



**SCIENTIFIC COMMITTEE
TWENTY-SECOND REGULAR SESSION**
11-19 August 2026
Apia, Samoa (Hybrid)

**INVESTIGATION OF THE IMPACTS OF REGIONAL GROWTH VARIATION ON THE
2023 BIGEYE TUNA STOCK ASSESSMENT**

WCPFC-SC22-2026-SA-IP11

11 July 2026

Submitted by John Hampton¹²³, Nick Davies¹⁴ and Paul Hamer¹

¹ Oceanic Fisheries Programme of the Pacific Community (SPC)

² Thunnidae Consulting, Brisbane, Australia

³ University of Wollongong, Wollongong, Australia

⁴ Te Takina Ltd, Whangarei, New Zealand

Investigation of the impacts of regional growth variation on the 2023 bigeye tuna stock assessment

John Hampton, Nick Davies and Paul Hamer

Executive summary

Integrated age-structured stock assessment models with spatial structure typically assume that demographic parameters such as growth are uniform across the entire stock area, despite evidence that growth in large pelagic species often varies spatially. This paper investigates the potential impact of regional growth variation on the 2023 Western and Central Pacific bigeye tuna (*Thunnus obesus*) stock assessment conducted using MULTIFAN-CL (MFCL). Regional growth curves were estimated for eight assessment regions (combining the small region 9 with adjacent region 5) using standalone single-region MFCL models fitted to size and conditional age-at-length data. These region-specific growth estimates were used to derive regional catches-at-age, which were then incorporated into a full spatial assessment model (the “regional growth model”) and compared against a control model in which a common growth curve was applied across all regions. Growth curves for the northern regions (1 and 2) and, to a lesser extent, the southwest region (5+9) showed markedly higher asymptotic lengths and slower growth rates than the tropical regions, with these differences more pronounced in weight-at-age. Despite only modest differences in catch age composition between models, the regional growth model produced lower estimates of population scale and a moderately more pessimistic stock assessment, with recent spawning biomass depletion estimated at approximately 0.22 compared to 0.30 for the control model. The results suggest that regional growth variation can meaningfully influence stock assessment outcomes. Further investigation using models with reduced spatial complexity is recommended to better understand the mechanisms driving these differences and to inform future assessments. Further development of MULTIFAN-CL to allow for regional estimation or specification of natural mortality and maturity-at-age would also assist in further understanding the impacts of regional growth variation.

Introduction

Age-structured stock assessment models with spatial structure can estimate parameters such as movement and recruitment distribution so that estimates of recruitment, spawning biomass and fishing mortality are available by the regions defined in the model (Hampton and Fournier, 2001). This can provide potentially important information for the management of the fisheries that occur throughout the stock area.

While such models have spatial structure, typically through the definition of a limited number of regions (2–9 in most WCPFC tuna assessments), demographic parameters such as growth and maturity need to be assumed common across the entire spatial extent of the model. Growth is frequently influential on stock assessment results and is known to vary spatially, either because

of environmental variation, genetic differences, or both. Nevertheless, spatial variability in growth is extremely difficult to model effectively in age-structured models that incorporate movement among regions (Punt et al., 2020).

In this paper, we develop a version of the 2023 diagnostic case bigeye tuna stock assessment for the western and central Pacific Ocean (WCPO) using MULTIFAN-CL (MFCL) (Day et al., 2023) to test the importance of regional variation in growth. Regional growth variation is accommodated in the test model by first estimating growth and fishery catch-at-age in standalone single region models corresponding to the assessment model regions; and secondly, incorporating these catch-at-age estimates into the full regional model as catch-at-age samples, replacing the length- and weight-frequency data of the original model. Versions of this test model with (i) fishery catch-at-age determined assuming a common growth curve across regions; and (ii) fishery catch-at-age determined from the individual region models where growth is separately estimated, are compared to infer the impact of regionally variable growth.

