Gulf of Alaska Pacific Ocean Perch
September 2025 Groundfish Plan Team

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1 Executive Summary

The Gulf of Alaska Pacific Ocean Perch stock assessment is scheduled for a full operational model in 2025. This assessment has a new lead author this year, leading to only incremental changes in the assessment. Relative to the last full assessment in 2023 (Model 2020.1) the following iterative changes have been made with Model 25.2a recommended for review in November:

- Model 25.0: The assessment model has been migrated from the ADMB framework to RTMB,
  - Moves maturity estimation outside the model,
- Model 25.1: Uses the full form of the lognormal negative log-likelihood for catch and survey biomass,
- Model 25.2: The 2nd (of 4) fishery selectivity time block is estimated using a gamma function (dome-shaped) instead of the averaged logistic-gamma from the 1st and 3rd time blocks,
- Francis reweighting is used to update composition data weights for all models examined, indicated with an "a" (e.g., Model 25.0a).

These models are not anticipated to greatly impact management advice but they follow best practices and remove arbitrary data weights (e.g., annual catch $\lambda = 50$). All examinations originate from the ADMB base model (Model 2020.1) using 2023 data inputs.

2 Model Bridging

2.1 ADMB to RTMB - Model 25.0

The Gulf of Alaska Pacific Ocean Perch stock assessment is currently in a bespoke ADMB model framework. The ADMB program is in the process of an 'orderly shutdown of development' (see: ADMB) and Template Model Builder (TMB) 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++ (RTMB 2024).

The RTMB assessment model and the associated comparison code are available on GitHub.

- RTMB Model Code:
- ADMB vs. RTMB Comparison Code:.

A key difference between the ADMB and RTMB models is that parameters for the logistic function describing maturity-at-age are estimated conditionally in the ADMB model. These parameter values are identical to estimating maturity-at-age independently via GLM. Estimating maturity-at-age parameters conditionally influences the model only through the evaluation of uncertainty, as the MCMC procedure includes variability in the maturity parameters in conjunction with variability in all other parameters, rather than assuming the maturity parameters are fixed. Thus, estimation of maturity-at-age within the ADMB assessment model allows for uncertainty in maturation to be incorporated into uncertainty for key model results (e.g., SSB), though estimates of other parameters are not effected. Moving maturity estimation outside of the model permits easier implementation of alternative functional forms and does not impact estimation of other model parameters.

Using ADMB Model 2020.1 MLE estimates as input values in Model 25.0 produces the same model predictions (Table 1), and when optimized from there the same standard errors (uncertainties) for parameters and derived quantities. Negative log-likelihood values are nearly identical, differing by a few decimal points (Table 2). Comparison shows that the RTMB model results are consistent with the ADMB version (Figure 1, Figure 2), with negligible differences that arise from numerical precision.

Table 1: Key parameters and output values for comparing the GOA Pacific ocean perch assessment coded in ADMB and RTMB.

Item	ADMB	RTMB	Difference
M	0.0743	0.0743	0.0000
q	1.7361	1.7361	0.0000
Log mean recruitment	4.4492	4.4492	0.0000
Log mean F	-2.6131	-2.6131	0.0000
a50_1	6.2965	6.2965	0.0000
delta_1	1.9582	1.9582	0.0000
a50_3	2.5239	2.5239	0.0000
delta_3	5.0275	5.0275	0.0000
a50_4	2.7987	2.7987	0.0000
delta_4	9.6824	9.6824	0.0000
a50_survey	5.4801	5.4801	0.0000
delta_survey	5.8192	5.8192	0.0000
2024 Total biomass	649,941.00	649,941.11	-0.1070
2024 Spawning biomass	227,991.00	227,991.19	-0.1945
B40	137,447.00	137,447.18	-0.1781
2024 OFL	47,466.30	47,466.28	0.0154
2024 F OFL	0.1192	0.1192	0.0000
2024 ABC	39,718.90	39,718.89	0.0104
2024 F ABC	0.0990	0.0990	0.0000

Table 2: Model negative log likelihood (nLL) values for comparing the GOA Pacific ocean perch assessment coded in ADMB and RTMB. Note that 'Sub total' is used as the ADMB model also has nLL values for 2 maturity parameters that are not present here.

nLL	ADMB	RTMB	Difference
Catch	0.2181	0.2181	0.0000
Survey biomass	16.4416	16.4416	0.0000
Fishery age comp	25.0028	25.0028	0.0000
Survey age comp	29.2822	29.2822	0.0000
Fishery length comp	66.2258	66.2259	-0.0001
Recruitment devs	10.6027	10.6027	0.0000
F regularity	6.1405	6.1405	0.0000
SPR penalty	0.0000	0.0000	0.0000
M prior	1.8299	1.8299	0.0000
q prior	0.4241	0.4241	0.0000
Sigma R prior	7.9849	7.9849	0.0000
Sub total	164.1526	164.1527	-0.0001
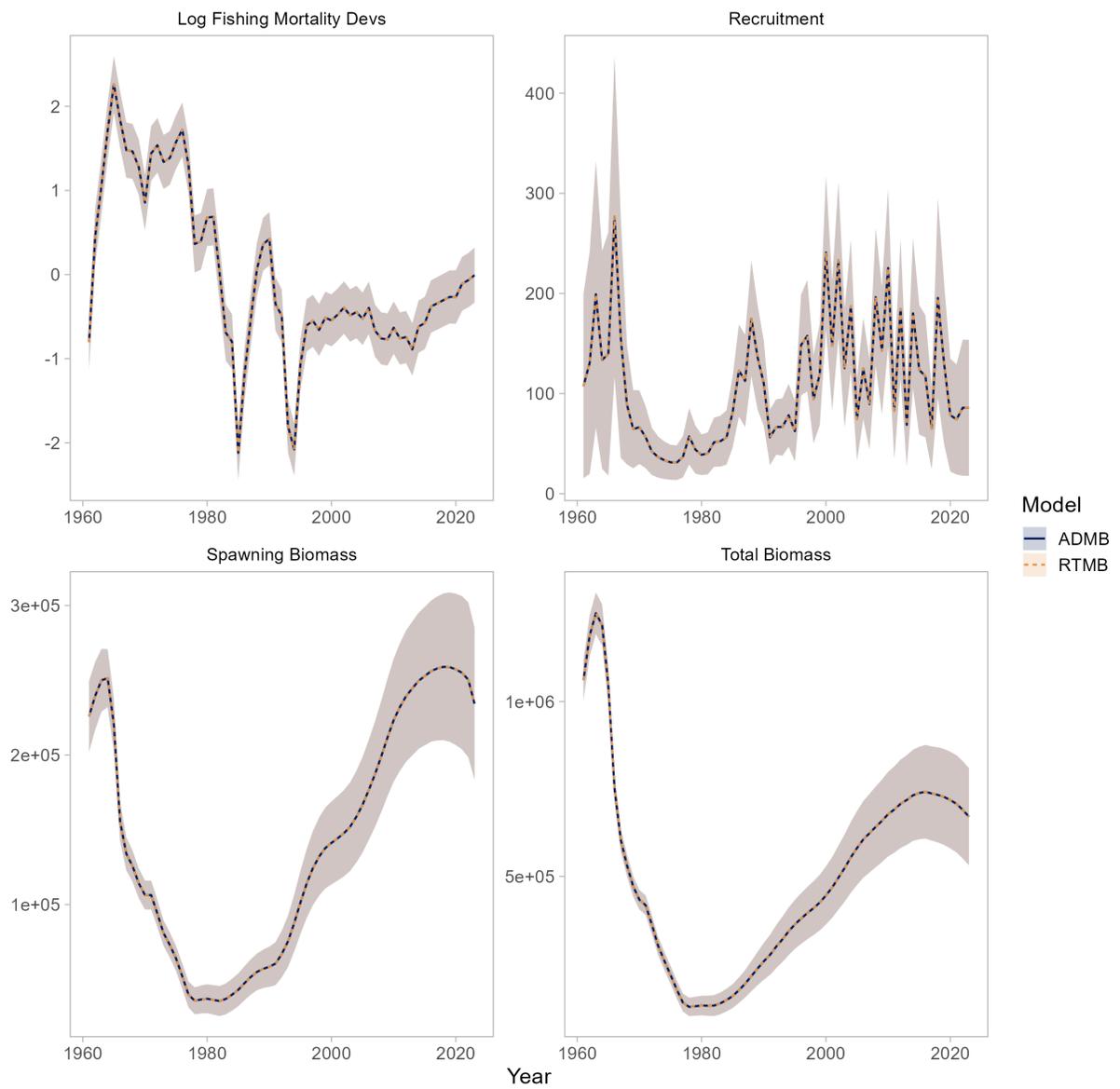
Figure 1: Comparison of key model outputs from the ADMB and RTMB Pacific ocean perch assessment models with associated standard deviations (shaded areas).
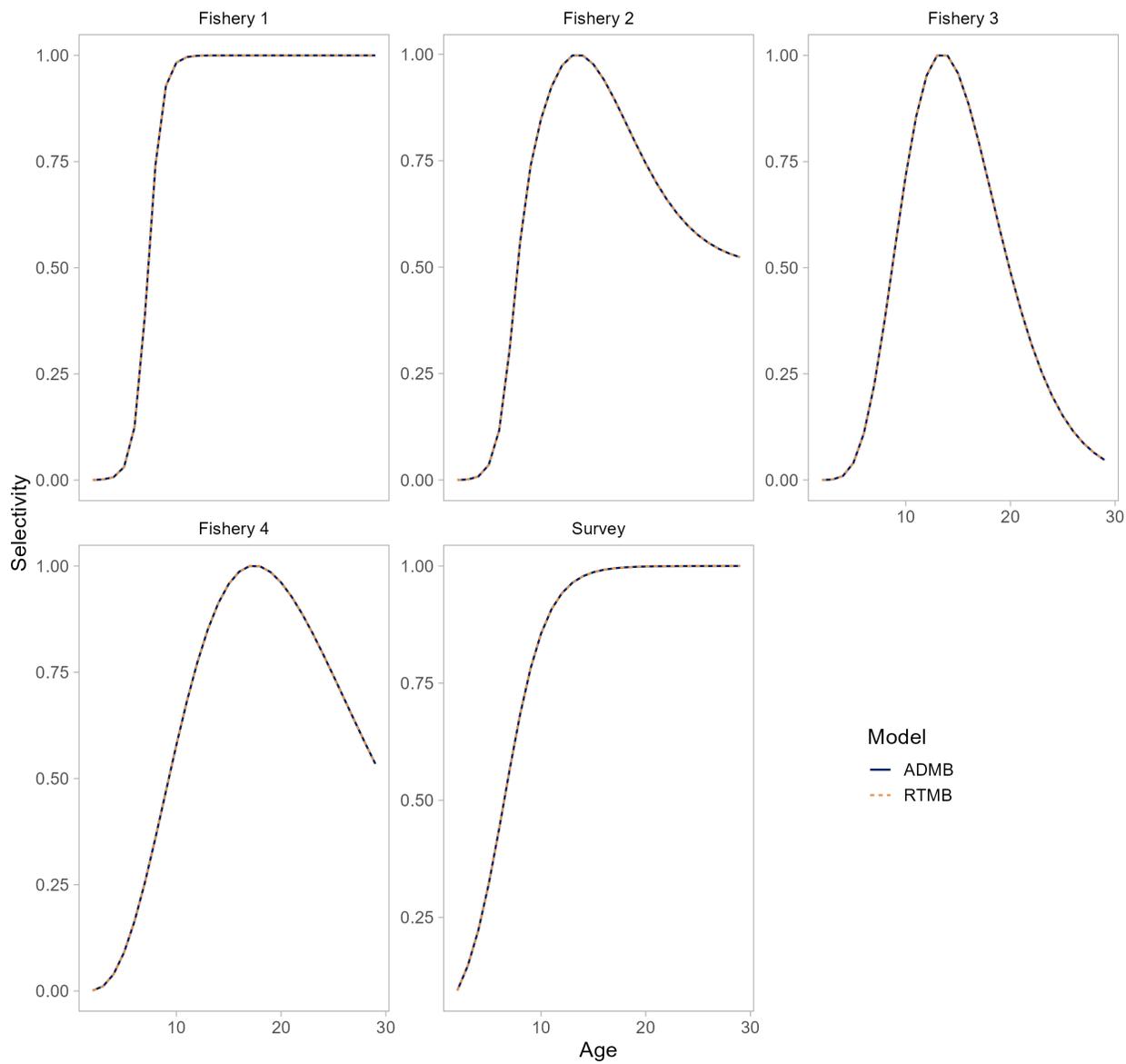
Figure 2: Comparison of fishery (4 time blocks) and survey selectivity from the ADMB and RTMB Pacific ocean perch assessment models.

