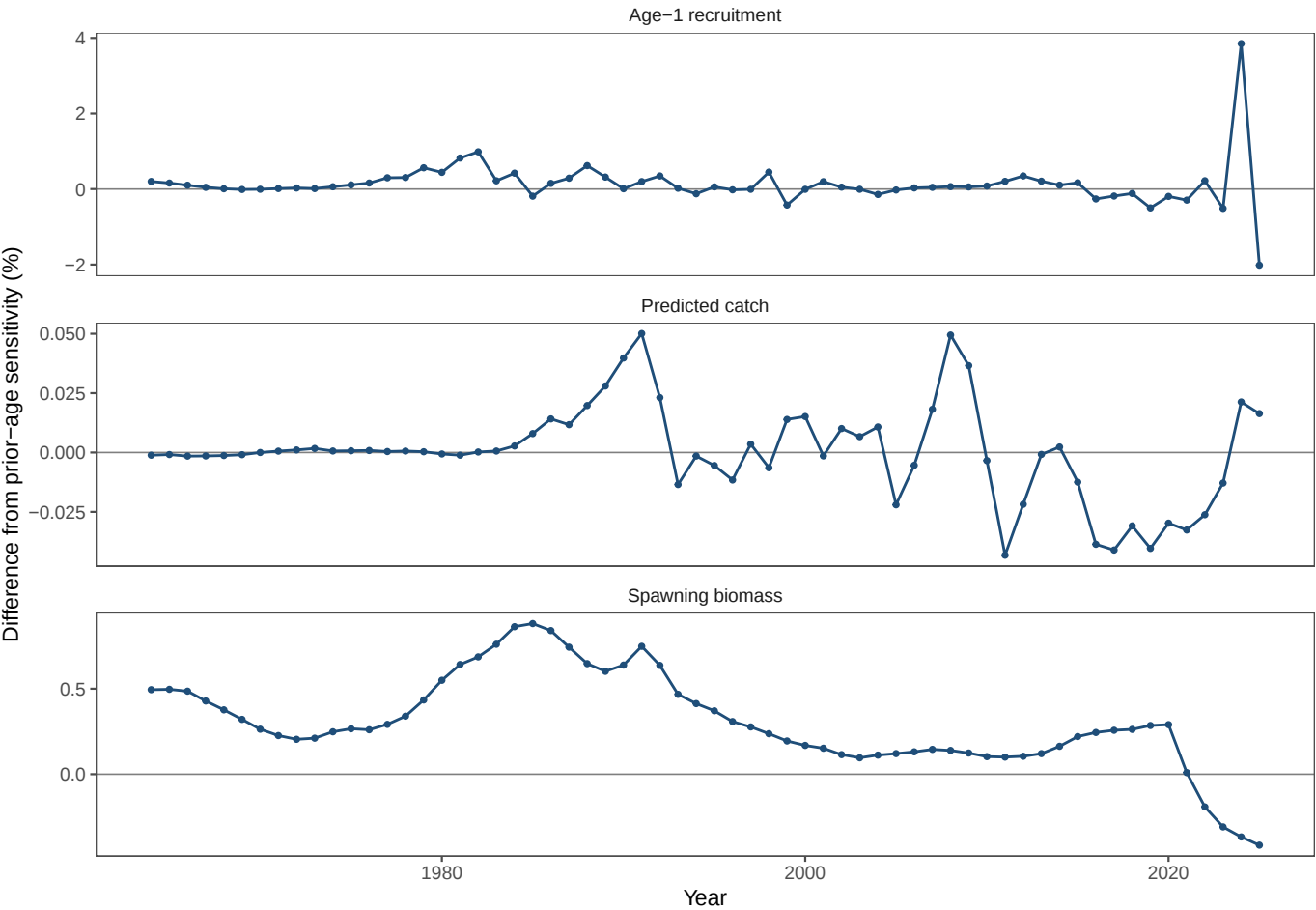


Figure 10.2: Percent differences in spawning biomass, age-1 recruitment, and predicted catch between the 2025 model using tinyVAST BTS proportions and the sensitivity using original BTSProp proportions for 1982-2024. The horizontal line marks no difference.

Table 10.8: RTMB convergence diagnostics for the full tinyVAST model and nine retrospective peels. Optimizer code 0 indicates normal completion; maximum absolute gradient is the primary convergence criterion.

tinyVAST Nine-peel Retrospective Diagnostics

Peel	Terminal year	Optimizer code	Objective	Maximum gradient	Optimization passes
0	2024	0	6,295.649	8.07×10^{-5}	2
1	2023	0	6,017.816	1.68×10^{-4}	2
2	2022	1	4,746.727	8.75×10^{-5}	2
3	2021	0	3,208.292	7.17×10^{-4}	1
4	2020	1	1,377.361	1.46×10^{-4}	2
5	2019	0	254.949	6.73×10^{-4}	1
6	2018	0	-1,058.540	9.22×10^{-4}	1
7	2017	0	-2,439.845	9.05×10^{-4}	1
8	2016	1	-4,073.266	2.12×10^{-4}	2
9	2015	0	-5,707.352	2.65×10^{-4}	2

Table 10.9: Mohn’s rho for spawning biomass and age-1 recruitment across nine RTMB retrospective peels using the tinyVAST BTS proportions.

tinyVAST Retrospective Mohn’s Rho

Quantity	Mohn’s rho	Peels
Spawning biomass	0.283	9
Age-1 recruitment	0.311	9

Nine-peel tinyVAST retrospective

The RTMB retrospective uses the exact 1982-2024 **both**-region proportions from **tinyVAST_props_new.csv**. Peel 0 terminates in 2024 and nine successive peels terminate in 2023 through 2015. Each peel removes observations after its terminal year and initializes from the preceding fitted peel.

All ten RTMB fits have maximum absolute gradients below 0.001. Peels 2, 4, and 8 ended with optimizer code 1 after tighter restarts, but their gradients were below the reporting criterion. Mohn’s rho is 0.283 for spawning biomass and 0.311 for age-1 recruitment. Both values indicate a positive retrospective pattern.

Replacing the historical BTS proportions with tinyVAST has a small effect on terminal spawning biomass and predicted catch in the controlled ADMB bridge, and a somewhat larger effect on recruitment. The positive retrospective pattern remains an important stability caveat when considering adoption.

A-2 Evaluation of time-varying BTS availability

This diagnostic isolates the biomass variation induced by the fitted time-varying bottom-trawl survey (BTS) selectivity. It holds population abundance and weight at age constant across years. The fixed abundance vector for ages 1–15 is the arithmetic mean of the model-estimated numbers at each age across 1982–2024. The fixed weight vector is the mean BTS weight at each age across the survey observations. This centers the controlled calculation on the estimated population age structure over the analysis period while removing annual changes in population abundance.

For year t , the selectivity-only vulnerable biomass is

$$B_t^{\text{sel}} = \sum_{a=1}^{15} \bar{N}_a \bar{w}_a s_{t,a},$$

where $\bar{N}_a$ is mean estimated numbers at age across 1982–2024, $\bar{w}_a$ is mean BTS weight at age, and only BTS selectivity $s_{t,a}$ varies. This is an availability index rather than an estimated stock biomass trajectory.

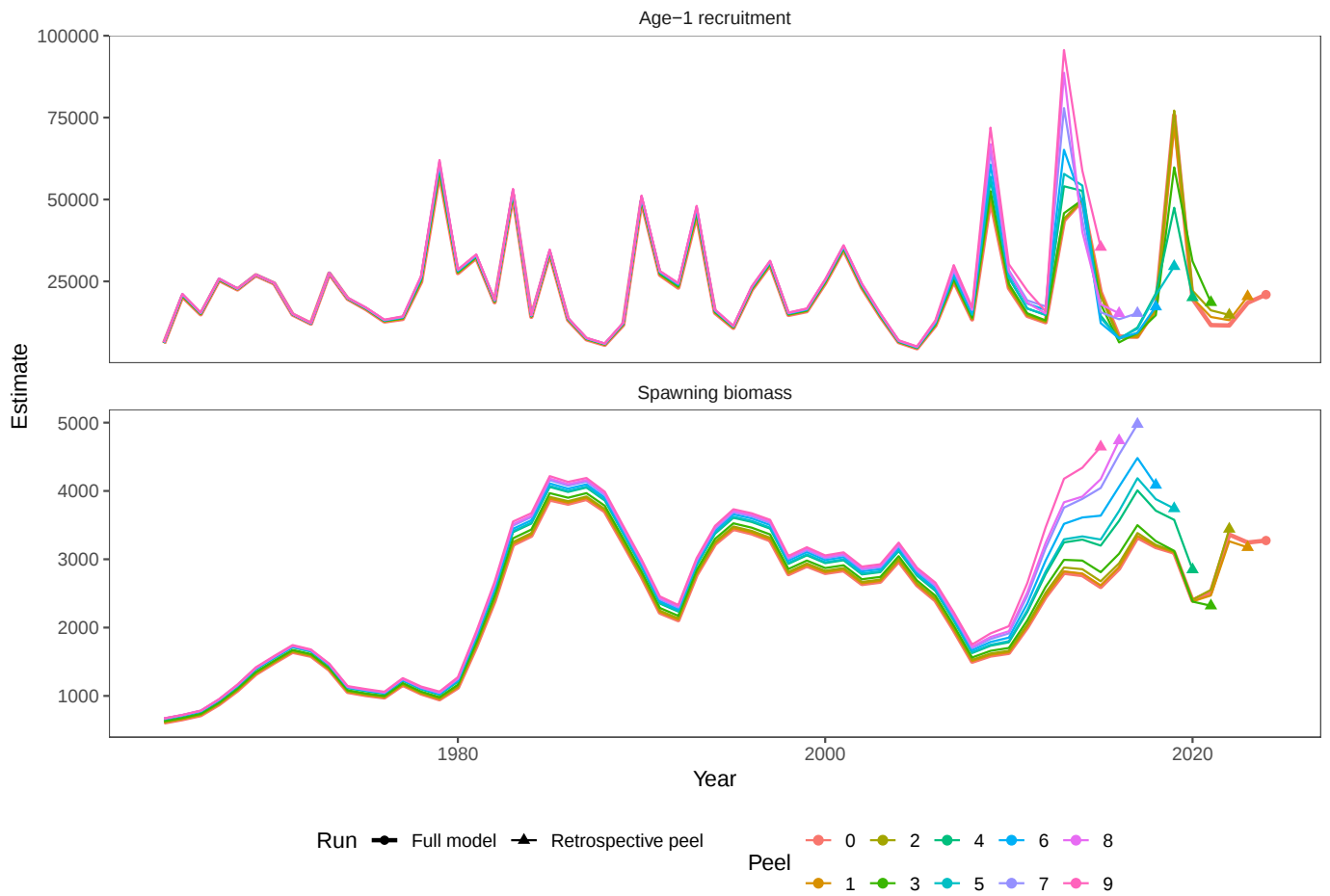


Figure 10.3: RTMB spawning-biomass and age-1 recruitment trajectories for the full 2024 model and nine retrospective peels using tinyVAST BTS proportions. Points mark the terminal year of each trajectory.