Methods

Control model

The control model was developed from the 2023 bigeye tuna diagnostic case model (Day et al., 2023) using the following procedure:

1. Estimates of catch-at-age for each fishing incident were obtained from the fitted 2023 diagnostic case model. These estimates are found in the *ests.rep* output file beneath the label “Predicted catch at age by fishing incident”. They are produced by the diagnostic case model using the estimated growth curve and the weight-length relationship specified in the model. The derived catch-at-age is used in the model’s catch equations to support estimation of fishing mortality and other model parameters.
2. The catch-at-age estimates were divided by 1,000 and placed into a new MFCL input file *bet.frq* and the original length and weight composition data removed. These now represent perfectly representative “observed” age-frequency samples of the catch from each fishing incident.
3. In MFCL, fisheries may have catches represented as number or weight of fish caught. To avoid complications in subsequent testing, all catches that were recorded in weight in the diagnostic case model (all non-longline fisheries) were recast in numbers of fish simply by summing the estimated catch-at-age (before division) across ages for each fishing incident.
4. The model was then re-fitted but now using the catch-at-age “samples” replacing the length and weight composition data of the diagnostic case model. The catch-at-age data were fitted using a lognormal likelihood for the age-frequencies. The model included the same CPUE index and tagging data as used in the 2023 assessment but did not include the conditional age-at-length data. This new model becomes our **control model** where no regional variation in growth occurs. Note that for a model fitting to “observed” catch-at-age, the estimation (or specification) of a growth curve is required only for the very limited purposes of assigning tag releases to age classes and computing spawning biomass using mean weights-at-age.

Regional growth model

The objective of the regional growth model was to incorporate regional growth variation into the estimates of catch-at-age. The procedure used to develop this model was as follows:

1. Growth models and corresponding catches-at-age were estimated for each assessment region individually through external analyses of the available size and conditional age-at-length data. These “external analyses” were single-region MFCL models, corresponding to each region of the 2023 bigeye tuna assessment, with the exception that the very small region 9 was combined with the surrounding region 5 for this purpose. The fisheries and data corresponding to each of these single-region models were identical to those in the 2023 diagnostic case model. Further details of these models are given in the next section.
2. The catch-at-age estimates for the regional fisheries from these models were assembled in the *bet.frq* file in the same way as in step 2 for the control model. The difference now is that these catch-at-age estimates reflect regional differences in growth through the separately estimated growth curves. All other data in the *bet.frq* file, including the specified catches in number of fish, were identical to that for the control model.
3. The model was fitted to the integrated data equivalent to the control model.
4. The region-specific growth curves were used to compute mean weights-at-age and the proportion mature-at-age by region, which in turn were incorporated into the computation of spawning biomass. Region-specific growth curves were not used in the allocation of tag releases to age-classes; this was done using the common growth curve.

Estimating regional growth curves

As noted above, growth curves for each region of the 2023 bigeye tuna assessment (Figure 1) were estimated based on the same catch (converted to number of fish were required), CPUE, size and conditional age-at-length data as used in the assessment. For this purpose, region 9 was combined with region 5; therefore, eight separate growth models were estimated.

Some constraints on the estimation of the eight single-region models needed to be applied to obtain stable estimates that were reasonably consistent. These included:

- The population scaling parameter ($\text{LN}(R_0)$) for each regional model was fixed according to the diagnostic case model and not estimated;
- Natural mortality scaling parameter was fixed and not estimated;

The size data for selected fisheries showing the best growth structure were upweighted in the likelihood, and other less informative fisheries down weighted. These settings are summarised in Table 1. Fisheries defined in the 2023 bigeye tuna assessment.

1. LL ALL 1	10. LL AU 5	19. PS JP 1	28. PL ALL 7	37. Index 5
2. LL ALL 2	11. LL ALL 5	20. PL JP 1	29. LL ALL 9	38. Index 6
3. LL US 2	12. LL ALL 6	21. PL ALL 3	30. PS ASS 7	39. Index 7
4. LL ALL 3	13. PS ASS 3	22. PL ALL 8	31. PS UNA 7	40. Index 8
5. LL OS 3	14. PS UNA 3	23. MISC ID 7	32. MISC VN 7	41. Index 9
6. LL OS 7	15. PS ASS 4	24. PS PHID 7	33. Index 1	
7. LL ALL 7	16. PS UNA 4	25. PS ASS 8	34. Index 2	
8. LL ALL 8	17. MISC PH 7	26. PS UNA 8	35. Index 3	

9. LL ALL 4	18. HL PHID 7	27. LL AU 9	36. Index 4	
-------------	---------------	-------------	-------------	--

- Table 2;
- The mean length of the youngest age class was not estimated and was fixed at the value obtained in the 2023 assessment (23.3 cm). The rationale for this was to anchor the estimated growth curves with the same length at age 1 quarter, so that differences in subsequent growth are coming from a common base.