3 Model Changes

3.1 Catch and Survey Negative Log Likelihood (Model 25.1)

Code for the September model runs is available on github.

Previously, the catch component of the negative log likelihood (nLL) was calculated using a weighted ($\lambda = 50$) sum-of-squares on log-transformed data expressed as:

$$\text{nll} = \lambda \sum_y \left(\log(C_y) - \log(\hat{C}_y) \right)^2$$

where (λ) is the annual weight for the catch data, C_y is the observed catch, $\hat{C}_y$ is the predicted catch.

While functional, this approach is a simplified approximation and does not represent the full probability density of a log-normal distribution. Furthermore, the variance of the catch observations is implicitly defined by the weighting term (λ), rather than being derived from an assumed coefficient of variation (CV).

To better align with statistical practices, this has been updated to use the full nLL for a log-normal distribution. This method improves precision by defining the uncertainty for each catch observation based on its unique CV. The former method used $\lambda = 50$ which is akin to a constant 10% CV for all years. This method explicitly defines the standard deviation on the log scale based on an input annual CV for the catch data. The updated nLL is:

$$\text{nll} = \lambda \sum_y \left[\log(\sigma_c) + \frac{1}{2\sigma_c^2} \left(\log(C_y) - \log(\hat{C}_y) \right)^2 \right]$$

where (λ) is the overall weight for the catch data (now set to 1), and σ_c is the standard deviation of the catch on the log scale, defined as:

$$\sigma_c = \sqrt{\log \left(1 + CV_{catch}^2 \right)}.$$

This formulation is statistically robust as it properly specifies the distributional assumption and directly incorporates the uncertainty of the catch data via its CV. The catch data are not bias-corrected, as their high assumed precision (i.e., a small CV) makes the lognormal bias term negligible.

Similarly, the GOA POP assessment has used a simplified nLL for survey biomass, which is a least-squares approximation of the lognormal distribution:

$$\text{nll} = \lambda \sum_y \frac{\left(\log(I_y) - \log(\hat{I}_y) \right)^2}{2 \left(\frac{SE(I_y)}{I_y} \right)^2}$$

This simplified form is computationally convenient but does not account for the non-zero mean bias inherent in a lognormal distribution. As a result, the expected value of the model's prediction may not correctly align with the survey data on the original arithmetic scale.

To address this, the likelihood function has been updated to the full form of the lognormal nLL. This approach incorporates a bias correction term to ensure the model's expectation is properly centered. The updated likelihood is:

$$\text{nll} = \lambda \sum_y \left[\log(\sigma_y) + \frac{1}{2} \left(\frac{\log \left(\frac{I_y}{\hat{I}_y^{bc}} \right)}{\sigma_y} \right)^2 \right]$$

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where, σ_y is the standard deviation on the log scale, and $\hat{I}_y^{bc}$ is the bias-corrected model prediction. These terms are defined as:

$$\sigma_y = \sqrt{\log\left(1 + CV_y^2\right)} \quad \text{and} \quad \hat{I}_y^{bc} = \exp\left(-\frac{\sigma_y^2}{2}\right)\hat{I}_y$$

Since the likelihoods have changed, the total nLL of Model 25.0 and Model 25.1 are not directly comparable (Table 3). However, best practices lean toward using the full nLL form. Overall, the changes in nLLs slightly increase total and spawning biomass, and the OFL and ABC (Table 4). There are no substantive differences in key parameters (e.g., M, q).

3.2 Fishery Selectivity (Model 25.2)

In the GOA POP assessment, fishery selectivity is modeled using four distinct time blocks. These time periods are:

- 1961-1976: This period represented the massive catches and overexploitation by the foreign fisheries which slowed considerably by 1976. Age data are not available for this period, but it is assumed the near pristine age-structure was much older than now, and that at the high rate of exploitation, all vulnerable age-classes were being harvested. For these reasons it is modeled using asymptotic selectivity.
- 1977-1995: This period represents the change-over from the foreign fleet to a domestic fleet, but was still dominated by large factory trawlers, which generally would tow deeper and further from port.
- 1996-2006: During this period is the emergence of smaller catcher-boats, semi-pelagic trawling and fishing cooperatives. The length of the fishing season was also greatly expanded.
- 2007-Present: This period coincides with the start of the Rockfish Program in the Central Gulf, a fishing cooperative that has influenced the behavior and composition (catcher versus factory trawlers) of the fishery.

The selectivity blocks and their respective modeling approaches are defined as:

- Block 1 ($\leq$ 1976): Estimated using a logistic selectivity curve.
- Block 2 (1977–1995): Calculated as the average of the curves from Block 1 and Block 3.
- Block 3 (1996–2006): Estimated using a gamma function selectivity curve.
- Block 4 ($\geq$ 2007): Estimated using a gamma function (dome-shaped) selectivity curve.

By averaging two curves, Block 2 is imposing a shape that may not accurately reflect the true selectivity during that period. This could lead to bias in the estimated fishing mortality at age and, consequently, the stock status. The updated approach for Block 2 is to model it using a gamma function selectivity curve, similar to Blocks 3 and 4. Selectivity for the different model outputs are available in (Figure 3), the likelihoods and parameters (are available in Table 3 and Table 4). Two additional parameters are needed to estimate the 2nd selectivity block.

One longstanding issue for this assessment has been a high q value (Kapur et al. 2023), it is worth noting that when the selectivity is estimated q decreases to 1.6, however, M remains consistent and somewhat elevated (0.0769) for such a long-lived species. Overall, biomass estimate increase from Model 25.1 with the 2nd selectivity block estimated having a fuller dome shape than the base model (Figure 3).

3.3 Francis composition data reweighting

The Francis reweighting method (Francis 2011; TA1.8) was used to objectively rebalance the influence of the age and size composition data relative to the abundance indices. This ensures the model fit is not being disproportionately driven by any single dataset. All composition data components were initially given a weight of 1.0. The analysis indicated that the age data was not influential enough, while the fishery size data was too influential. The method calculated the following multipliers to adjust the initial weights for all models to:

- Fishery age composition: ~2.8 (influence increased)
- Survey age composition: ~2.0 (influence increased)
- Fishery size composition: ~0.5 (influence decreased)

This rebalancing of data weights led to several important changes in the model's perception of the stock: The stock is estimated to be larger and more productive. Both total and spawning biomass increased, which in turn led to higher estimates for the OFL and ABC. Key parameters changed to support a larger stock. To account for the higher biomass, the model estimated a lower natural mortality (M) and survey catchability (q). The overall fits to age composition data did not drastically change from Model 25.0 to Model 25.2a (Figure 5 - Figure 19). Similarly, retrospective patters were consistent between models (Figure 23 and Figure 24).

Survey selectivity shifted to younger ages for all of the reweighted models. As the model was guided by a different balance of data, it estimated that the survey gear is catching slightly younger fish than previously thought (Figure 4).

Overall, the reweighted model provides a statistically sound and balanced fit across all data sources. Additionally, reweighting moves the q and M parameters closer to expected/assumed values for this species. Therefore, the reweighted model that incorporates assessment best practices is carried forward as the recommended base model (Model 25.2a) for providing management advice in November.

4 References

Kristensen, K. 2024. RTMB: R bindings for TMB. R package version 1.6

Kapur, M.S., Hulson, P-J., Williams, B.C., 2023. Assessment of the Pacific Ocean Perch Stock in the Gulf of Alaska. North Pacific Fishery Management Council, Anchorage, AK

Francis, R.C. 2011. Data weighting in statistical fisheries stock assessment models. Canadian Journal of Fisheries and Aquatic Sciences, 68(6), pp.1124-1138.
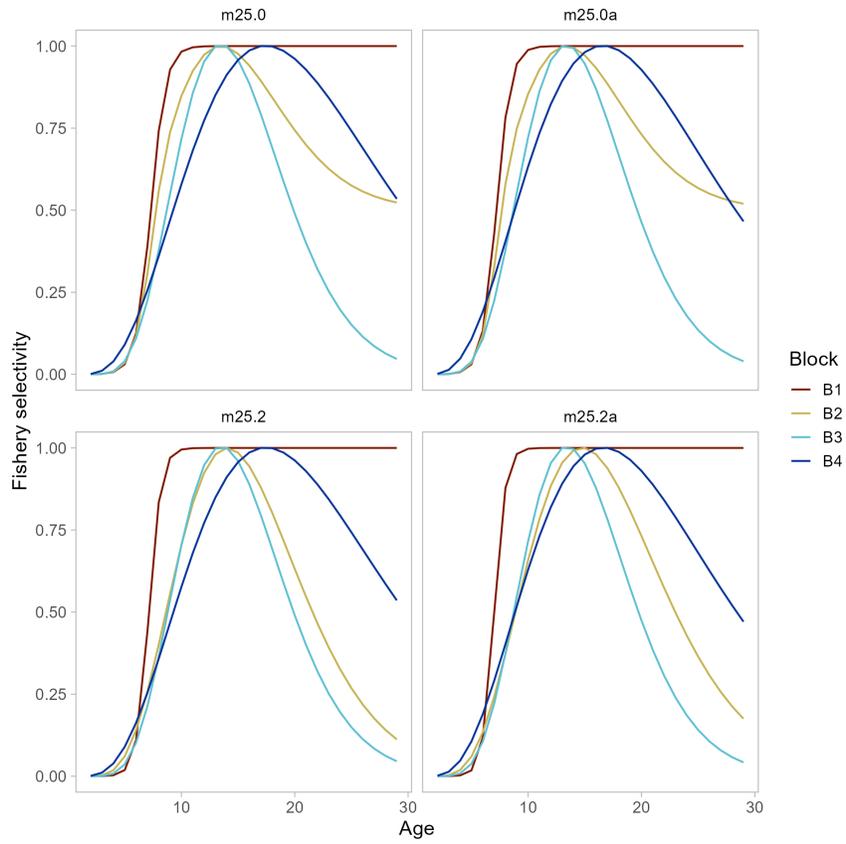
Figure 3: Fishery selectivity by time blocks. Models 25.0(a) and 25.1(a), have the 2nd time block set at the average of the 1st and 3rd time blocks, m25.2(a) estimates selectivity using a gamma function.
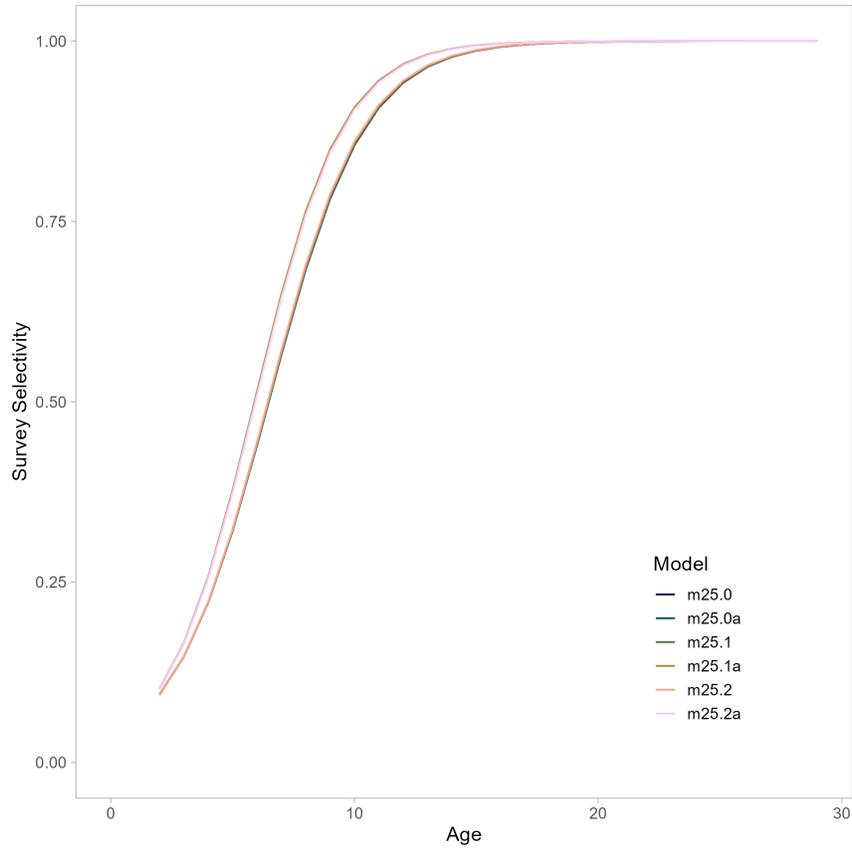
Figure 4: Survey selectivity using a double logistic model. Note that the reweighted model runs (suffix 'a') all have selectivity shifted to a younger age.