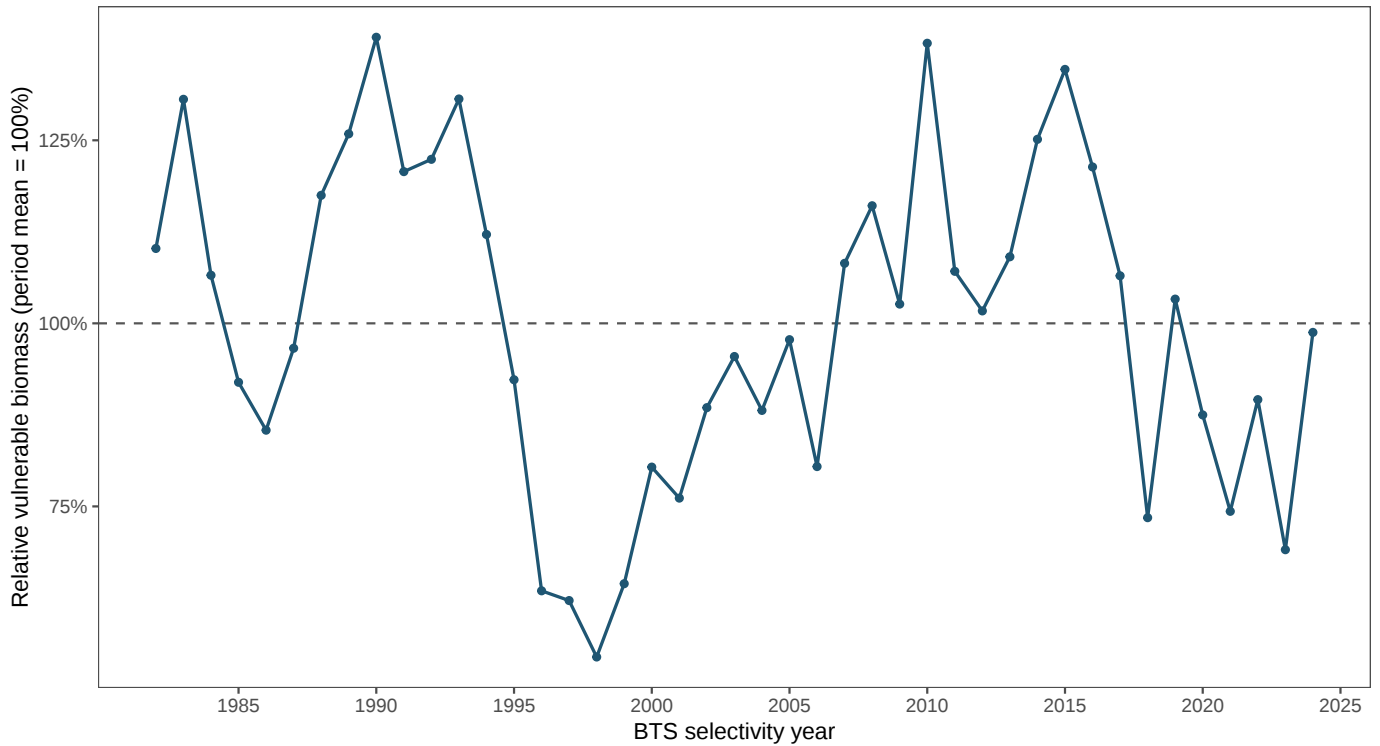


Figure 10.4: Relative BTS-vulnerable biomass attributable only to fitted annual BTS selectivity. Mean estimated numbers at ages 1–15 across 1982–2024 and mean BTS weight at age are held fixed. Values are divided by the 1982–2024 mean; the dashed horizontal line marks that mean.

With numbers and weights fixed, the selectivity-only index ranges from 54.4% to 139.1% of its period mean. Thus, fitted BTS selectivity alone produces deviations of approximately -45.6% to 39.1% around mean vulnerable biomass. This range describes changes in modeled survey availability caused by selectivity and should not be interpreted as population biomass change.

An analogous weight-only calculation holds mean estimated numbers at age and BTS selectivity fixed. Selectivity is averaged at each age over 1982–2024, while the observed BTS weight-at-age vector varies among the 42 survey years. There is no BTS weight observation for 2020, so the plotted series moves directly from 2019 to 2021.

With mean estimated numbers at age and mean selectivity fixed, annual BTS weights alone produce a relative vulnerable-biomass range of 80.8% to 124.5%, equivalent to deviations of -19.2% to 24.5% around the mean.

The third calculation holds both BTS selectivity and BTS weight at age at their period means and varies only the model-estimated numbers at ages 1–15. It therefore describes how the estimated population age structure and scale would change BTS-vulnerable biomass under a constant observation process.

With mean selectivity and mean weight fixed, estimated numbers at age alone produce a relative vulnerable-biomass range of 48.1% to 152.7%, equivalent to deviations of -51.9% to 52.7% around the mean. Unlike the first two controlled calculations, this third series reflects estimated population change rather than observation-process variation.

The combined comparison in Figure 10.7 places the three controlled series from Figure 10.4, Figure 10.5, and Figure 10.6 on the same scale as the observed BTS biomass index. Each series is divided by its own period mean, so 100% represents the mean for that series rather than a common biomass level. The BTS observation series retains the 2020 survey gap.

The pairwise display in Figure 10.8 removes the time axis and compares the four normalized series directly. Diagonal panels show each marginal distribution, lower panels show paired annual values, and upper panels report Pearson correlations based on the years available for each pair. These correlations describe shared temporal variation among the normalized indices; they do not identify causal contributions to observed survey biomass.

A-3 SparseNUTS MCMC

This analysis applies **SparseNUTS** to the **hierarchical Form-2 double-logistic candidate model** (`fishery_sel_form = 2`). The Form-2 model declares annual selectivity deviations as random effects, which permits **SparseNUTS** to construct the sparse precision metric. The sampler uses `metric = "sparse"` and `adapt_delta = 0.95`; chains, cores, sampling iterations, warmup, and initialization remain at the package defaults. The model name and `globals = list(data = model_data)` are also supplied.

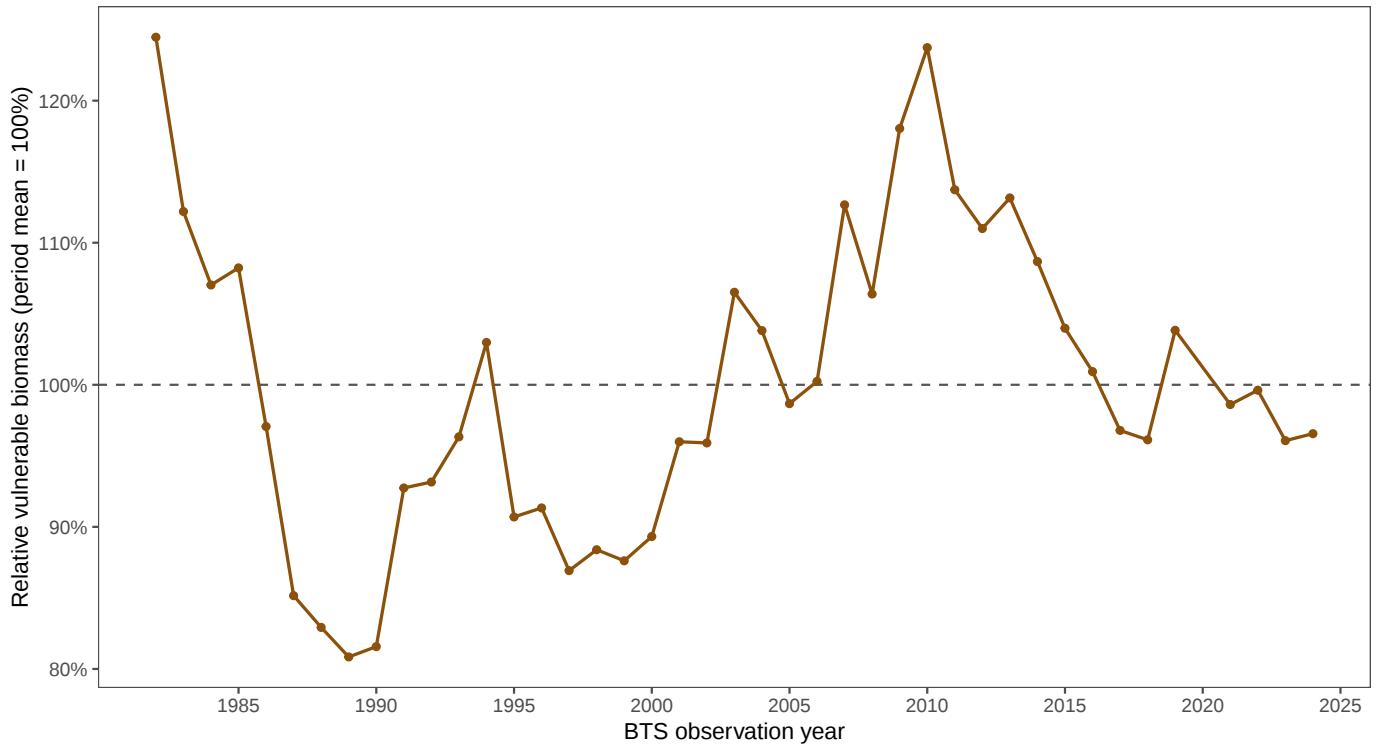


Figure 10.5: Relative BTS-vulnerable biomass attributable only to annual BTS weight at age. Mean estimated numbers at ages 1–15 across 1982–2024 and mean 1982–2024 BTS selectivity at age are held fixed. Values are divided by the mean across the 42 BTS observation years; the dashed horizontal line marks that mean.