Results

Adequately converged fits were obtained for each of the eight regional models, and the eight estimated growth curves are shown in

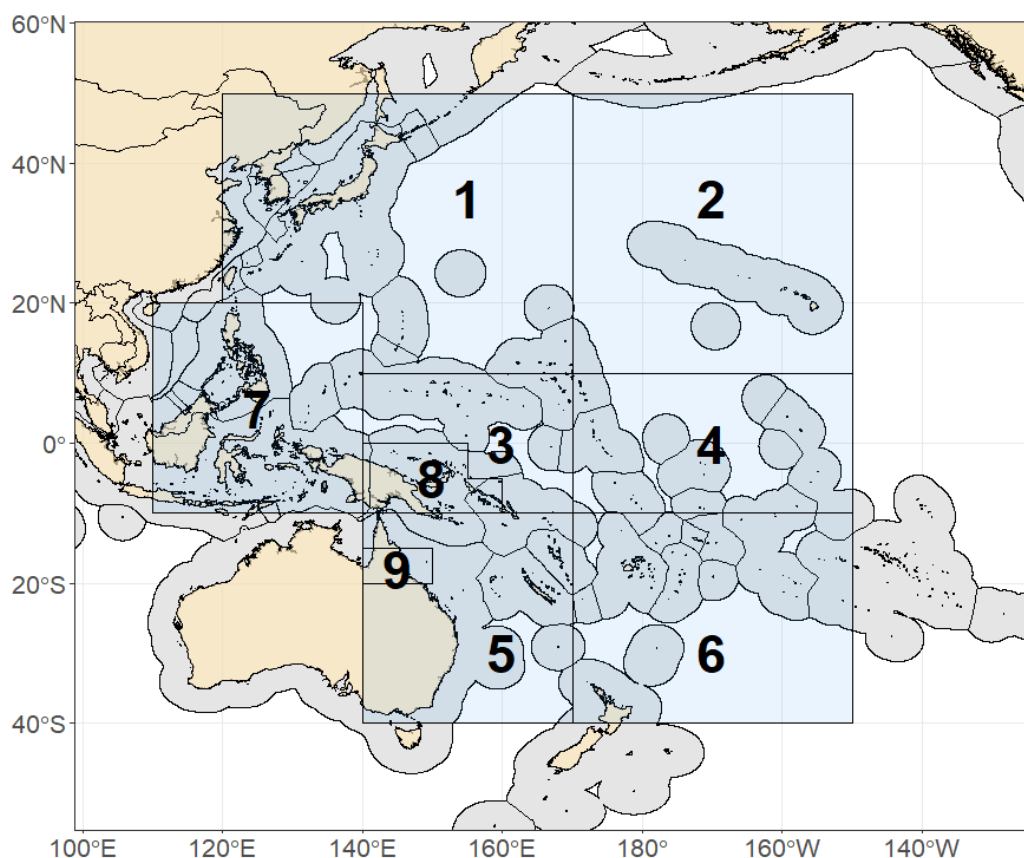


Figure 1. The nine-area model used for the 2023 bigeye tuna assessment.

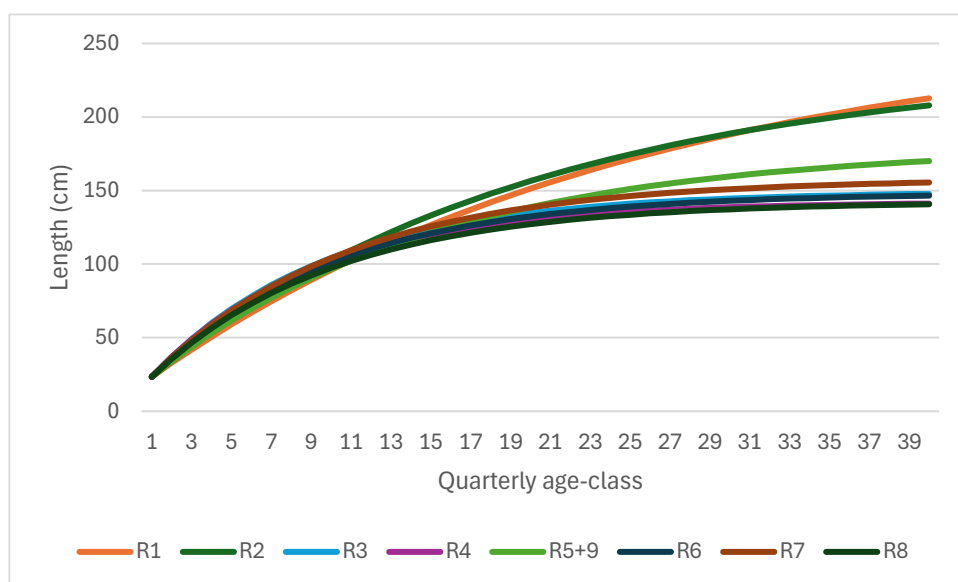


Figure 2. Similar curves were estimated for the tropical regions and the southeast region (3, 4, 7, 8, 6), and these estimated curves were also similar to the common growth curve estimated in the 2023 assessment (Figure 3). In contrast, the northern regions (1, 2) and to some extent the southwest region (5+9) had higher estimates of L_{40} and lower estimates of k (Table 1. Fisheries defined in the 2023 bigeye tuna assessment.