Table 3: Model negative log-likelihood values (nLL) for comparing multiple GOA Pacific ocean perch assessments with data or model changes. Model changes are incremental: m25.0 is the base model, m25.1 updates the survey and catch likelihoods, m25.2 estimates the 2nd fishery selectivity time block using a gamma function. The 'a' suffix indicates results after accounting for Francis reweighting.

nLL	m25.0	m25.1	m25.2	m25.0a	m25.1a	m25.2a
Catch	0.2180	-87.1079	-87.1519	0.1346	-87.1916	-87.1940
Survey biomass	16.4416	7.1398	7.2336	17.1892	7.9515	7.9359
Fishery age comp	25.0028	25.0405	26.6269	64.6063	64.2468	65.4342
Survey age comp	29.2822	29.3050	29.4795	54.0828	53.7983	53.1489
Fishery length comp	66.2259	66.2495	65.7574	38.5566	38.5669	39.1706
Recruitment devs	10.6027	10.4306	8.8914	12.2152	11.9558	13.6457
F regularity	6.1405	6.1610	6.0169	6.3002	6.3238	5.7957
SPR penalty	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
M prior	0.4241	0.4524	0.2830	0.1485	0.1651	0.1829
q prior	1.8299	1.8760	2.5295	0.6144	0.6499	0.6904
Sigma R prior	7.9849	8.0188	8.3253	7.6706	7.7207	7.3971
Sub total	164.1527	67.5657	67.9916	201.5183	104.1873	106.2074
# Parameters	168	168	170	168	168	170

Table 4: Key parameters and output values for comparing multiple GOA Pacific ocean perch assessments with data or model changes. Model changes are incremental: m25.0 is the base model, m25.1 updates the survey and catch likelihoods, m25.2 estimates the 2nd fishery selectivity time block using a gamma function. The 'a' suffix indicates results after accounting for Francis reweighting.