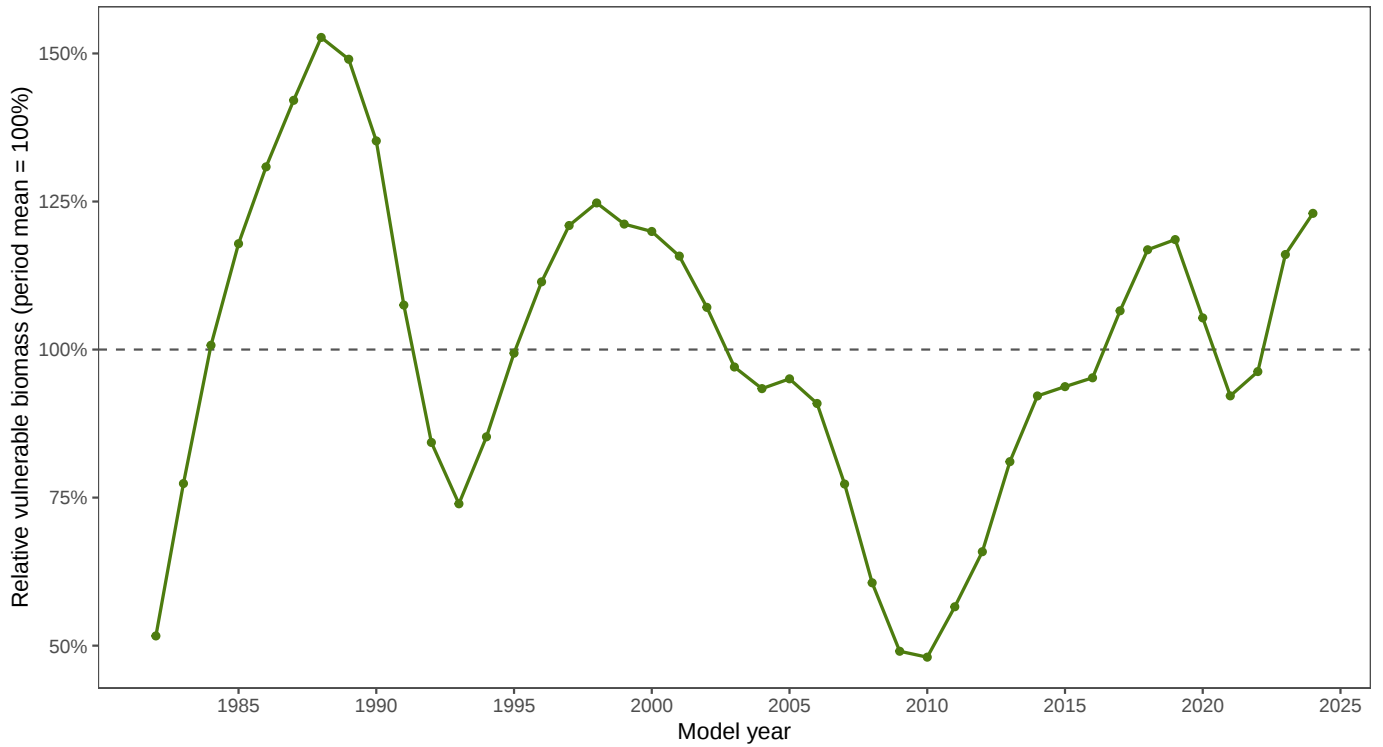


Figure 10.6: Relative BTS-vulnerable biomass attributable only to annual estimated numbers at ages 1–15. Mean BTS selectivity at age and mean BTS weight at age are held fixed. Values are divided by the 1982–2024 mean; the dashed horizontal line marks that mean.

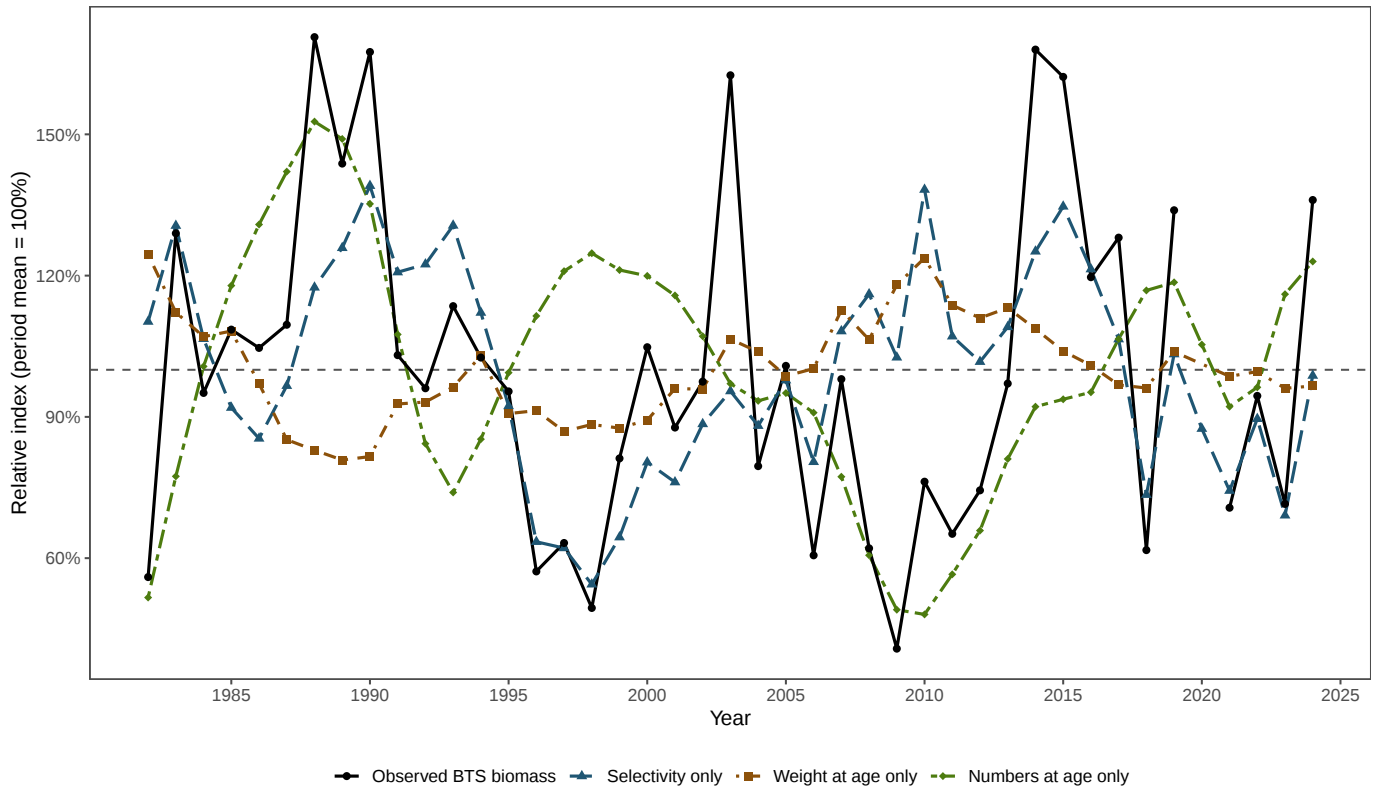


Figure 10.7: Relative BTS-vulnerable-biomass components and observed BTS biomass index. The selectivity-only, weight-only, numbers-at-age-only, and observed survey series are each normalized to their own 1982–2024 mean. The dashed horizontal line marks 100%; the observed BTS series has no 2020 value.

Table 10.10: Summary diagnostics for the current RTMB-ADMB base model.

Model Status Diagnostics

metric	value
RTMB output	analysis/output/corrected_full_age_bts/rtmb_base.rds
Report elements	42
Parameters in taped object	1205
Initial objective	7075.220
Saved total likelihood	7075.220
ADMB bridge report	repo/analysis/output/corrected_full_age_bts/admb_root/runs/full_age_bts/p
ADMB bridge parameters	repo/analysis/output/corrected_full_age_bts/admb_root/runs/full_age_bts/p
Interpretation	Saved report loads and the RTMB objective tapes successfully; full convergence