1. LL ALL 1	10. LL AU 5	19. PS JP 1	28. PL ALL 7	37. Index 5
2. LL ALL 2	11. LL ALL 5	20. PL JP 1	29. LL ALL 9	38. Index 6
3. LL US 2	12. LL ALL 6	21. PL ALL 3	30. PS ASS 7	39. Index 7

4. LL ALL 3	13. PS ASS 3	22. PL ALL 8	31. PS UNA 7	40. Index 8
5. LL OS 3	14. PS UNA 3	23. MISC ID 7	32. MISC VN 7	41. Index 9
6. LL OS 7	15. PS ASS 4	24. PS PHID 7	33. Index 1	
7. LL ALL 7	16. PS UNA 4	25. PS ASS 8	34. Index 2	
8. LL ALL 8	17. MISC PH 7	26. PS UNA 8	35. Index 3	
9. LL ALL 4	18. HL PHID 7	27. LL AU 9	36. Index 4	

Table 2. Various settings used for the individual single-region models, identified by Region. Fishery numbers correspond to those in Table 1. FF(49) - LF and FF(50) – WF refers to the effective length frequency (LF) and weight frequency (WF) sample size scalars applied to each fishery. “na” indicates were no data of that type were available for each fishery.

Region	Fisheries	LN(R0)	FF(49) - LF	FF(50) – WF
1	1, 19, 20, 33	1.474317	na, 100, 100, na	1, na, na, 1
2	2, 3, 34	1.438107	na, na, na	1, 1, 1
3	4, 5, 13, 14, 21, 35	1.452590	na, na, 100, 100, 100, na	1, 1, na, na, na, 1
4	9, 15, 16, 36	1.429888	na, 1, 1, na	1, na, na, 1
5+9	10, 11, 27, 29, 37	1.275700	na, na, na, na, na	1, 100, 100, 100, 100
6	12, 38	1.416663	na, na	1, 1
7	6, 7, 17, 18, 23, 24, 28, 30, 31, 32, 39	1.547590	na, na, 1, 1, 1, 1, 1, 1, 1, 1, na	1, 1, na, 1, na, na, na, na, na, na, 1
8	8, 22, 25, 26, 40	1.377807	na, 100, 1, 1, na	1, na, na, na, 1

Table 3, Figure 3). These differences are more pronounced for weight-at-age (Figure 4).

Differences in regional growth also influence the conversion of the proportion mature by length to the proportion mature-at-age, with the tropical regions having higher proportions mature for most age classes (Figure 5).

Examples of fits to the size (weight-frequency) data are shown in Figure 6. Most of the data show a distinctive modal structure (2 or 3 modes), with the modes very likely to represent annual cohorts arising from seasonal spawning. For the most part, the fitted models separate the modes, where present, by 4 quarters, indicating a consistent interpretation of annual cohorts.

A comparison of the age-frequency “data” (summed over time) for the control model (derived from the catch-at-age estimates of the 2023 diagnostic case model) and the regional growth model (derived from the catch-at-age estimates from the eight individual regional models) is shown in Figure 7. The differences are mostly subtle, but where they do occur, are skewed towards slightly older age distributions for the regional growth model. The most significant differences are seen in two region 1 fisheries, JP PS 1 and JP PL 1, where the regional growth model catch age distribution is shifted about one year older relative to the control model.

Both the control and regional growth models fit the age-frequency “data” very well. In the case of the control model, the fit is close to perfect (Figure 8). For the regional growth model, the fit also appears to be very good (Figure 9), although the log-likelihood value is substantially greater than that for the control model (Table 4). The regional growth model also had somewhat degraded log-likelihood values for both the tagging data and CPUE indices compared to the control model.