Item	m25.0	m25.1	m25.2	m25.0a	m25.1a	m25.2a
M	0.0743	0.0745	0.0769	0.0686	0.0688	0.0691
a50-1	6.2965	6.2958	6.1283	6.1884	6.1881	6.0098
a50-2	2.5239	2.5228	2.5690	2.5148	2.5141	2.6210
a50-3	2.7987	2.7987	2.5286	2.7460	2.7461	2.5202
a50-4	-	-	2.8002	-	-	2.7496
delta-1	1.9582	1.9563	1.5857	1.8663	1.8655	1.4743
delta-2	5.0275	5.0222	5.9092	4.9106	4.9064	6.4689
delta-3	9.6824	9.6681	4.9872	9.2424	9.2347	4.9449
delta-4	-	-	9.6805	-	-	9.2765
a50 survey	5.4801	5.4723	5.4425	4.9025	4.8998	4.9312
delta survey	5.8192	5.8043	5.7522	5.2794	5.2732	5.3115
q	1.7361	1.7598	1.6100	1.4673	1.4870	1.5072
sigma R	0.7644	0.7631	0.7517	0.7767	0.7747	0.7877
Log mean recruitment	4.4492	4.4562	4.5778	4.4765	4.4845	4.4737
Log mean F	-2.6131	-2.6188	-2.6663	-2.7271	-2.7330	-2.6963