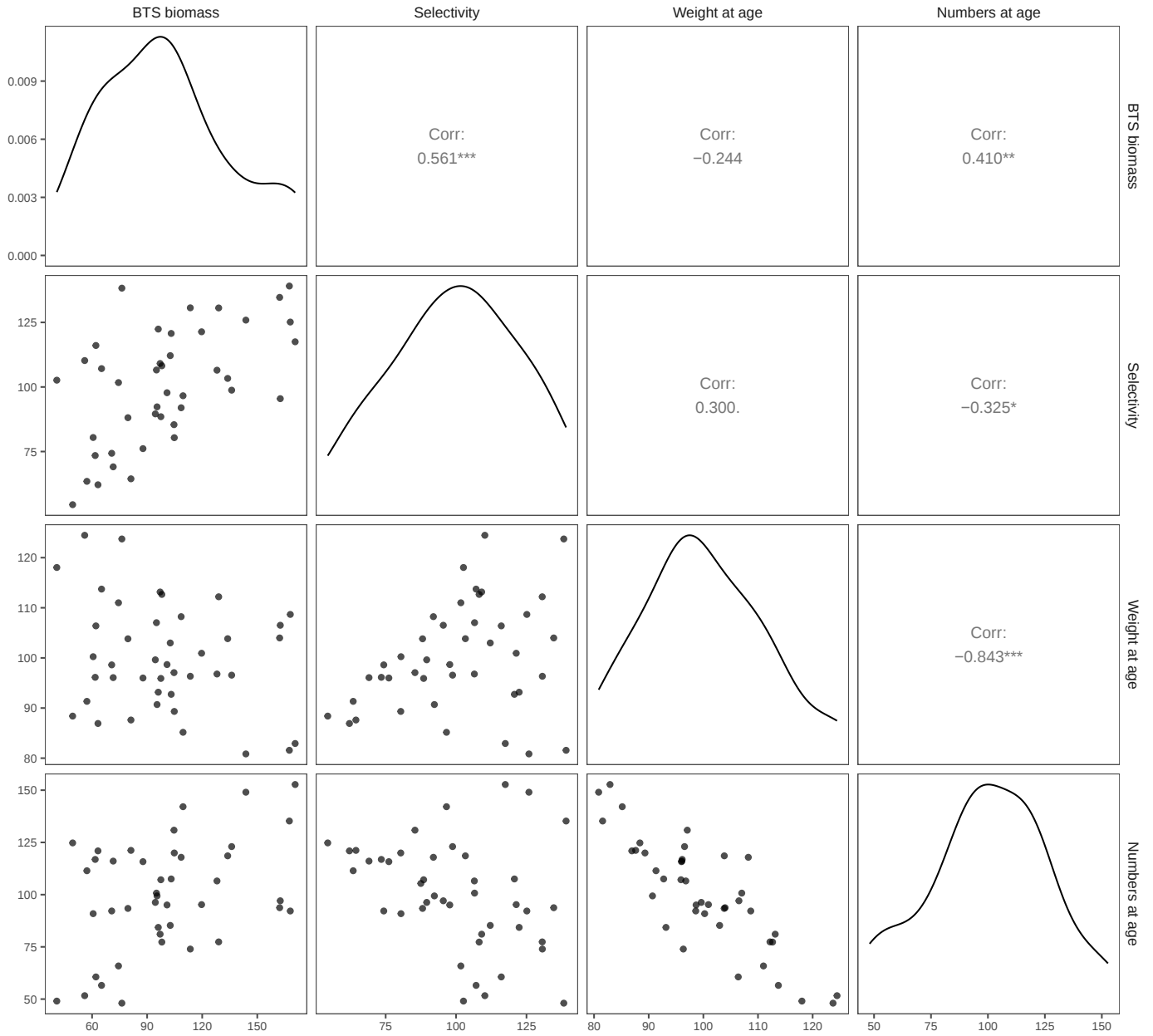


Figure 10.8: Pairwise relationships among observed BTS biomass and the selectivity-only, weight-at-age-only, and numbers-at-age-only relative indices shown in Figure Figure 10.7. Values are percentages of each series' 1982–2024 mean. Upper panels report Pearson correlations using available paired years.

Table 10.11: RTMB-ADMB likelihood diagnostics by component.

Likelihood Diagnostics by Component

component	value
Catch	2.521
BTS index	31.814
ATS index	9.282
ATS age-1 index	11.103
CPUE	1.080
AVO	9.028
Fishery age composition	157.798
BTS age composition	204.294
ATS age composition	30.088
Recruitment	34.684
Fishing mortality penalty	9.317
Selectivity penalty	209.039
Weight-at-age	6,344.865
Priors	20.118
Total	7,075.220

Exporting that RTMB data object allows the chains to run concurrently. These results characterize posterior sampling behavior for the candidate Form-2 model and do not replace the accepted assessment configuration.

With `metric = "sparse"` and `adapt_delta = 0.95`, the run produced 4 divergences during adaptation and **3 divergences among the 4,000 retained transitions**. Maximum R-hat was 1.007, and minimum bulk effective sample size was 1,199. The chain-mixing statistics are good, but 3 retained divergences remain; its location should be checked before treating the posterior as final. Substantive posterior checks and comparison with deterministic uncertainty remain appropriate before using the draws in assessment decisions.

A-4 Data and output

Downloadable CSV files

The following reader-facing files provide machine-readable versions of key inputs, diagnostics, and results used in this report:

- [Model-level summary](#)
- [Tidy model parameters](#)
- [Tidy model observations and predictions](#)
- [BTS age-data bridge comparison](#)
- [BTS age-data bridge diagnostics](#)
- [BTS age-data bridge time series](#)
- [tinyVAST retrospective diagnostics](#)
- [tinyVAST retrospective Mohn's rho](#)
- [Corrected-run downstream lineage](#)
- [Fishery-selectivity model summary](#)
- [One-step-ahead residual summary](#)
- [Retrospective data-availability audit](#)
- [SPM projection summary](#)
- [Tier-3 seven-scenario projection table](#)
- [Length-frequency summary counts](#)

Table 10.12: SparseNUTS sparse-metric run status for the hierarchical Form-2 RTMB model.

SparseNUTS Hierarchical Form-2 Run Status

metric	value
Model configuration	hierarchical Form-2 double-logistic RTMB model
SparseNUTS installed	TRUE
SparseNUTS version	1.0.2
SparseNUTS GitHub commit	NA
Default call	SparseNUTS::sample_snuts(obj, metric = 'sparse', control = list(adapt_delta = 0.95))
Saved default output	TRUE
Output path	repo/analysis/output/sparsenuts/fishery_sel_forms/rtmb_ebswp_sparsenuts
Algorithm	SNUTS
Metric	sparse
Target acceptance probability	0.95
Chains	4
Parallel cores	4
Execution mode	parallel sampling requested with cores=4
Warmup iterations per chain	150
Post-warmup samples per chain	1000
Elapsed time (minutes)	4.0
Diagnostic object available	TRUE
Error	

Table 10.13: Diagnostics for the SparseNUTS sparse-metric run of the base RTMB model with adapt_delta = 0.95. R-hat values near 1 and larger effective sample sizes indicate good between-chain mixing. Divergences identify inadequate exploration of posterior geometry and require resolution before final inference.

SparseNUTS Hierarchical Form-2 Diagnostics

diagnostic	value
Post-warmup draws	4,000.000
Warmup divergences	4.000
Post-warmup divergences	3.000
Post-warmup divergent transitions (%)	0.070
Maximum R-hat	1.007
Minimum bulk ESS	1,199.486
Median bulk ESS	4,918.121
Minimum tail ESS	362.772
Maximum-treedepth transitions (%)	0.000

Table 10.14: SparseNUTS parameters selected for slow-order MCMC diagnostic plots.

Slow-Order Diagnostic Parameters

variable	mean	sd	rhat	ess_bulk	ess_tail
log_initdevs[4]	4.888	1.040	1.007	1,199.486	362.772
log_initdevs[10]	3.285	1.705	1.006	2,448.587	3,021.838
sel_devs_ats[195]	0.462	0.251	1.005	5,709.143	2,688.595
log_initdevs[6]	4.787	0.970	1.005	1,415.214	1,149.880
sel_devs_ats[70]	0.511	0.267	1.005	5,500.928	2,920.277
sel_devs_ats[140]	0.440	0.297	1.005	5,647.538	2,675.394
sel_devs_ats[165]	0.453	0.277	1.004	6,021.631	2,804.628
sel_slp_bts_dev[9]	0.608	0.321	1.004	2,072.783	1,163.322
sel_devs_ats[131]	0.479	0.279	1.004	5,481.697	2,803.103
sel_double_logistic_dev_fsh[159]	0.018	0.155	1.004	5,179.005	2,651.110
sel_devs_ats[75]	0.425	0.276	1.004	5,067.671	2,361.184
coh_eff[5]	0.005	1.030	1.004	4,730.591	2,690.509

Table 10.15: Input spawning weight-at-age values used in the terminal model year.

Terminal-Year Spawning Weight at Age

year	age	weight
2024	1	0.08488
2024	2	0.19587
2024	3	0.32155
2024	4	0.53394
2024	5	0.62078
2024	6	0.70710
2024	7	0.82220
2024	8	0.94591
2024	9	1.05120
2024	10	1.11338
2024	11	1.17845
2024	12	1.29002
2024	13	1.33154
2024	14	1.36674
2024	15	1.41524

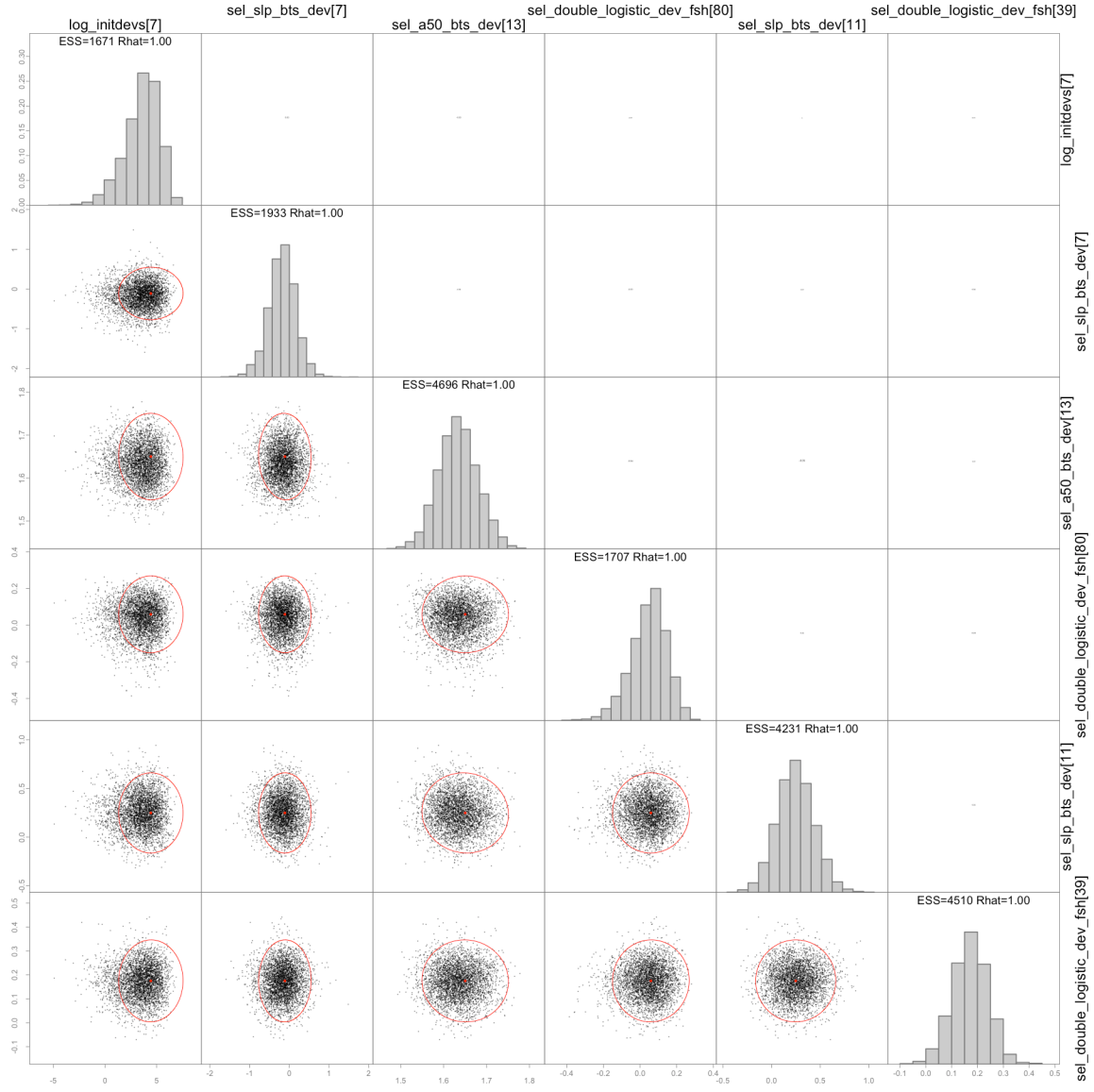


Figure 10.9: SparseNUTS package pairs plot for the six slowest RTMB-ADMB parameters by Rhat/ESS ranking, generated through the package S3 method `pairs.tmbfit` via `pairs(sparsenuts_fit, order = 'slow')`.