A comparison of selected parameter estimates from the two models is provided in Appendix 1. Points of note include:

- The estimates of natural mortality at age are practically identical. Note however that natural mortality is a global model estimate and the Lorenzen age-specific schedule of natural mortality cannot respond to the regional growth estimates in that model. The scaling of M however is independently estimated and is almost identical.
- The average regional distribution of total biomass is very similar for the two models. This would largely reflect the common CPUE indices that are a part of both models.
- The average distribution of recruitment across regions is quite different for the two models, with a much larger proportion of recruitment allocated to region 3 and a smaller proportion allocated to region 7 in the regional growth model.
- Estimates of selectivity-at-age vary for the two models, reflecting the differences in catch-at-age used as data.
- The estimates of overall population scaling, via the $\text{LN}(R_0)$ parameter, are very similar for the two models – 16.552 and 16.636 (or R_0 of 15.4 million and 16.8 million) for the control and regional growth models, respectively.

A summary of the main stock assessment results for the 2023 diagnostic case model, the control catch-at-age model and the regional growth catch-at-age model are provided in Figure 10. The trends in SB, SB depletion and recruitment are very similar across the three models. However, there are moderate differences in scaling across the models, with the 2023 model having the highest recruitment and SB, and more moderate depletion (higher depletion ratio). Differences between the 2023 diagnostic case model and the control catch-at-age model might be expected because the composition and weighting of the respective likelihood components is different. Notwithstanding this, comparisons between the control model and the regional growth model does provide an indication of how regional growth differences might impact the assessment results. Recent depletion ratios are estimated at around 0.3 for the control model and 0.22 for the regional growth model. In this instance, acknowledging differences in regional growth as they have been estimated here makes the assessment more pessimistic.

The differences in estimates of SB (Figure 11) and SB depletion (Figure 12) by region are generally consistent with this overall picture, with lower levels of regional SB and higher regional SB depletion estimated by the regional growth model. Interestingly, the largest divergences between the two models do not necessarily occur in the regions where the differences in growth are greatest. The largest differences in SB are seen in regions 3, 4 and 8 (all tropical), while the largest differences in SB depletion are in regions 1 and 5.

Discussion

This study provides a first attempt to estimate the possible impact of regional variation in bigeye tuna growth, and the consequential effects on estimates of catch-at-age, mean weight-at-age,

and proportion mature-at-age, on stock assessment results. Comparison of results from the control (common growth) model and the regional growth model indicates that, despite relatively small differences in catch age composition, incorporating regional growth results in reduced population scaling and a moderately more pessimistic assessment overall, but with variable differences depending on the model region. Not surprisingly in a complex spatial model such as this, it is difficult to ascribe the divergence in assessment results to particular model processes. It is possible that the larger size-at-age estimated for the northern regions under the regional growth hypothesis implies higher fishing impacts (and lower population size), consistent with the sensitivity to growth frequently observed in tuna stock assessments. However, there is considerable data conflict between the tagging and age composition data (see likelihood profile in Appendix 1), like the conflict between tagging and weight composition data in the 2023 assessment. The different assessment outcomes may also reflect, in part, the general complexity of the model and its sensitivity to relatively small changes in inputs — in this case mediated through the catch-at-age data.

Further work is recommended using models with reduced spatial complexity (such as planned for the 2026 bigeye tuna assessment) that are nevertheless able to capture the clear regional differences in growth estimated in this study. It would also be useful to further develop MFCL to allow for region-specific natural mortality, weight-length relationship and maturity at age, so that the growth-related effects on these processes could be incorporated. Also, it would be useful to develop a multinomial or Dirichlet multinomial likelihood function for the catch-at-age data, which seems a more natural likelihood for such data.

Finally, this test is indicative that future model software developments, such under **WCPFC Project 123: next generation tuna models**, should be mindful of the likely importance of accounting for spatial variation in growth as an option in tuna assessments.

References

- Day, J, Magnusson, A., Tears, T., Hampton, J., Davies, N., Castillo Jordán, C., Peatman, T., Scott, R., Scutt Phillips, J., McKechnie, S., Scott, F., Yao, N., Natandra, R., Pilling, G., Williams, P., and Hamer, P. 2023. Stock assessment of bigeye tuna in the western and central Pacific Ocean: 2023 (6Aug2023) – Final (Rev.02). WCPFC SC19-SA-WP-05.
<https://meetings.wcpfc.int/node/19353>.
- Hampton, J, and Fournier, D.A. 2001. A spatially-disaggregated, length-based, age-structured population model of yellowfin tuna (*Thunnus albacares*) in the western and central Pacific Ocean. Mar. Freshw. Res. 52:937–963.
- Punt, A.E., Dunn, A., Elvarsson, B.P., Hampton, J., Hoyle, S.D., Maunder, M.N., Methot, R.D., and Nielsen, A. 2020. Essential features of the next-generation integrated fisheries stock assessment package: A perspective. Fisheries Research 229: 105617.
<https://doi.org/10.1016/j.fishres.2020.105617>.