2024 Total biomass	649,939	654,617	720,106	734,920	739,725	731,703
2024 Spawning biomass	227,991	229,412	251,853	268,324	269,872	266,341
2024 OFL	47,466	47,883	53,959	49,483	49,909	49,574
2024 F OFL	0.1192	0.1196	0.1229	0.1078	0.1081	0.1086
2024 ABC	39,719	40,066	45,133	41,659	42,016	41,718
2024 F ABC	0.0990	0.0993	0.1020	0.0901	0.0904	0.0907
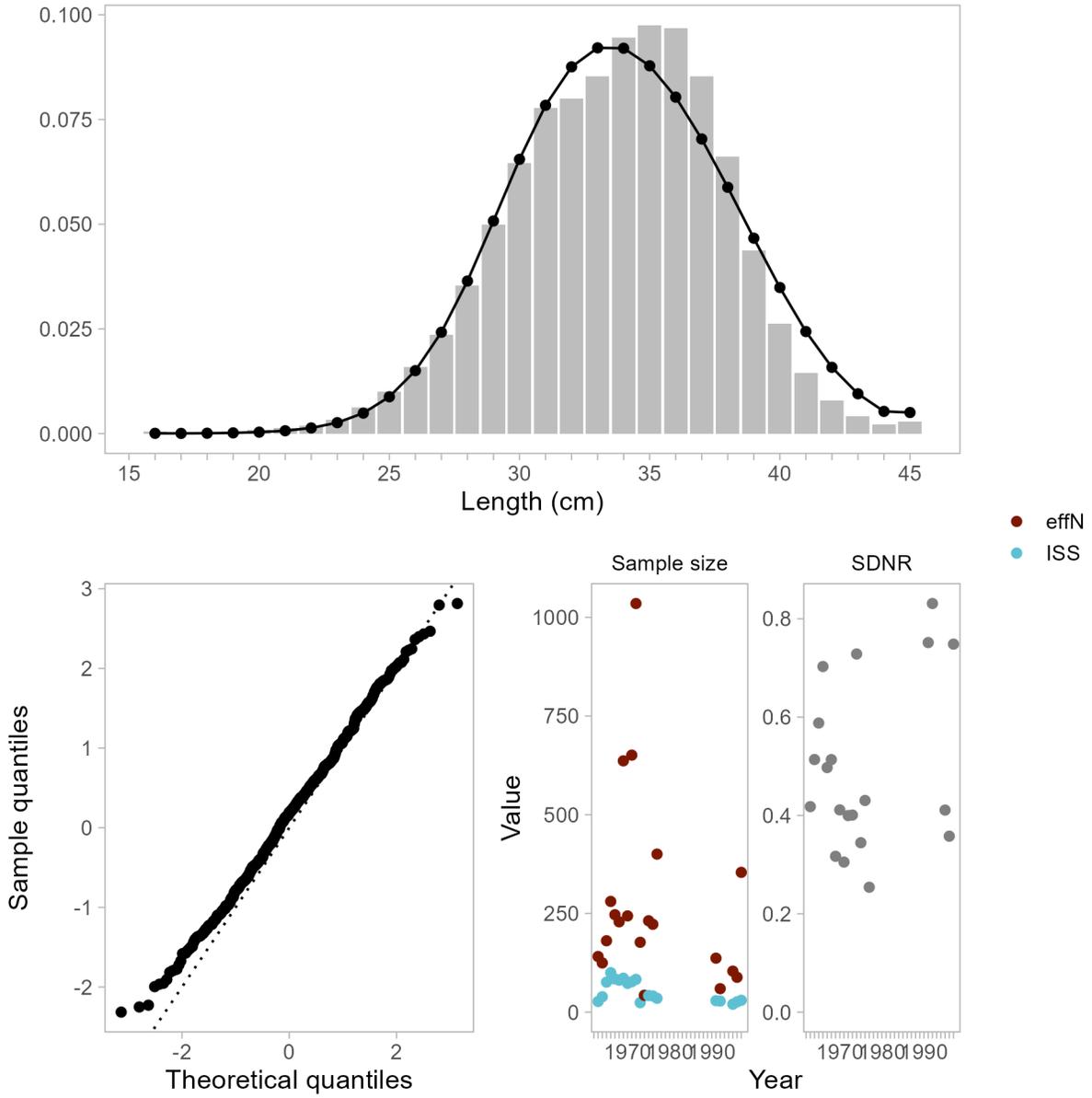
Figure 5: Fishery size composition aggregate composition data for Model 25.0.
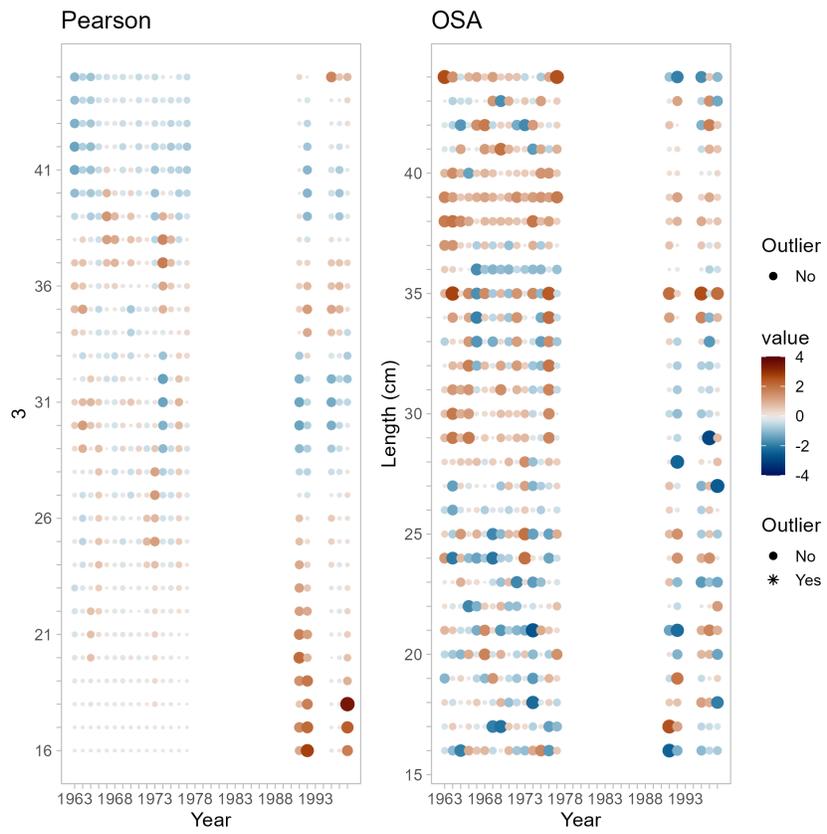
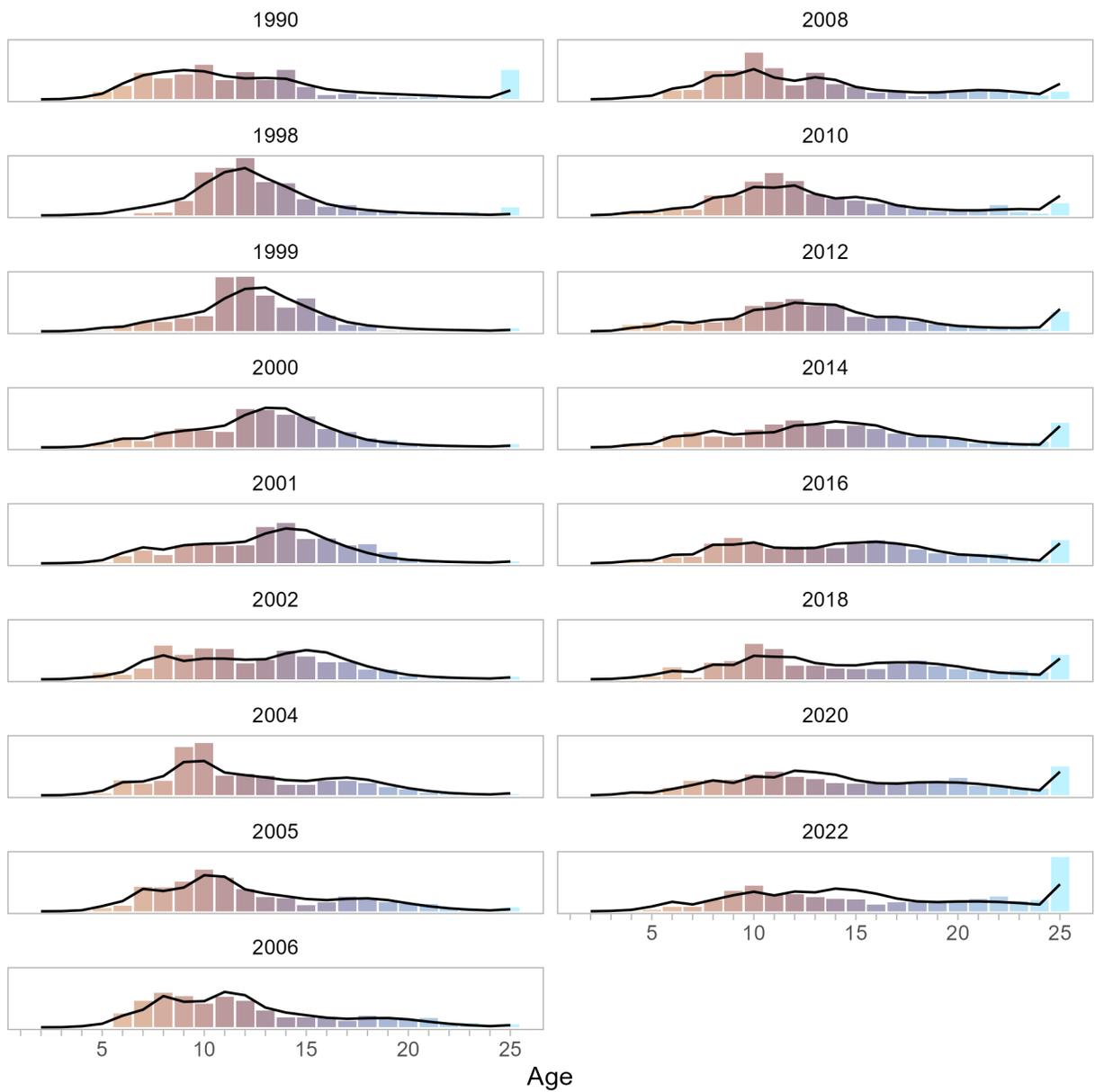Figure 6: Fishery size composition Pearson and one-step ahead (OSA) residuals for Model 25.0.
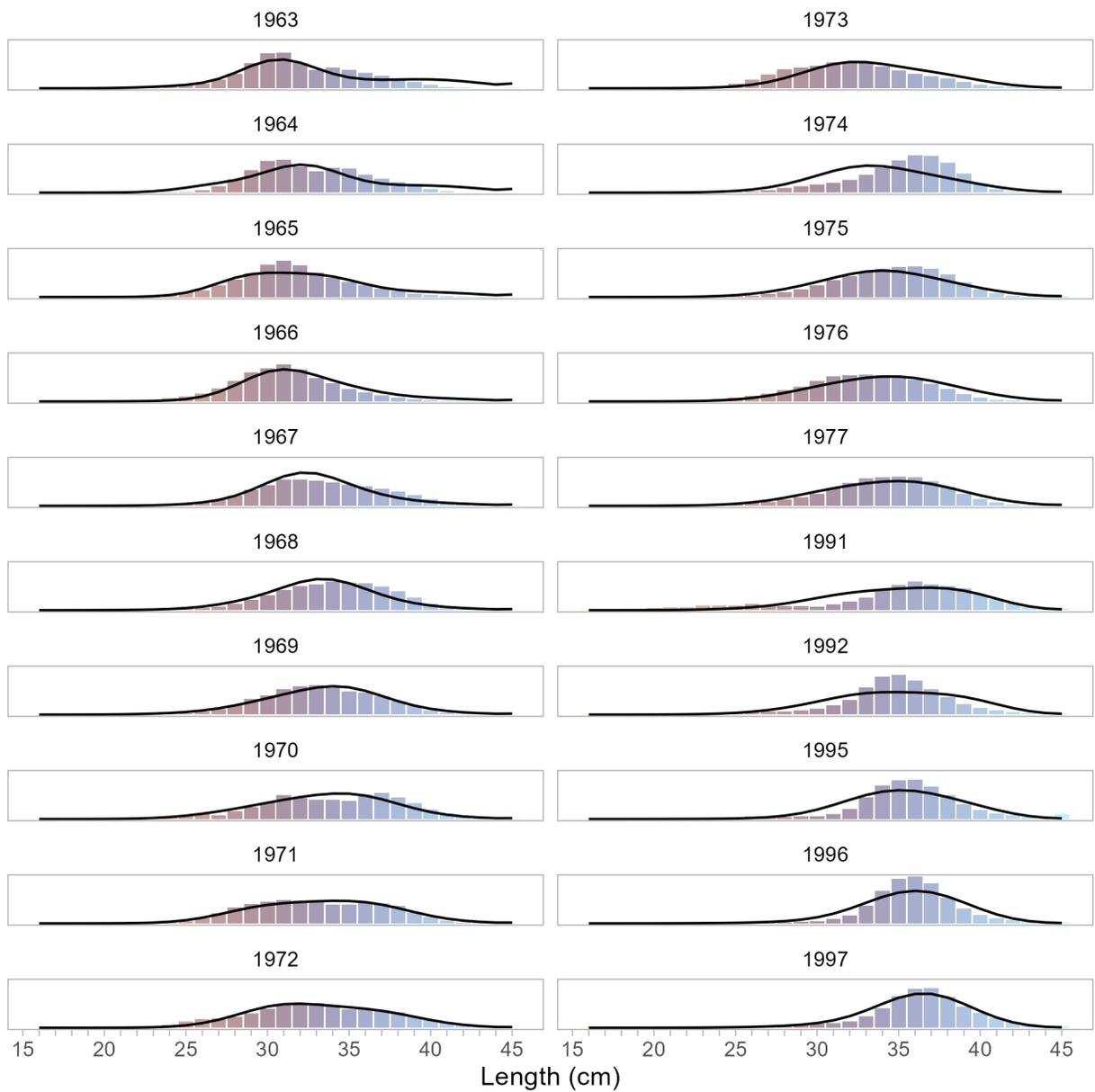
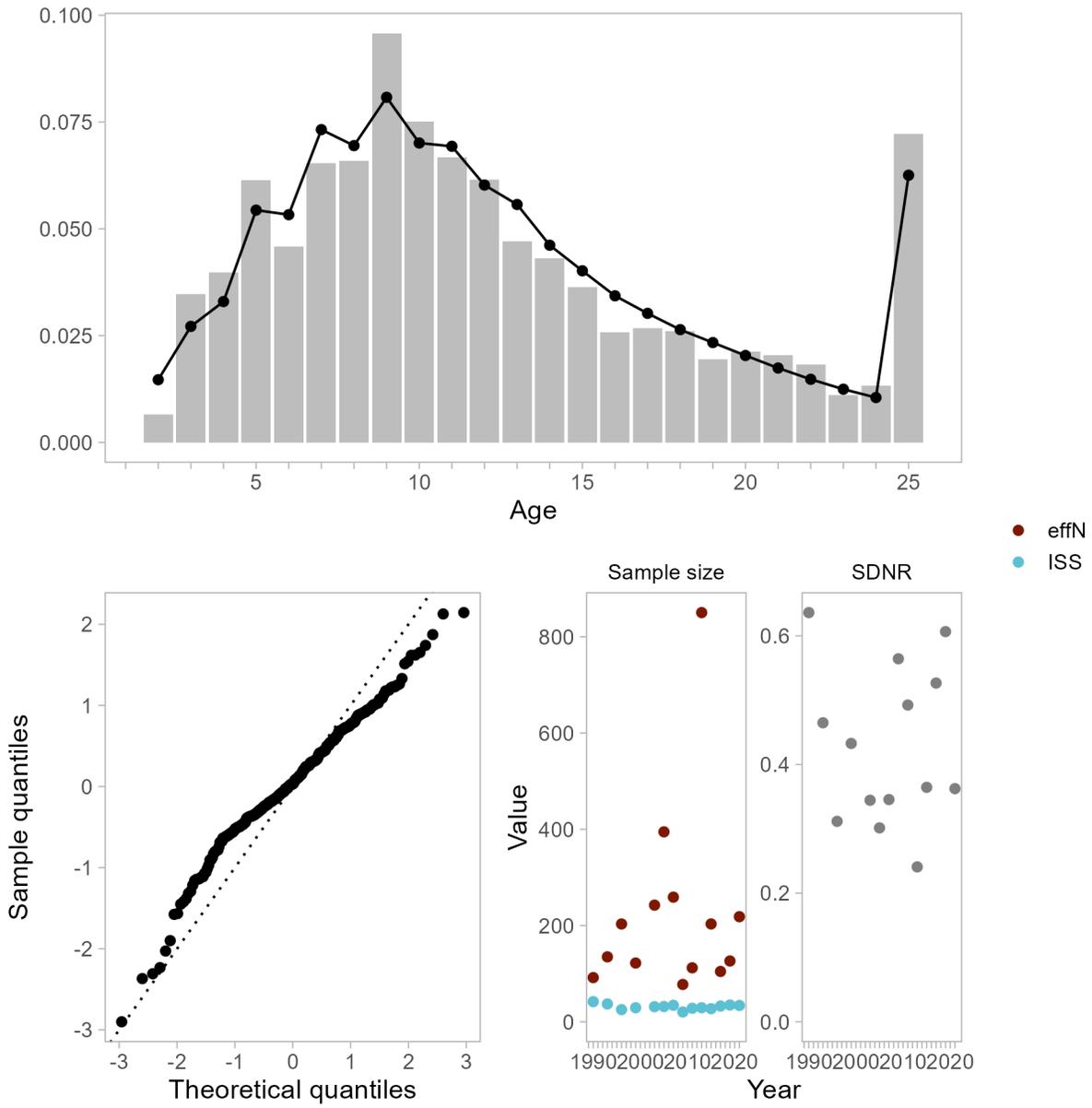Figure 7: Annual fishery size composition observations and estimates for Model 25.0.