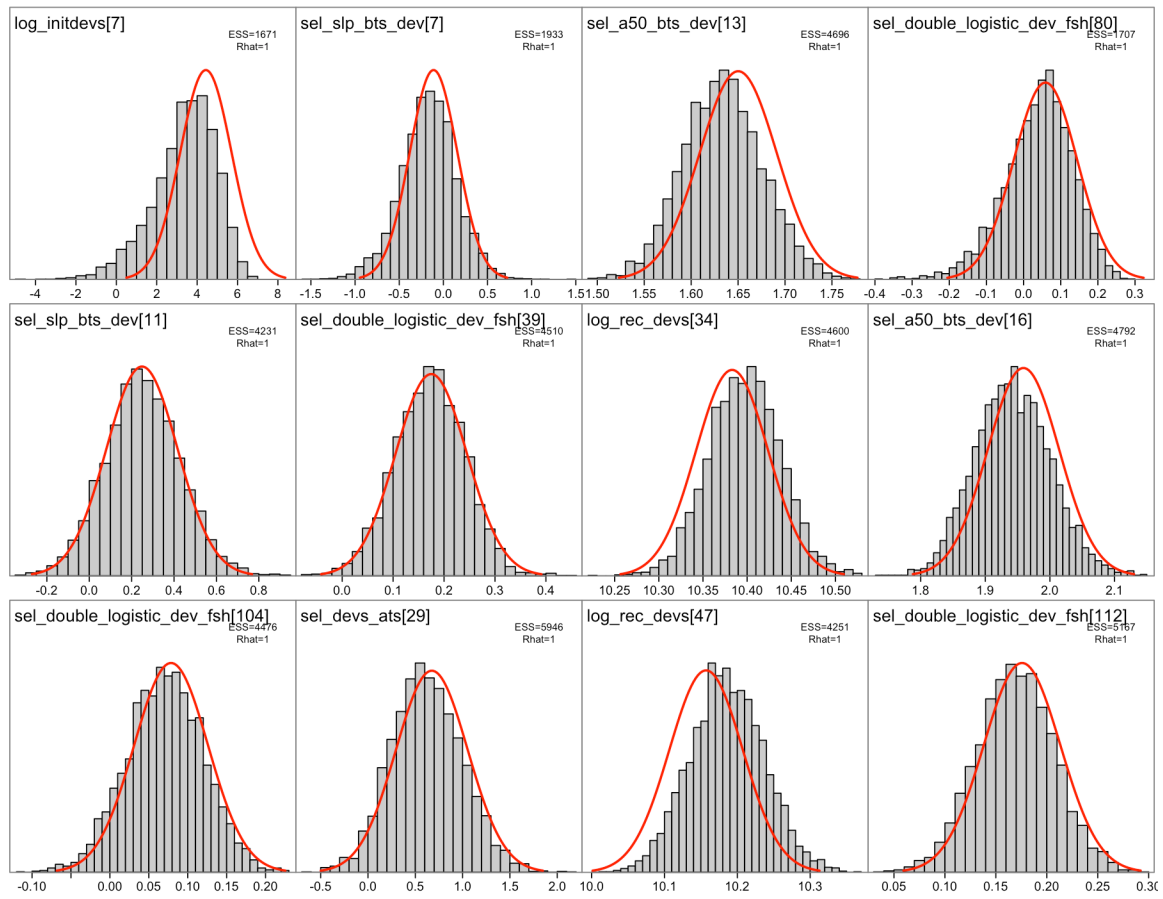


Figure 10.10: SparseNUTS::plot_marginals output from the default RTMB-ADMB SparseNUTS run using `order = 'slow'` for the selected parameter set.

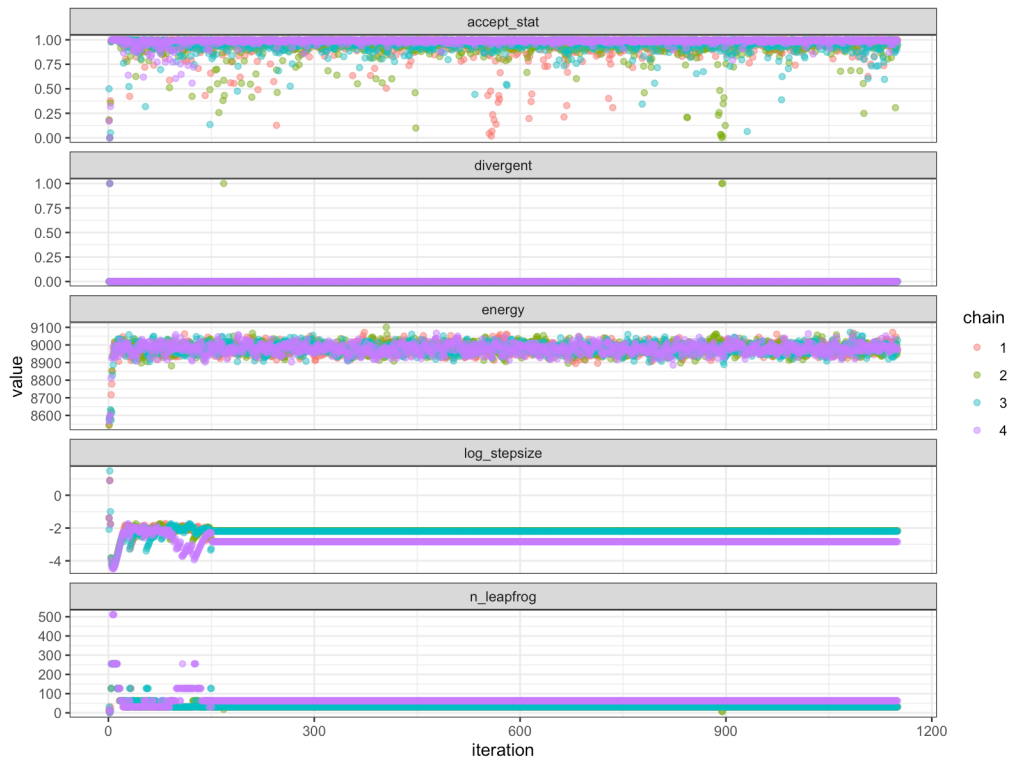


Figure 10.11: SparseNUTS sampler-parameter diagnostics from the default RTMB-ADMB run.

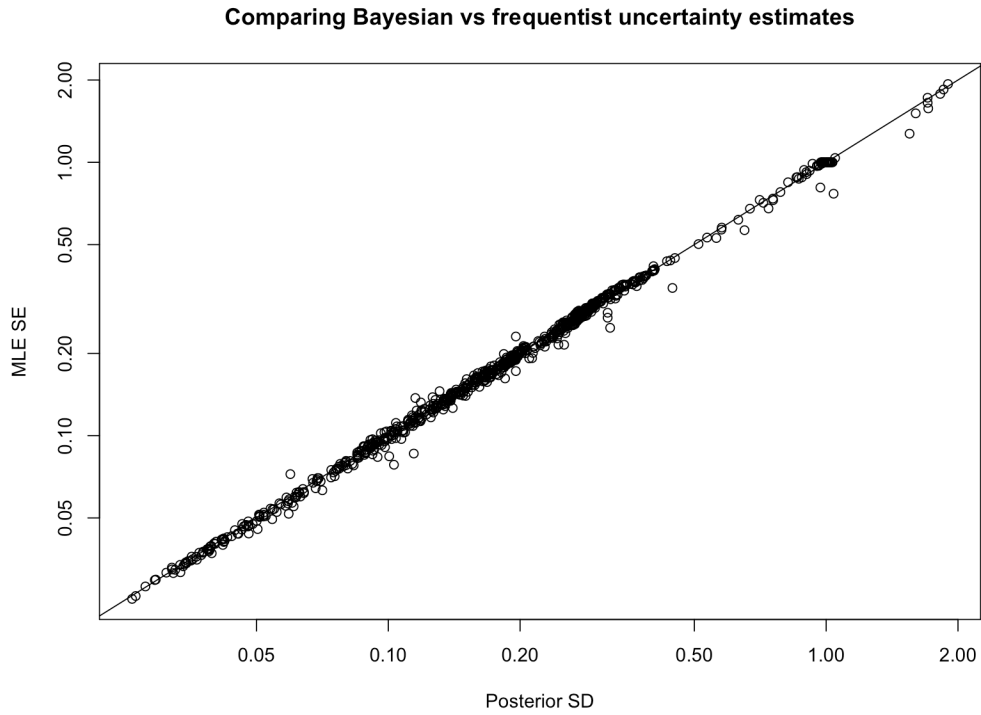


Figure 10.12: SparseNUTS::plot_uncertainties output from the default RTMB-ADMB run.

Table 10.16: Input maturity-at-age schedule used in the RTMB-ADMB model.

Maturity at Age

age	maturity
1	0.00000
2	0.00800
3	0.28900
4	0.64100
5	0.84200
6	0.90100
7	0.94700
8	0.96300
9	0.97000
10	1.00000
11	1.00000
12	1.00000
13	1.00000
14	1.00000
15	1.00000

Table 10.17: Inventory of named elements in the saved RTMB report object.

Saved RTMB Report Inventory

element	class	length	dimensions
N	matrix/array	915	61 x 15
Z	matrix/array	915	61 x 15
F	matrix/array	915	61 x 15
M	matrix/array	915	61 x 15
S	matrix/array	915	61 x 15
C	function	1	
pred_catch	numeric	61	
obs_catch	numeric	61	
SSB	numeric	61	
phizero	numeric	1	
Bzero	numeric	1	
steepness	numeric	1	
pred_cpue	numeric	12	
pred_avo	numeric	18	
eb_bts	numeric	42	
eb_ats	numeric	19	
sel_fsh	matrix/array	915	61 x 15
sel_bts	matrix/array	645	43 x 15
sel_ats	matrix/array	465	31 x 15
sam_fsh	numeric	60	
sam_bts	numeric	42	
sam_ats	numeric	19	
phat_fsh	matrix/array	900	60 x 15
phat_bts	matrix/array	630	42 x 15
phat_ats	matrix/array	285	19 x 15
age_like	numeric	3	
age_like_offset	numeric	3	
cat_like	numeric	1	
bts_like	matrix/array	1	1 x 1
ats_like	numeric	1	
ats_age1_like	numeric	1	
cpue_like	numeric	1	
avo_like	numeric	1	
avgsel_like	numeric	1	
wt_nll	numeric	4	
wt_like	numeric	1	
rec_like	numeric	7	
Fpen_like	numeric	1	
sel_like	numeric	3	
sel_like_dev	numeric	3	
Priors	numeric	4	
tot_like	numeric	1	

Input schedules

Report-object inventory

A-5 Length-frequency patterns

This appendix summarizes exploratory seasonal and spatial patterns in observed pollock length-frequency samples. It is intended to identify patterns that may warrant further investigation rather than to test an assessment-model configuration. The source analysis includes pollock observations from 1991 onward, excludes observations below 20 cm, and accumulates fish 65 cm and longer in a 65-cm-plus group. Length frequencies are normalized within each displayed year and grouping. A season includes samples collected before June; B season data are from June onward. Earlier years appear at the top of each figure.

Change from 2025 to 2026

The observed length distribution shifted toward smaller fish from 2025 to 2026. Across seasons, mean sampled length declined from 46.17 to 44.81 cm, while the median remained 46 cm. The percentage longer than 46 cm decreased from 46.40% to 43.96%, and the percentage at or below 35 cm increased from 4.03% to 9.86%.

The shift occurred primarily in the B-season samples. B-season mean length declined from 45.93 cm in 2025 to 42.55 cm in 2026, and the median declined from 46 to 43 cm. The proportion longer than 46 cm decreased from 48.90% to 34.76%, while the proportion at or below 35 cm increased from 6.79% to 17.54%. Both B-season area groups shifted toward smaller fish. In the western group (`NMFS_AREA > 519`), mean length declined from 44.26 to 39.39 cm and the percentage at or below 35 cm increased from 9.86% to 29.24%. In the eastern group (`NMFS_AREA < 520`), mean length declined from 48.55 to 45.62 cm and the percentage longer than 46 cm decreased from 70.13% to 49.88%.

The A-season change was smaller and differed in shape. Mean length declined from 46.39 to 45.82 cm and the median remained 46 cm, while the percentages longer than 46 cm and at or below 35 cm both increased. This indicates greater representation in the tails of the sampled A-season distribution in 2026. Sample coverage also changed: the A-season count increased from 91,912 to 101,038 observations, whereas the B-season count decreased from 80,749 to 45,057. These are unstandardized sample distributions, so the differences describe the available observations and may reflect changes in sampling as well as changes in the fish encountered by the fishery.

A- and B-season distributions

Combined-season distributions

B-season distributions by NMFS area

A-6 Sex-ratio patterns

This shortened BSAI-focused appendix summarizes exploratory patterns from fishery age samples and Bering Sea summer acoustic-survey samples. The source analysis covers 1986–2025, with catcher/processor A-season weekly summaries updated through 2026. Sex ratio is the proportion female among samples with a recorded female or male sex. Point sizes indicate sample size where shown. These unadjusted summaries identify seasonal, size-related, and interannual structure; they do not constitute a formal assessment-model test.

Pooled fishery patterns by age and length

A-season progression

Length patterns by age and season

The seasonal patterns vary with age and length. In particular, the unadjusted age-4 panels suggest that A-season samples contain slightly larger fish than B-season samples. The source analysis treats this as an exploratory visual pattern; its adjusted growth model reverses that simple interpretation and estimates a positive B-versus-A age-4 length contrast in the BSAI.

Pollock length-frequency by season

A season: before June 20; B season: June 20 or later

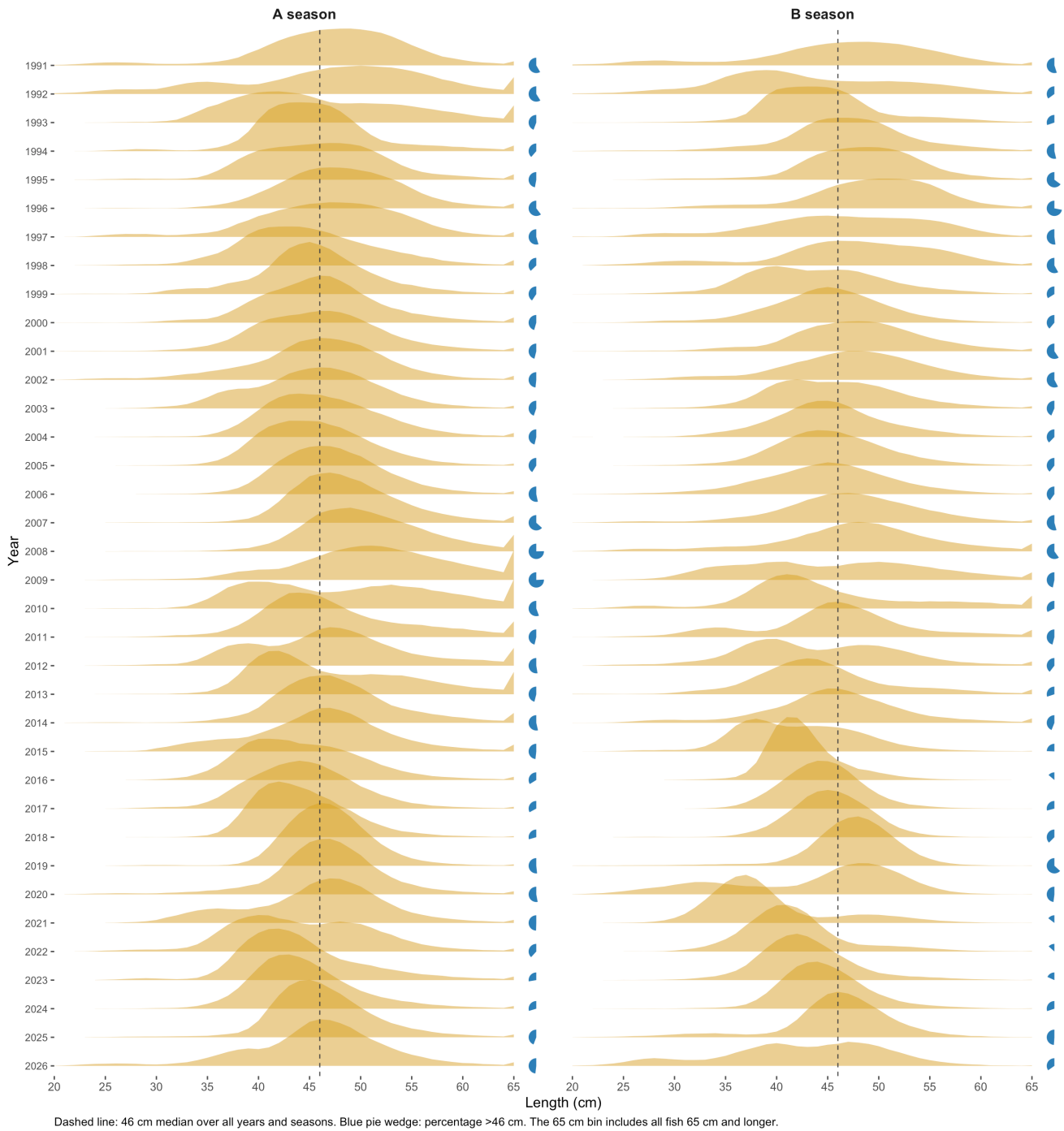


Figure 10.13: Pollock length-frequency proportions by season. The left panel shows samples collected before June; the right panel shows samples collected from June onward.

Combined pollock length-frequency
All sample dates

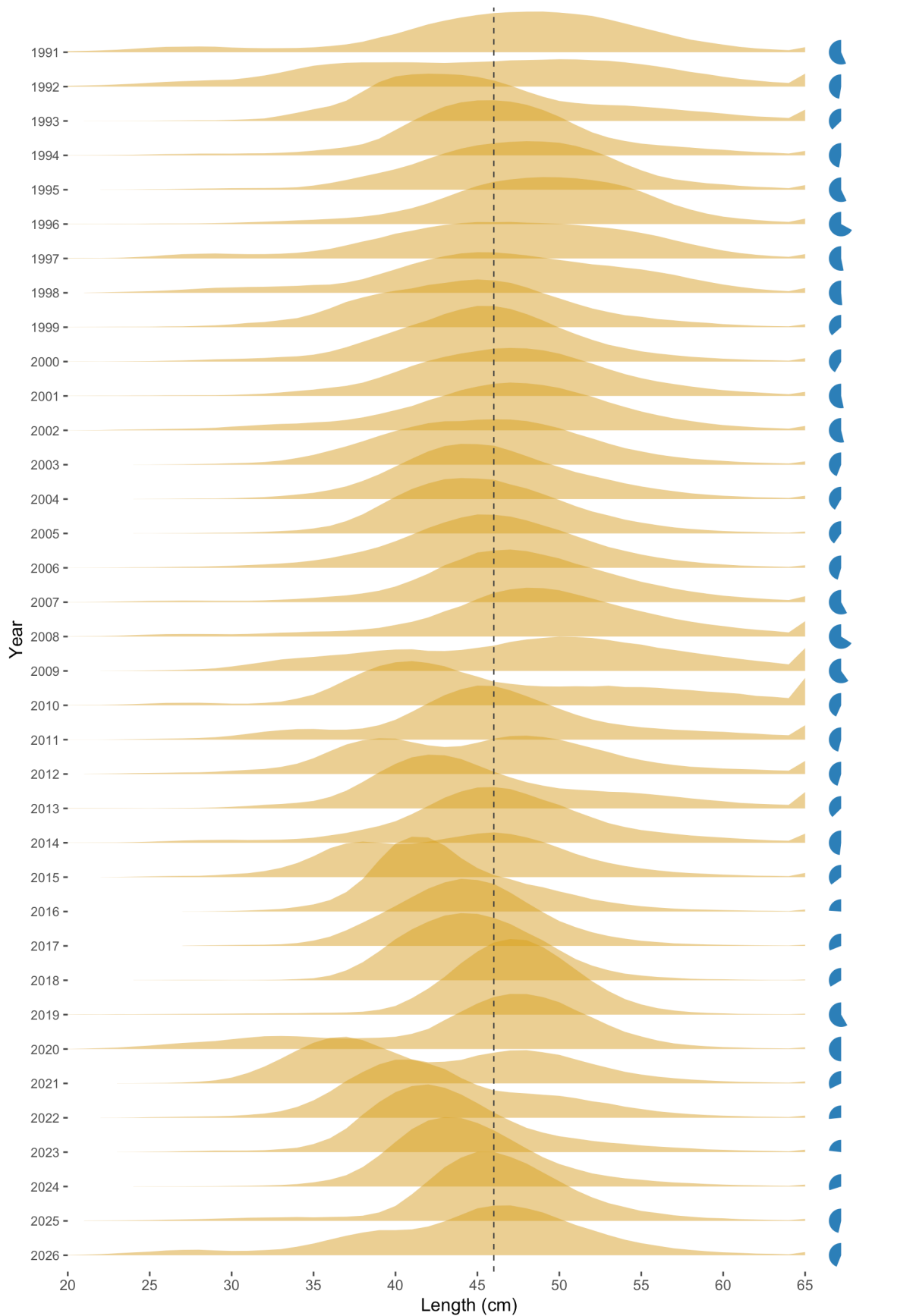


Figure 10.14: Pollock length-frequency proportions across both seasons.