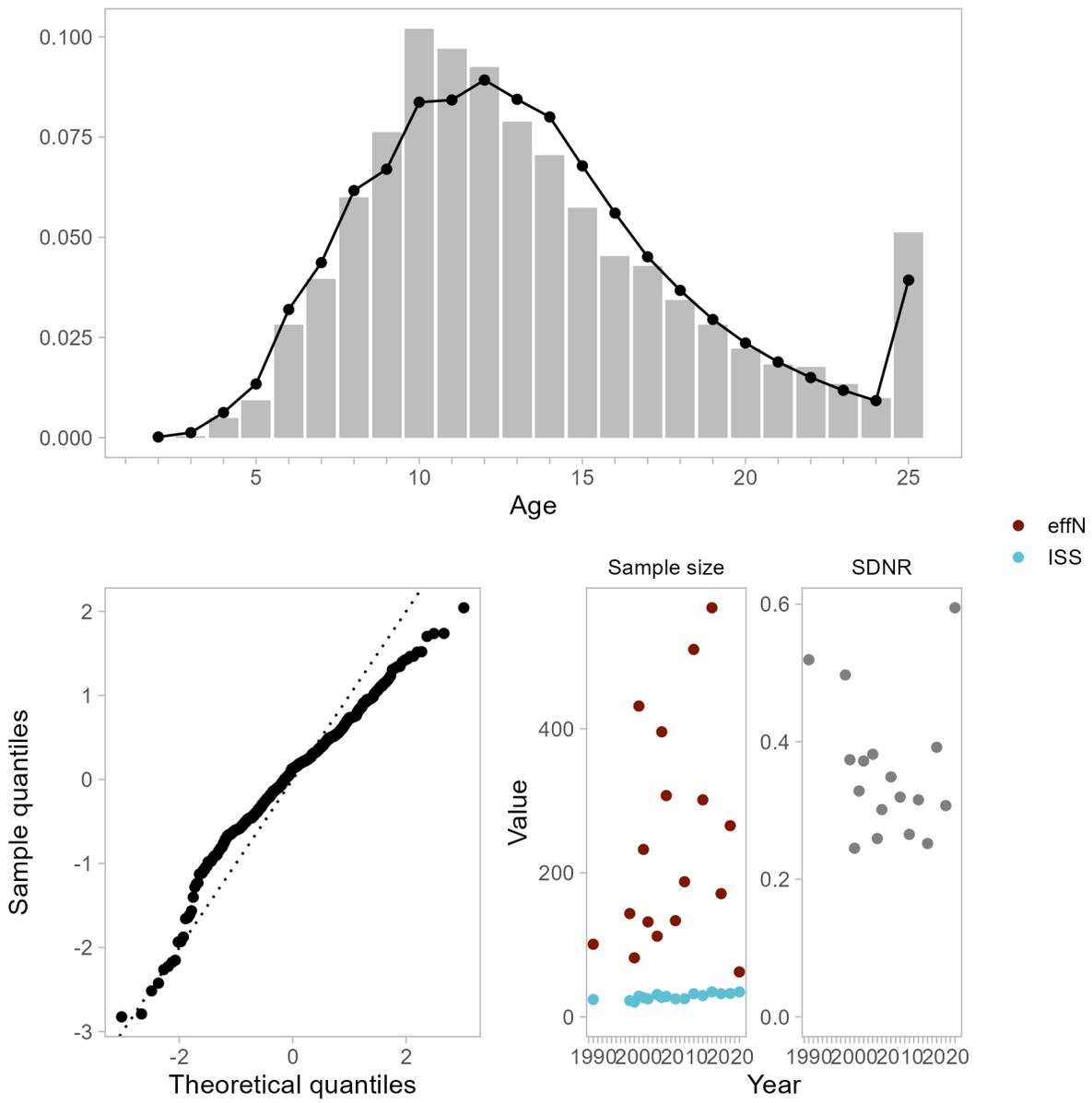
Figure 8: Fishery age composition aggregate composition data for Model 25.0.
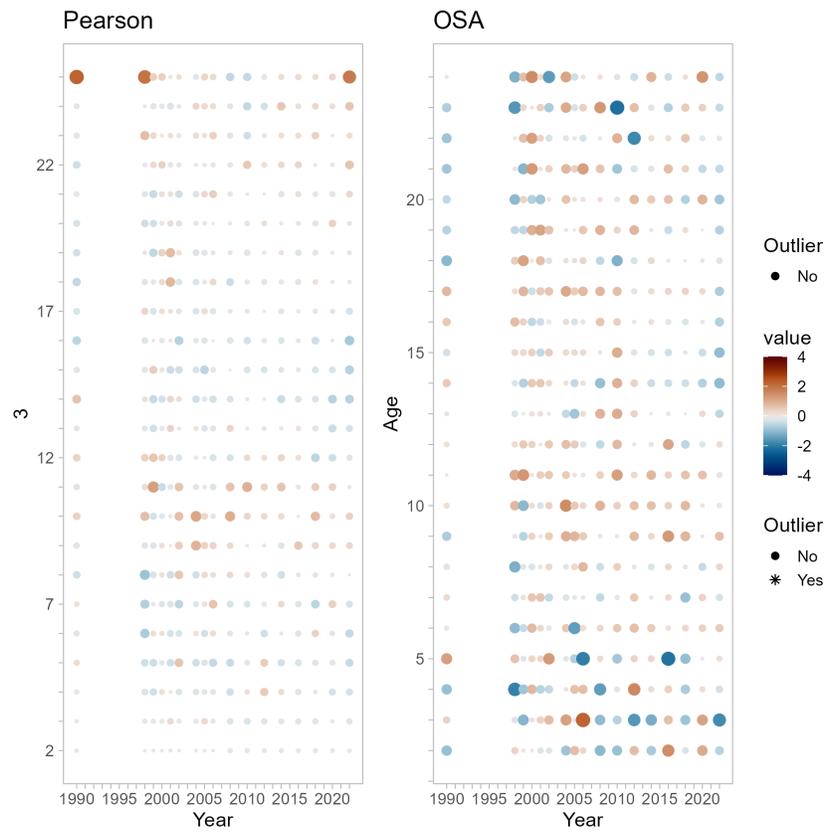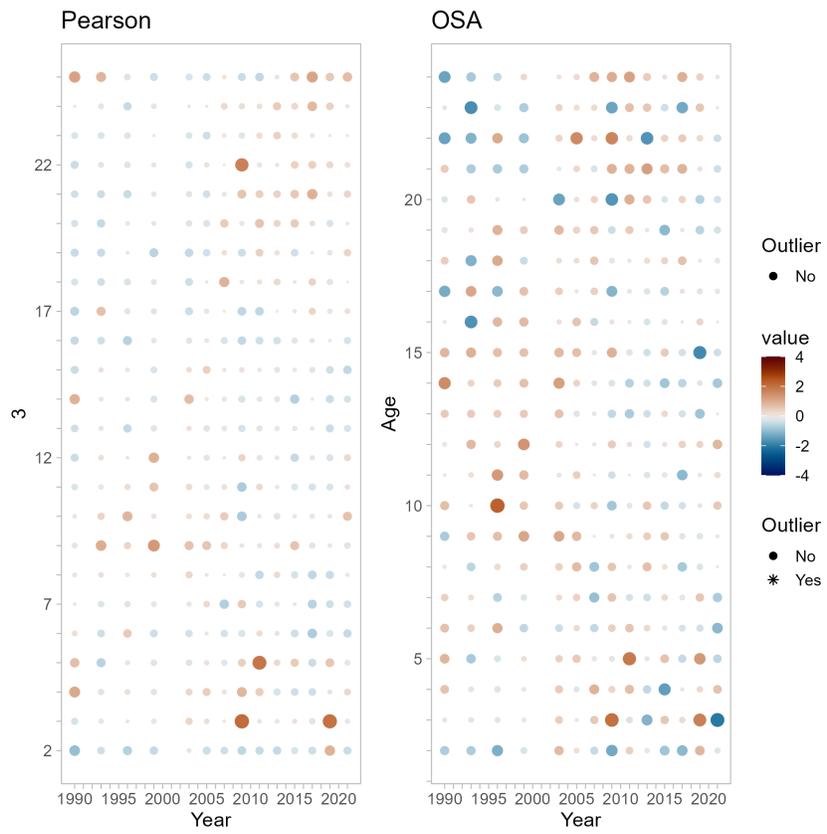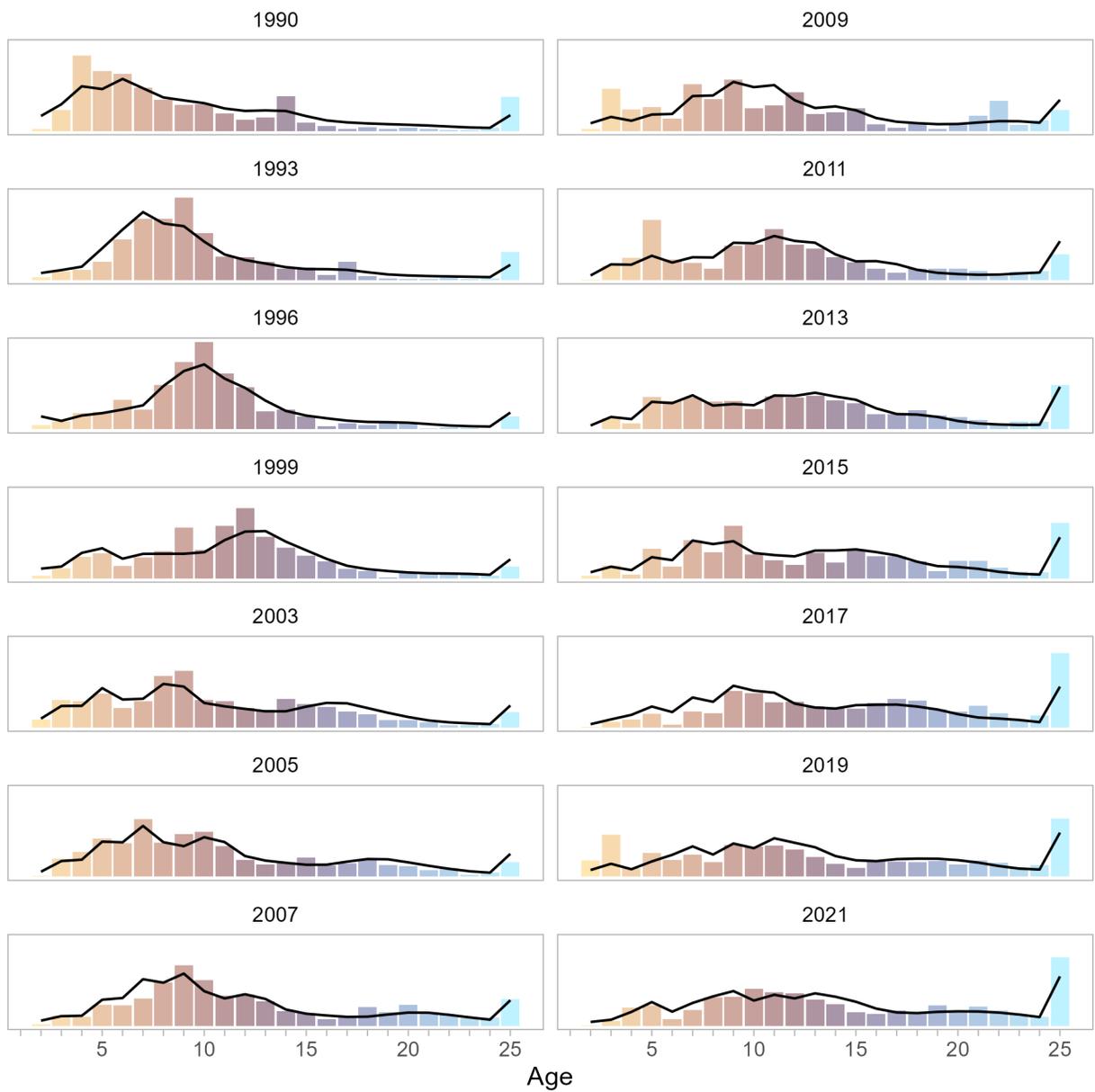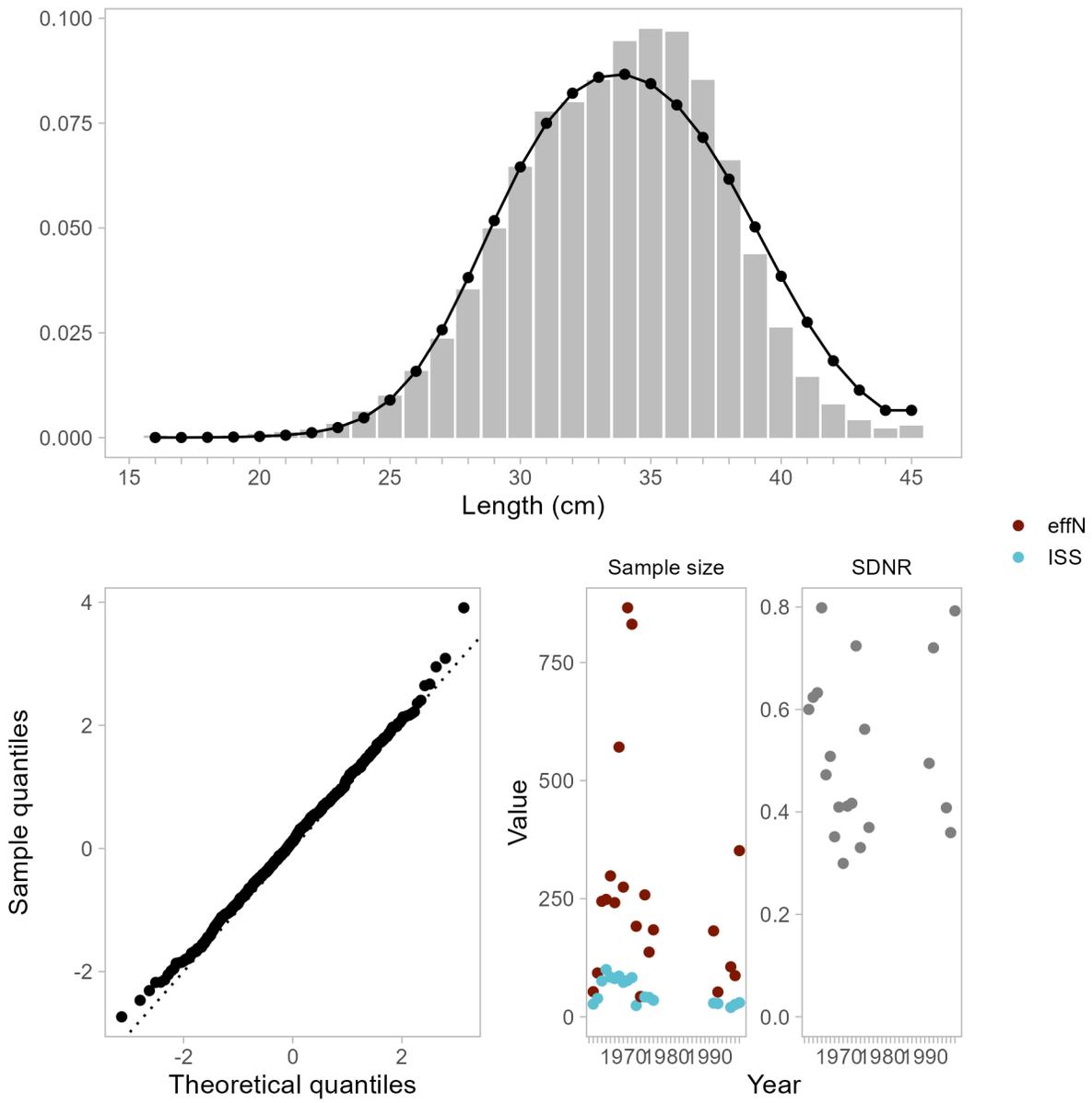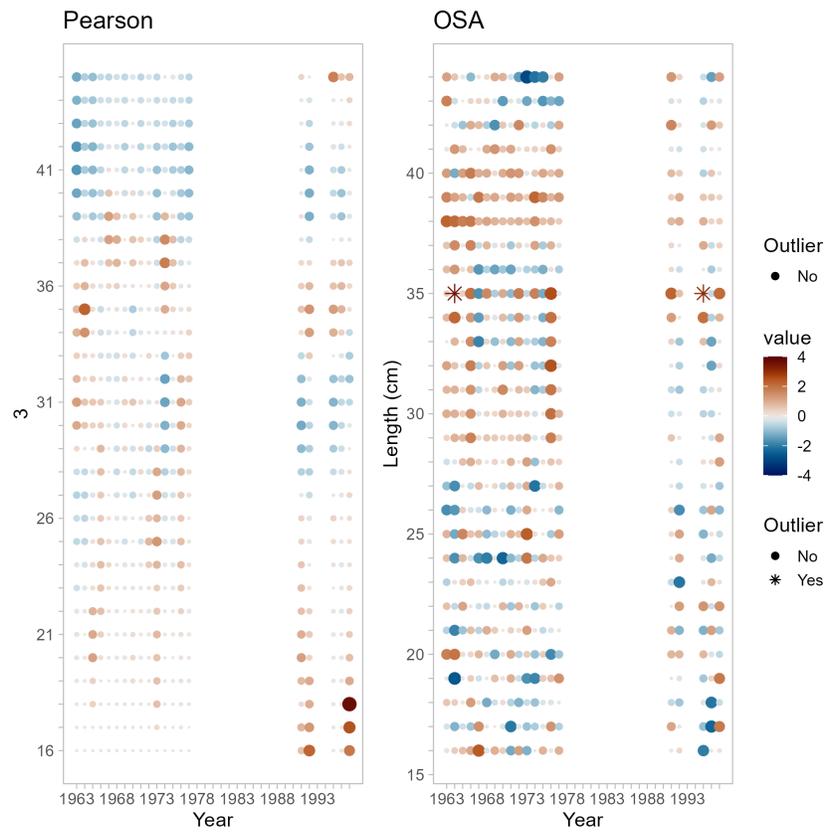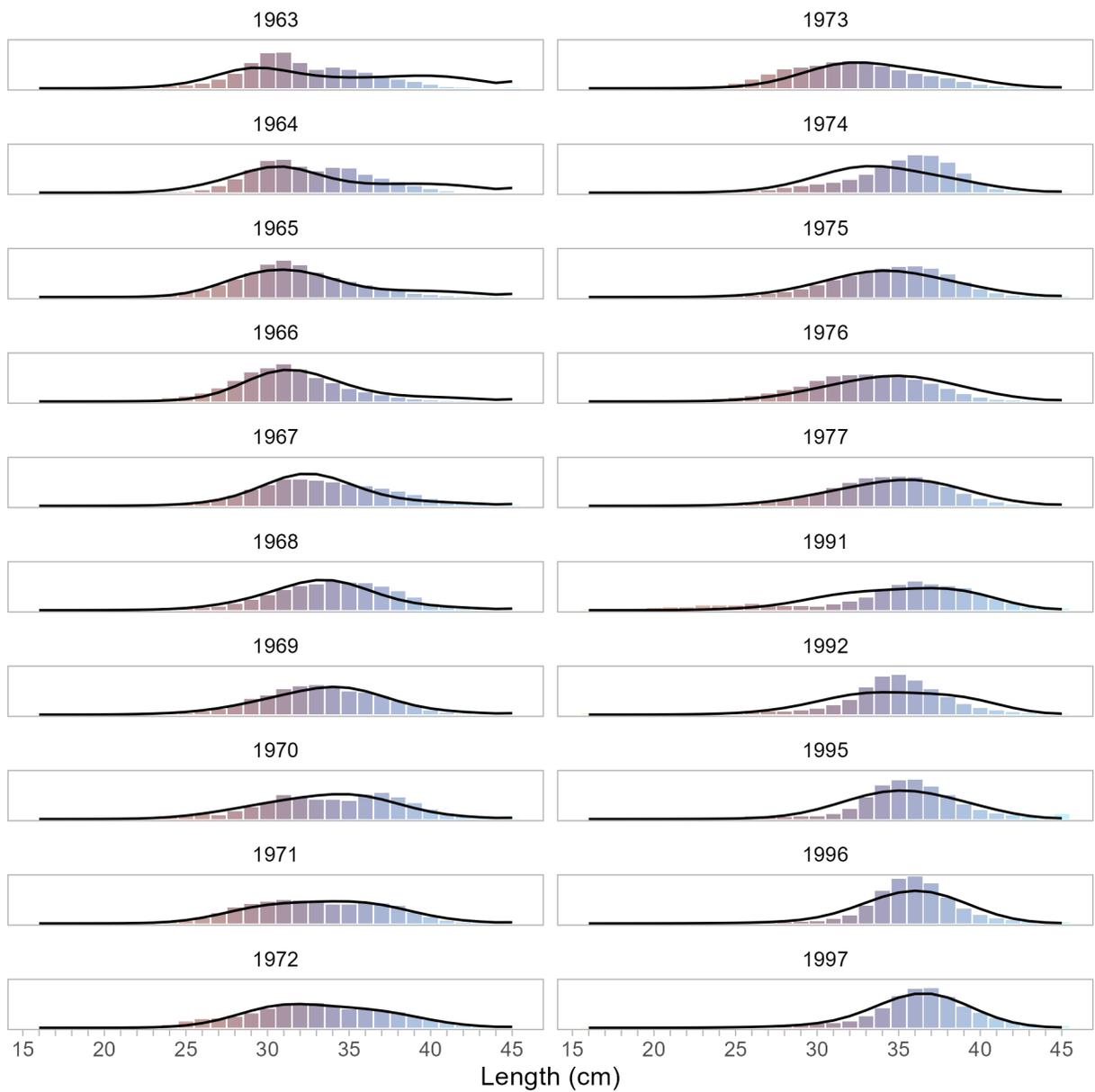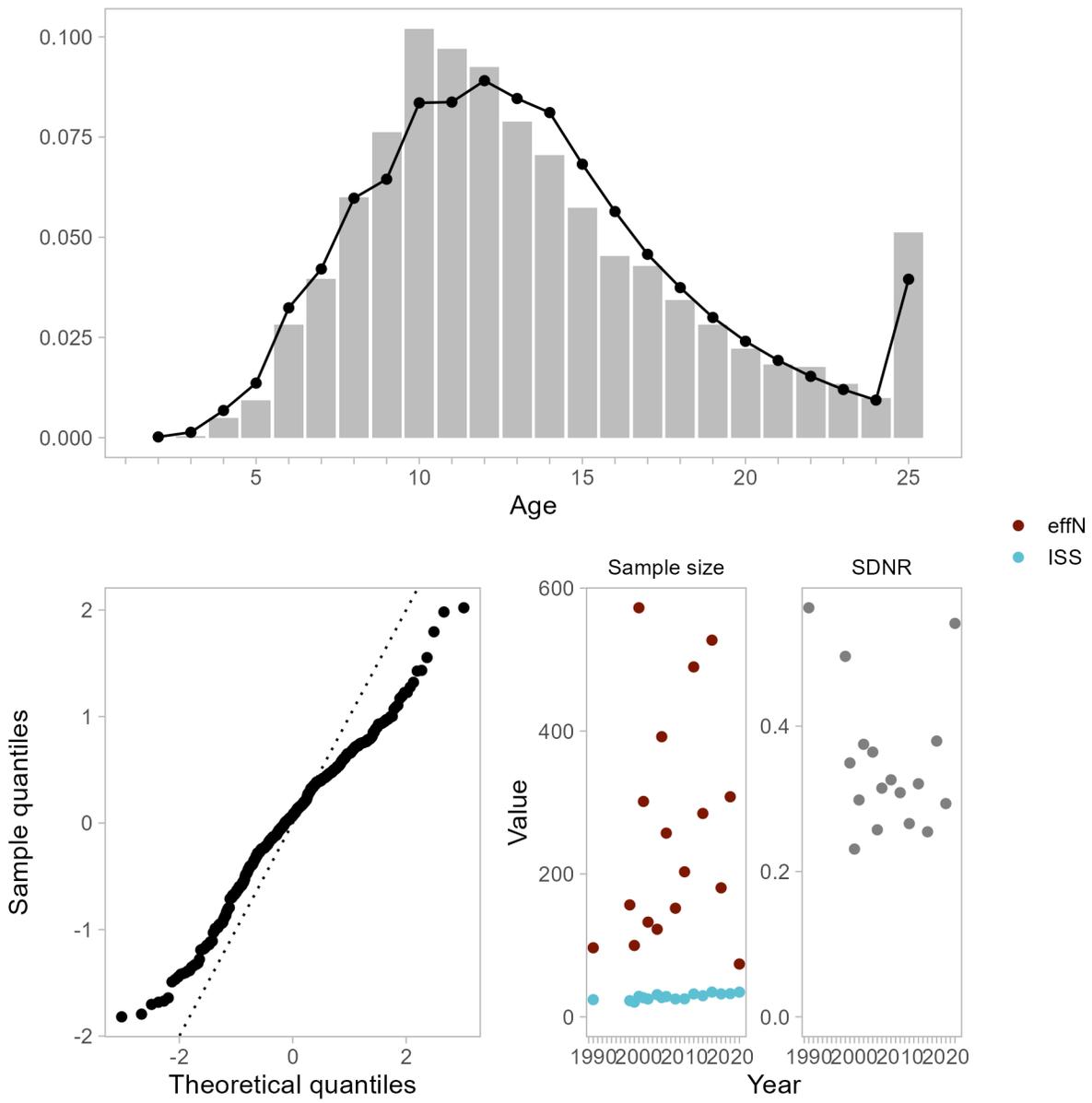
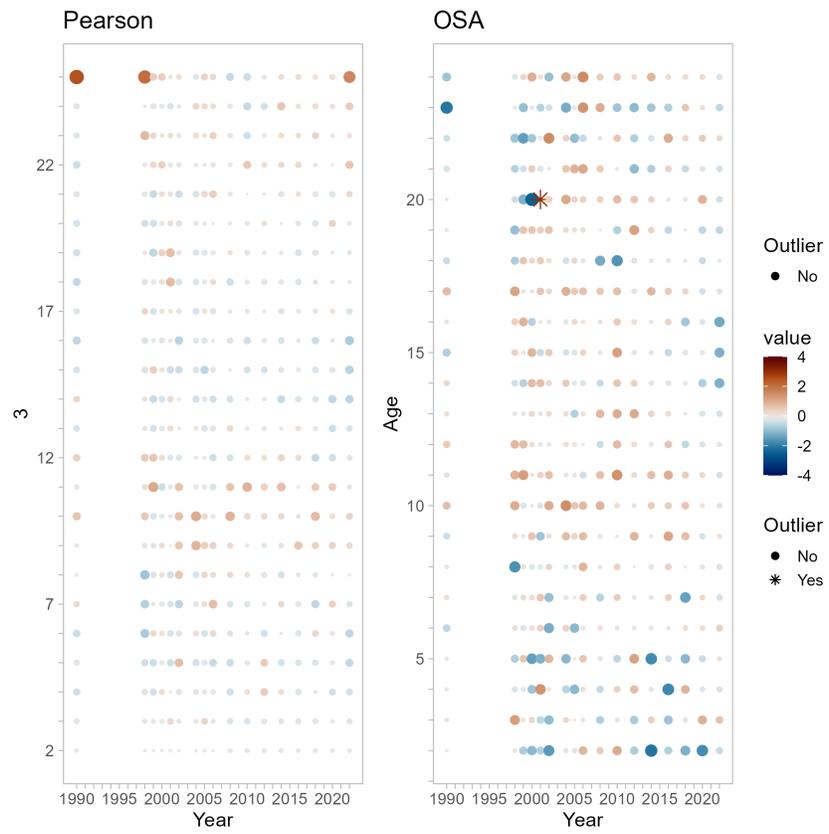Figure 9: Fishery age composition Pearson and one-step ahead (OSA) residuals for Model 25.0.
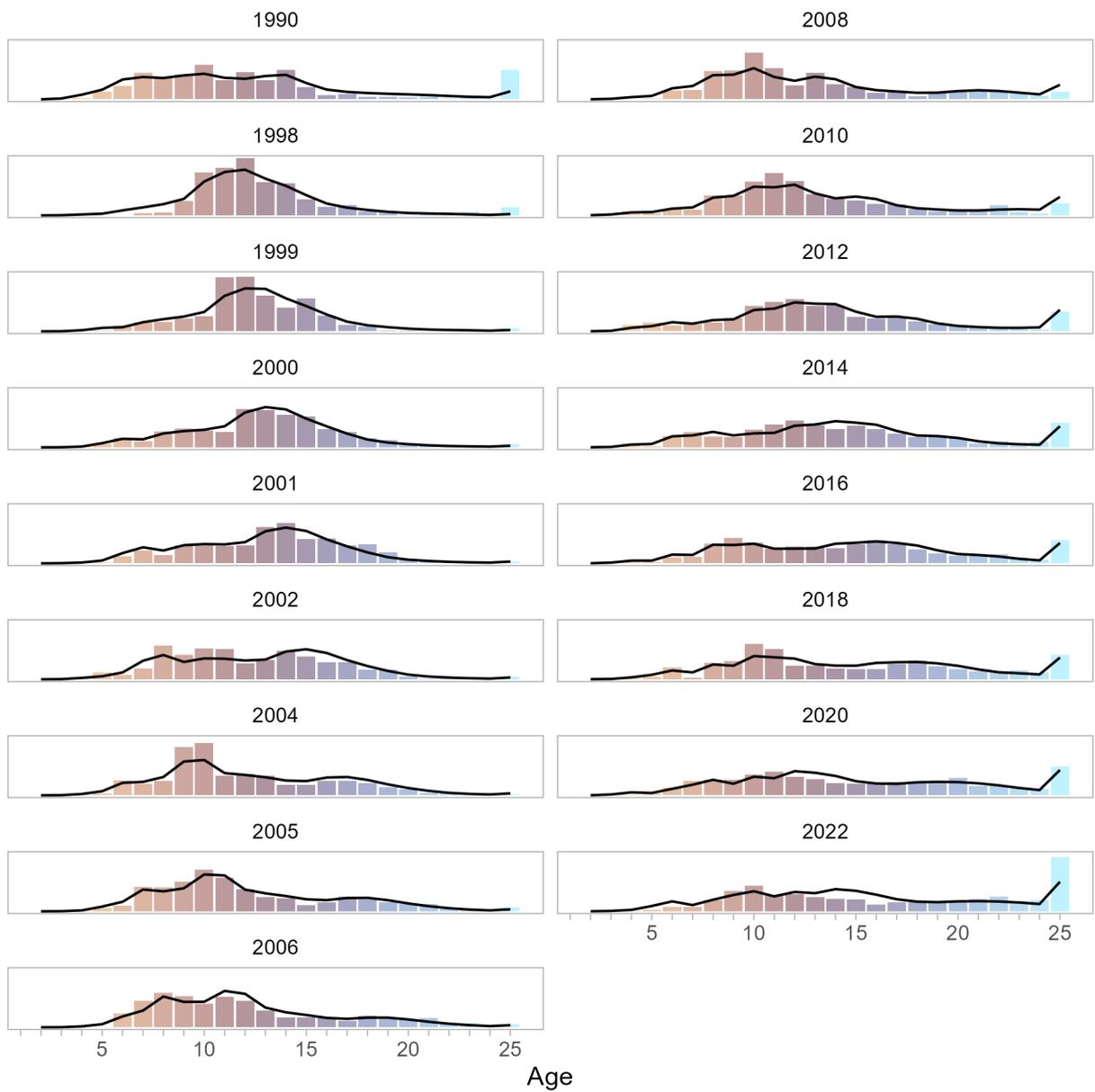
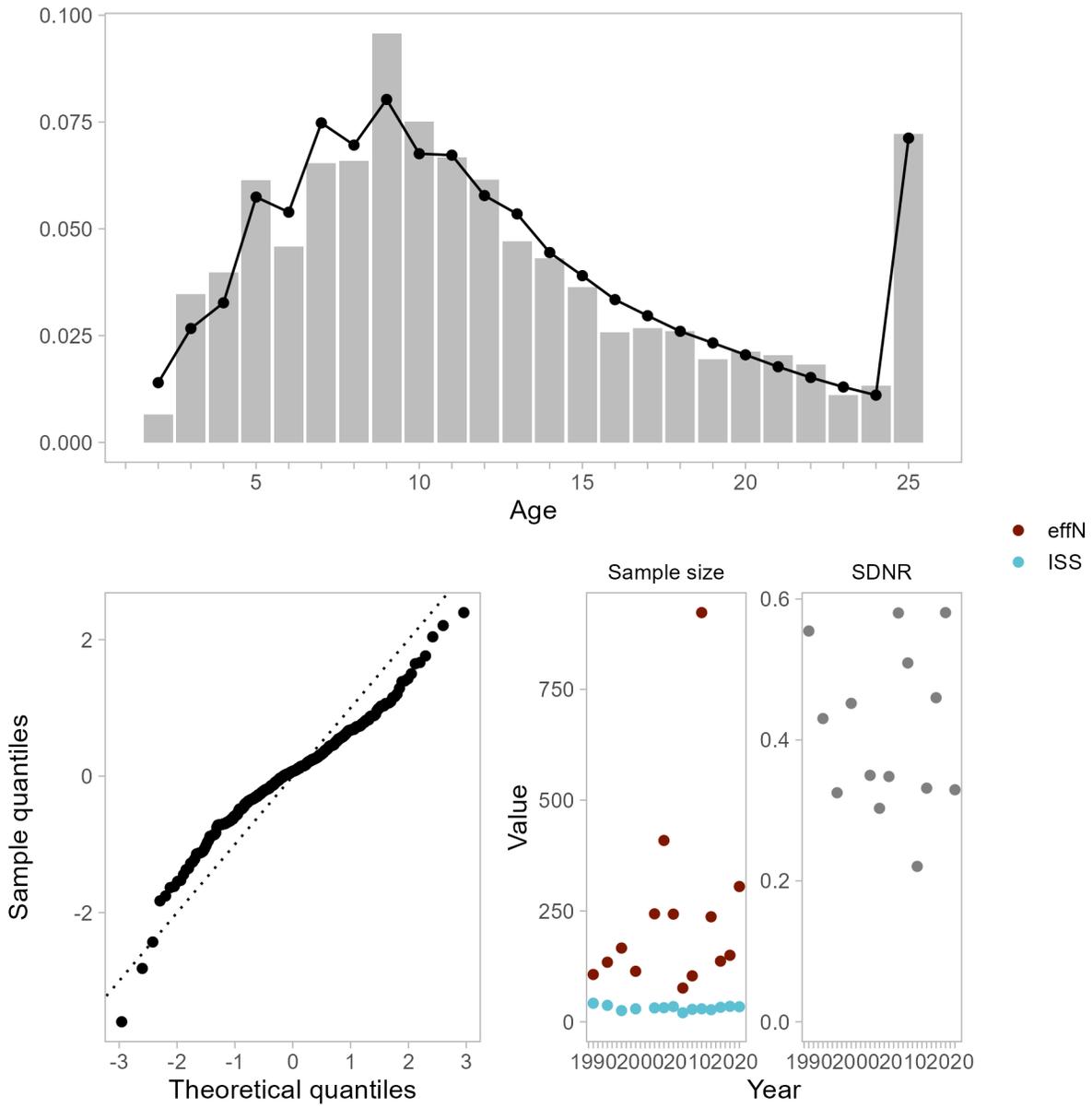Figure 10: Annual fishery age composition observations and estimates for Model 25.0.