B-season pollock length-frequency by NMFS area
June 20 or later; proportions normalized within year and area group

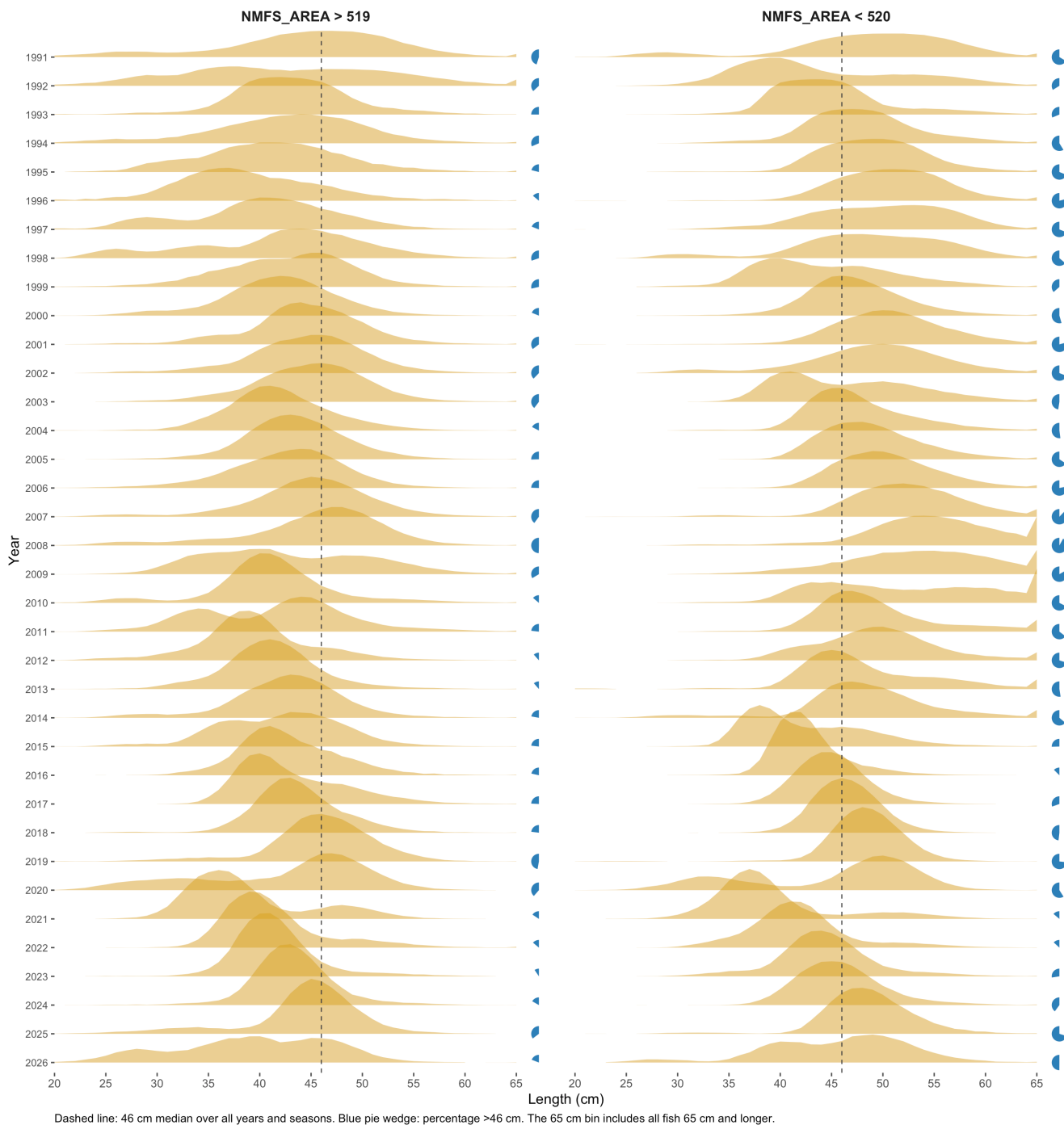


Figure 10.15: B-season pollock length-frequency proportions by NMFS area group. Samples were collected from June onward. The left panel represents samples west of 170 degrees W; the right panel represents samples east of 170 degrees W, approximately west and east of the Pribilof Islands.

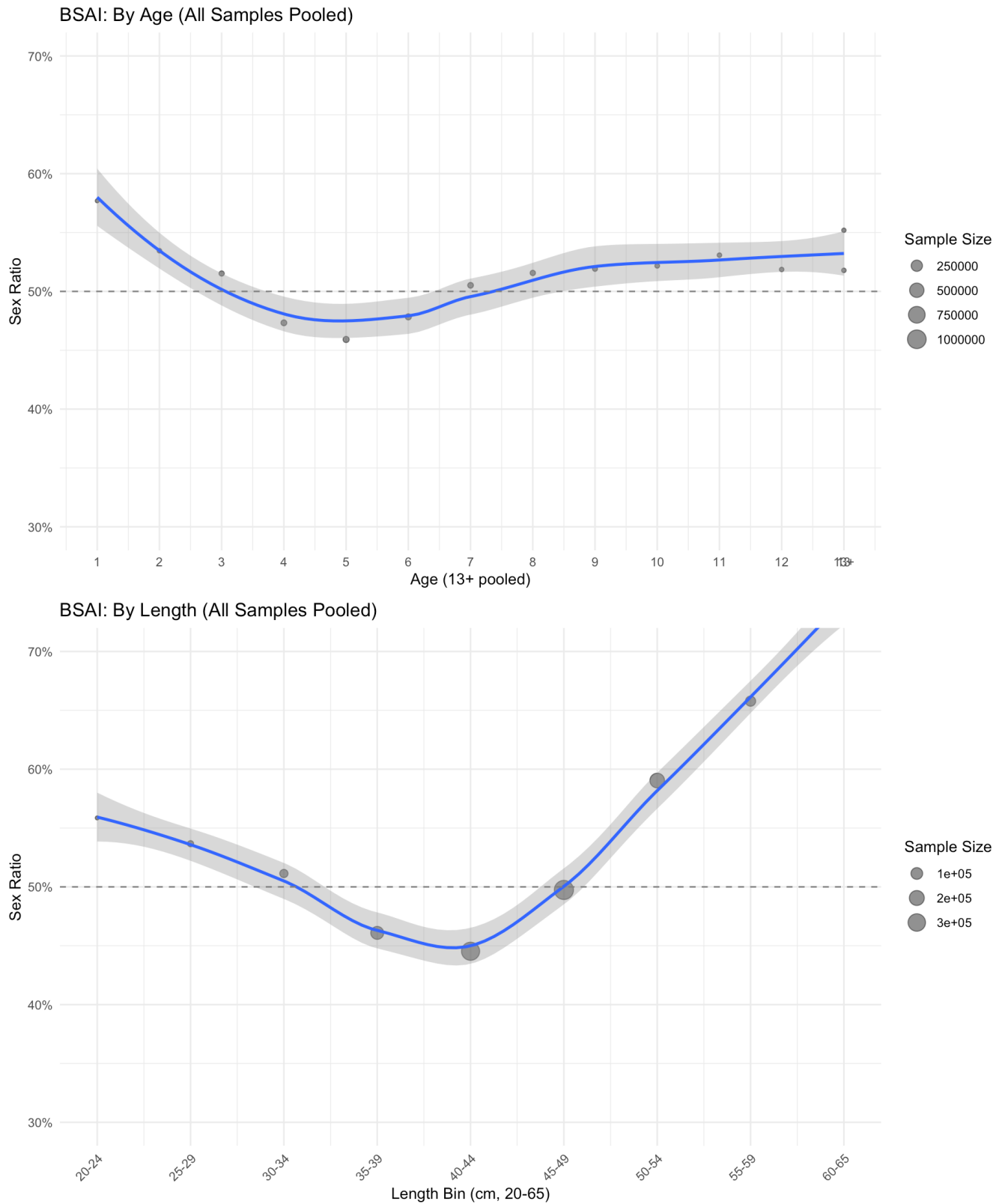


Figure 10.16: BSAI pooled fishery sex ratios across all samples: by age with ages older than 13 pooled to 13 plus (top), and by 5-cm length bins for lengths 20–65 cm (bottom).

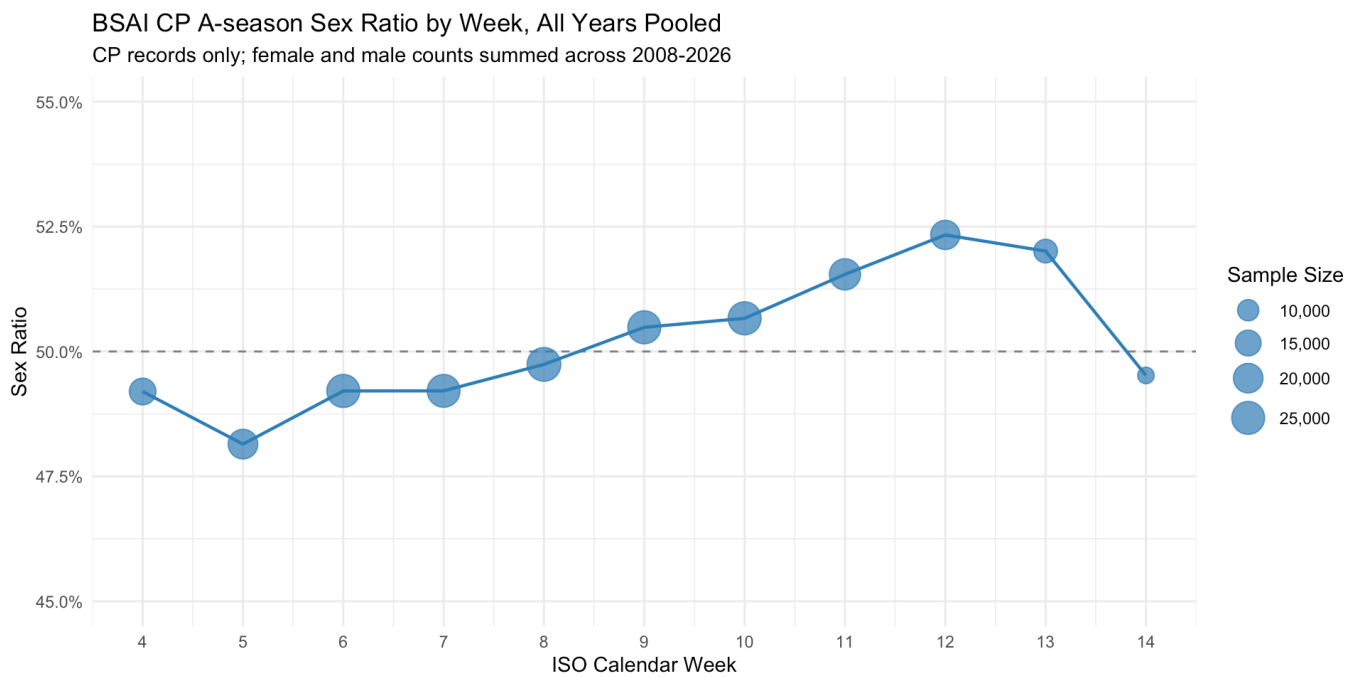


Figure 10.17: BSAI catcher/processor A-season sex ratio by ISO calendar week for weeks 4–14, pooled across 2008–2026.

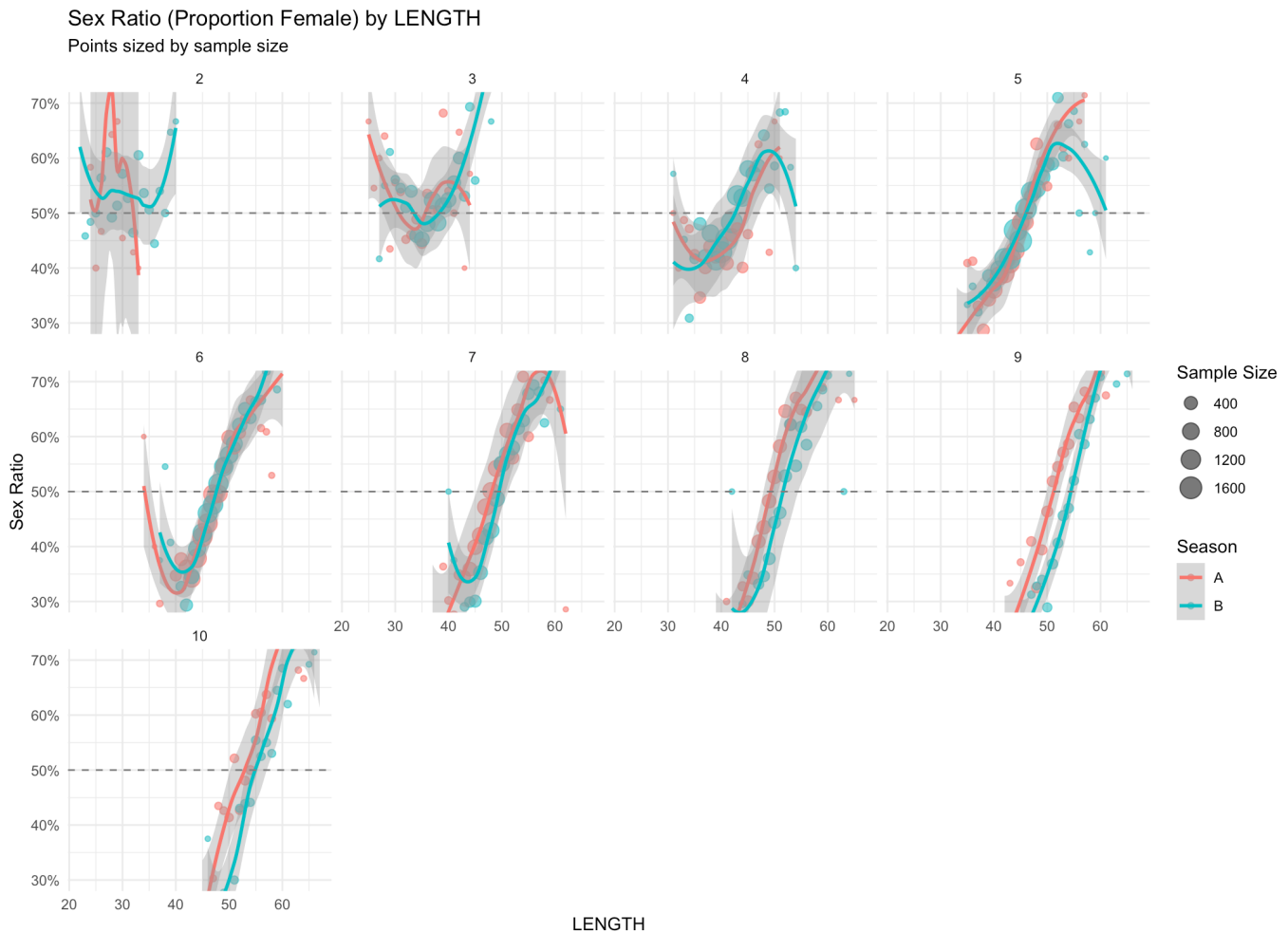


Figure 10.18: BSAI fishery sex ratio by length for ages younger than 11, with age in separate panels and season shown by color.

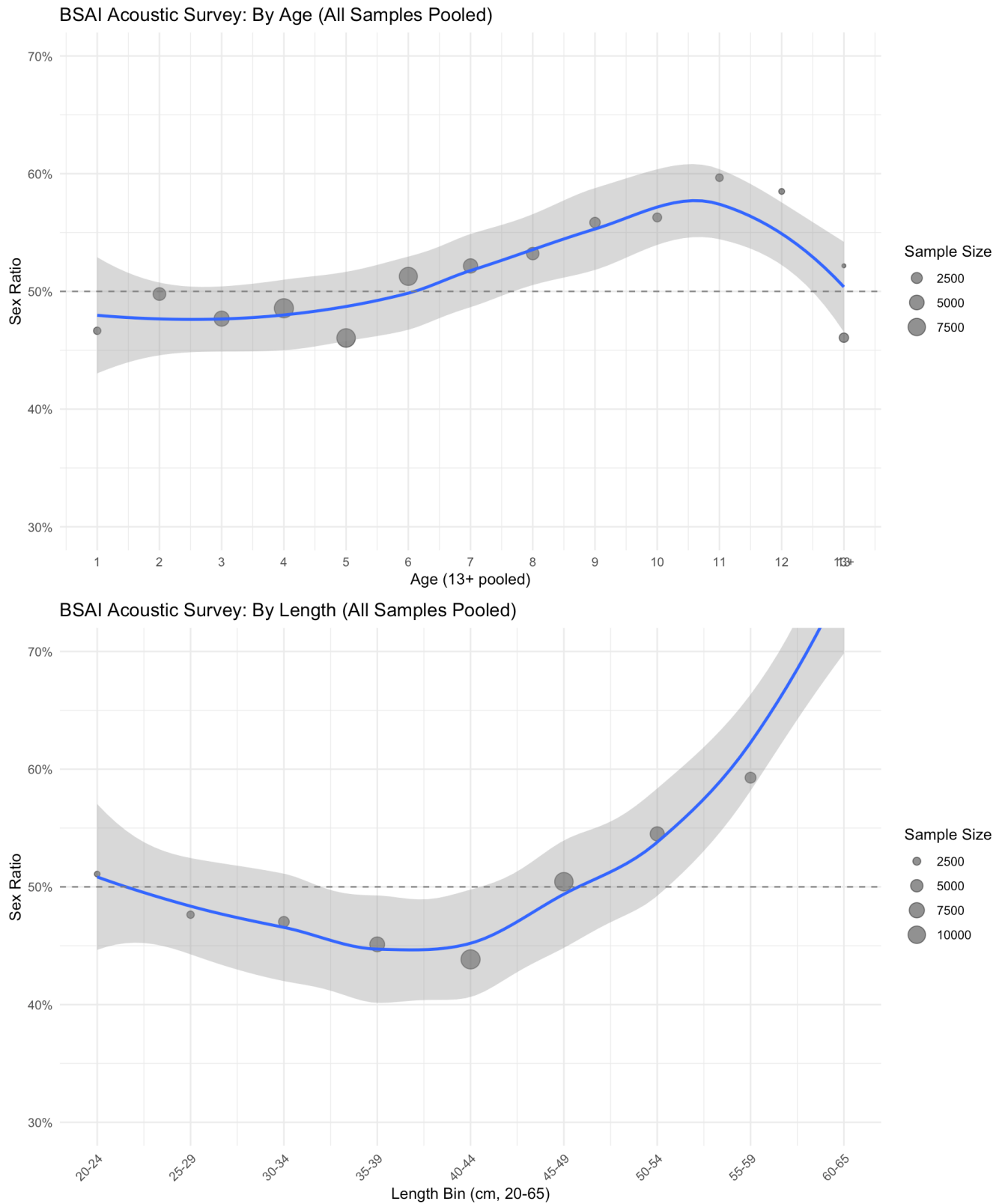


Figure 10.19: BSAI pooled acoustic-survey sex ratios across all samples: by age with ages older than 13 pooled to 13 plus (top), and by 5-cm length bins for lengths 20–65 cm (bottom).

Bering Sea summer acoustic survey

A-7 Notes

Operational consideration of the RTMB model requires satisfactory convergence, estimability, retrospective, sensitivity, and simulation results, followed by the established review process. The results presented here address several of these elements but do not constitute a recommendation to replace the accepted assessment model.