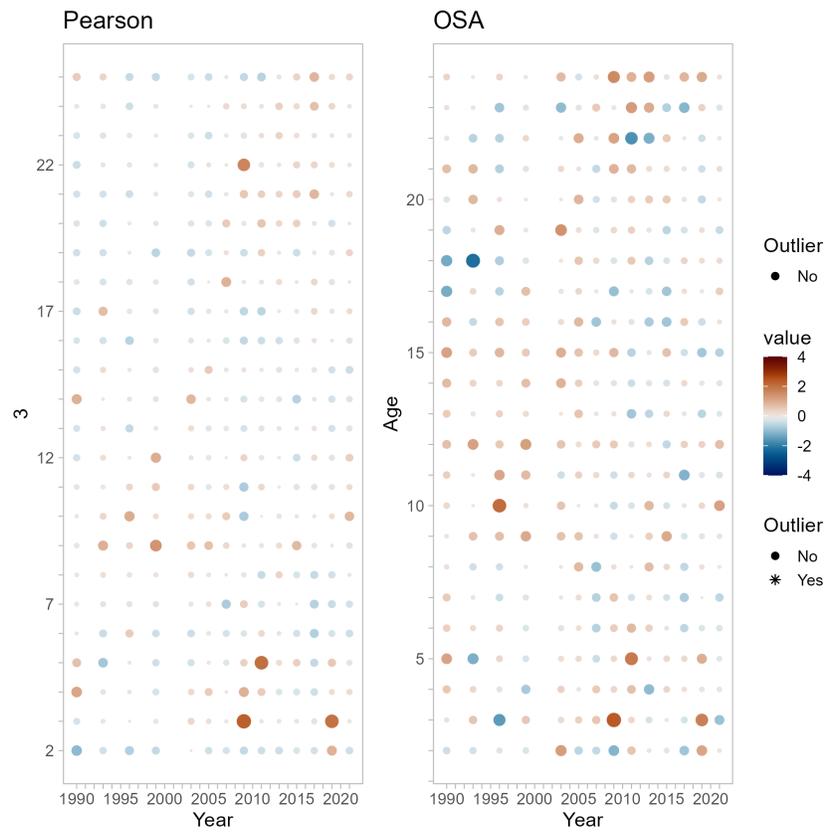Figure 11: Survey age composition aggregate composition data for Model 25.0.

Figure 12: Survey age composition Pearson and one-step ahead (OSA) residuals for Model 25.0.

Figure 13: Annual survey age composition observations and estimates for Model 25.0.

Figure 14: Fishery size composition aggregate composition data for Model 25.2a.

Figure 15: Fishery size composition Pearson and one-step ahead (OSA) residuals for Model 25.2a.

Figure 16: Annual fishery size composition observations and estimates for Model 25.2a.

Figure 17: Fishery age composition aggregate composition data for Model 25.2a.

Figure 18: Fishery age composition Pearson and one-step ahead (OSA) residuals for Model 25.2a.
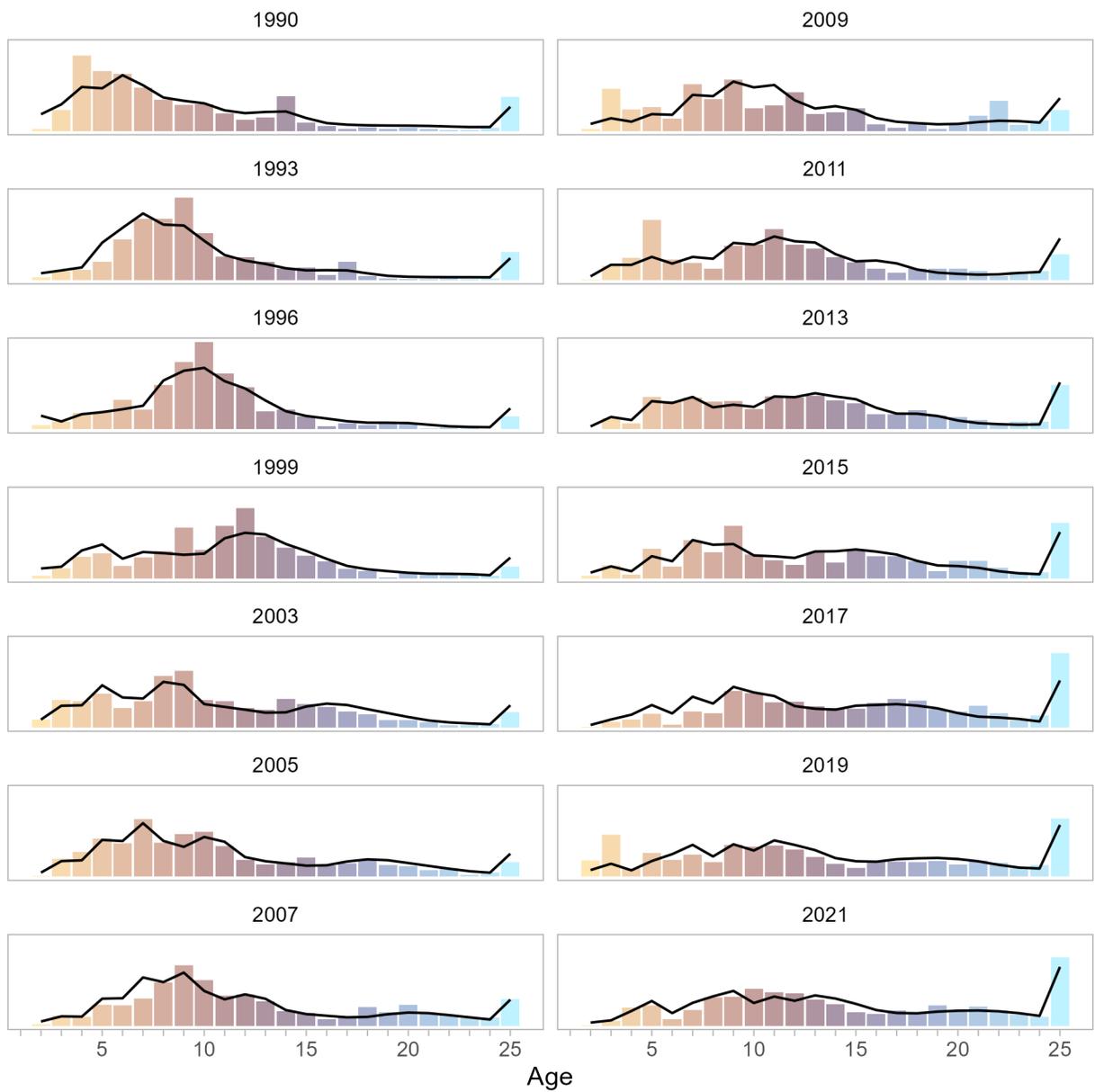
Figure 19: Annual fishery age composition observations and estimates for Model 25.2a.

Figure 20: Survey age composition aggregate composition data for Model 25.2a.

Figure 21: Survey age composition Pearson and one-step ahead (OSA) residuals for Model 25.2a.

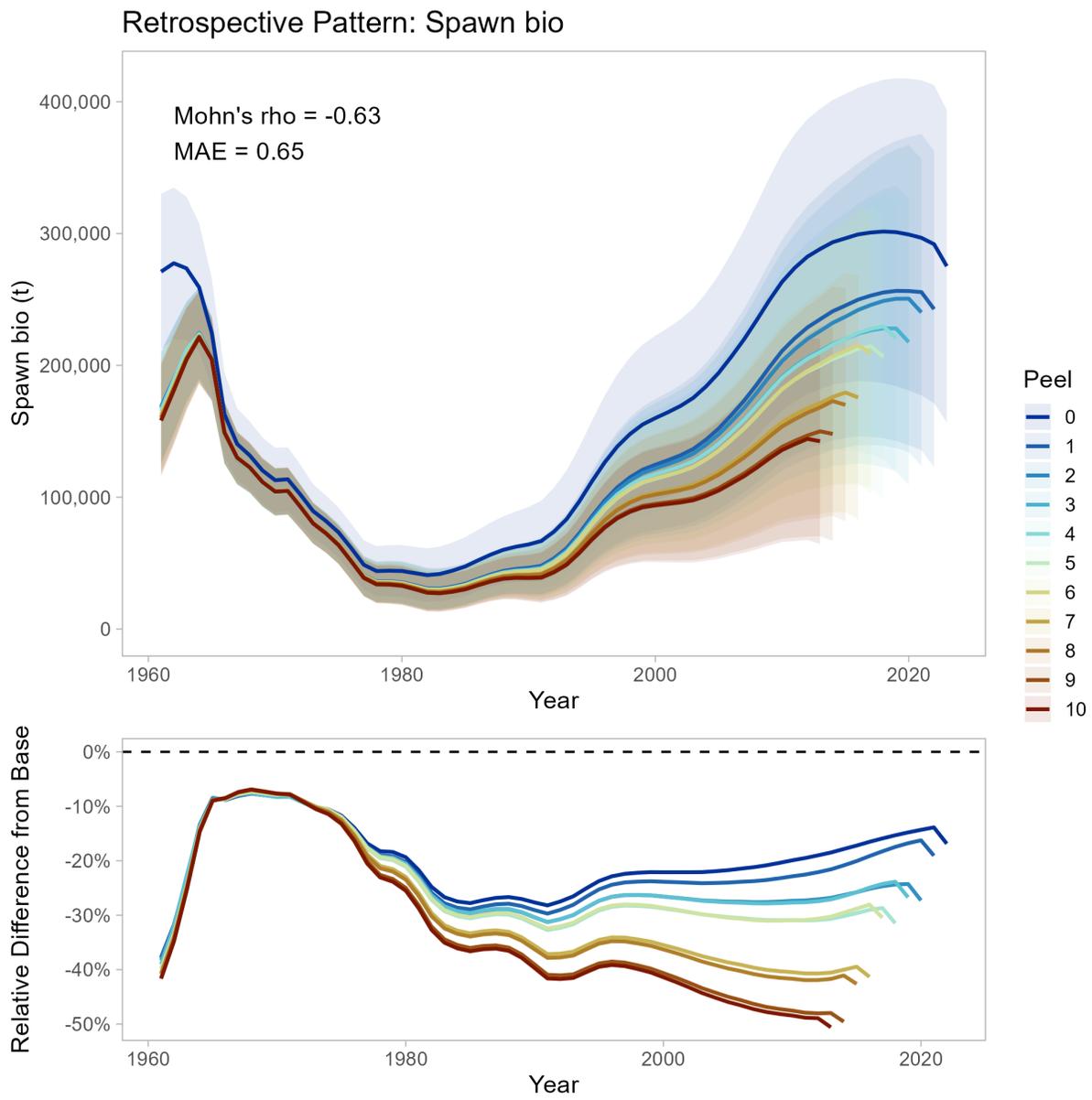Figure 22: Annual survey age composition observations and estimates for Model 25.2a.

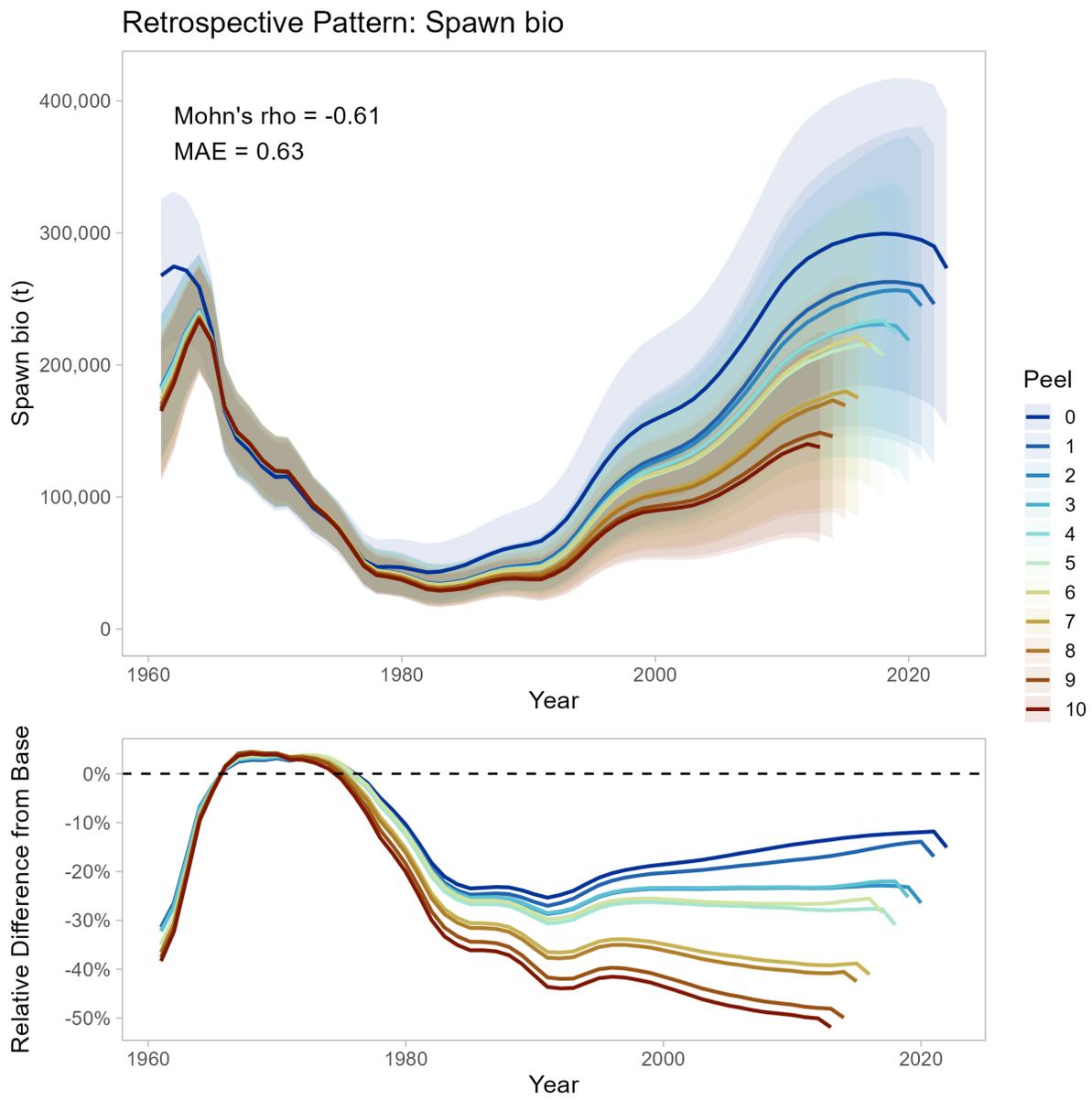Figure 23: Spawning biomass retrospective patterns for Model 25.0.

Figure 24: Spawning biomass retrospective patterns for Model 25.2a.