Declaration of generative AI and AI-assisted technologies in the SC paper preparation process

No AI technologies were used in the preparation of this paper

Acknowledgements

We are grateful to SPC-OFP colleagues for discussions and review of this paper, and to Nicholas Ducharme-Barth and Simon Hoyle for suggestions for this work at the 2026 Pre-Assessment Workshop. This work was supported by the WCPFC under the regular 'scientific services' and 'additional resourcing SPC' budget lines to the scientific services provider.

Table 1. Fisheries defined in the 2023 bigeye tuna assessment.

1. LL ALL 1	10. LL AU 5	19. PS JP 1	28. PL ALL 7	37. Index 5
2. LL ALL 2	11. LL ALL 5	20. PL JP 1	29. LL ALL 9	38. Index 6
3. LL US 2	12. LL ALL 6	21. PL ALL 3	30. PS ASS 7	39. Index 7
4. LL ALL 3	13. PS ASS 3	22. PL ALL 8	31. PS UNA 7	40. Index 8
5. LL OS 3	14. PS UNA 3	23. MISC ID 7	32. MISC VN 7	41. Index 9
6. LL OS 7	15. PS ASS 4	24. PS PHID 7	33. Index 1	
7. LL ALL 7	16. PS UNA 4	25. PS ASS 8	34. Index 2	
8. LL ALL 8	17. MISC PH 7	26. PS UNA 8	35. Index 3	
9. LL ALL 4	18. HL PHID 7	27. LL AU 9	36. Index 4	

Table 2. Various settings used for the individual single-region models, identified by Region. Fishery numbers correspond to those in Table 1. FF(49) - LF and FF(50) - WF refers to the effective length frequency (LF) and weight frequency (WF) sample size scalars applied to each fishery. "na" indicates were no data of that type were available for each fishery.

Region	Fisheries	LN(R0)	FF(49) - LF	FF(50) - WF
1	1, 19, 20, 33	1.474317	na, 100, 100, na	1, na, na, 1
2	2, 3, 34	1.438107	na, na, na	1, 1, 1
3	4, 5, 13, 14, 21, 35	1.452590	na, na, 100, 100, 100, na	1, 1, na, na, na, 1
4	9, 15, 16, 36	1.429888	na, 1, 1, na	1, na, na, 1
5+9	10, 11, 27, 29, 37	1.275700	na, na, na, na, na	1, 100, 100, 100, 100
6	12, 38	1.416663	na, na	1, 1
7	6, 7, 17, 18, 23, 24, 28, 30, 31, 32, 39	1.547590	na, na, 1, 1, 1, 1, 1, 1, 1, 1, na	1, 1, na, 1, na, na, na, na, na, 1
8	8, 22, 25, 26, 40	1.377807	na, 100, 1, 1, na	1, na, na, na, 1

Table 3. von Bertalanffy growth Parameter estimates for the eight regional models. Note that L1 was fixed at the value obtained in the 2023 assessment for all regional models.

Regional model	L1 (cm)	L40 (cm)	k (qtr ⁻¹)	V1 (cm)	V2	SD of length at age 40 qtr (cm)
1	23.3	212.7	0.0404	4.70	1.339	17.9
2	23.3	207.9	0.0517	4.63	0.678	9.1
3	23.3	147.7	0.1141	5.11	0.410	7.9
4	23.3	141.2	0.1198	6.69	0.745	14.1
5+9	23.3	170.0	0.0699	2.91	1.024	8.1
6	23.3	146.5	0.1083	3.78	0.858	8.9
7	23.3	155.4	0.1018	5.13	0.601	9.4
8	22.2	141.9	0.1056	4.34	0.250	5.6

Table 4. Likelihood components for the 2023 diagnostic case model, the control (common growth) and regional growth models.

Likelihood component	2023 diagnostic case model	Control (common growth) model	Regional growth model
Length-frequency	-74,401.35	-	-
Weight-frequency	-962,224.68	-	-
Age-frequency	-	144.62	14,186.64
Conditional age-at-length	2,119.84	-	-
Tagging	6,395.66	6,269.21	7,979.04
CPUE indices	-2,578.69	-2,643.78	-2,222.83
Penalties	303.81	287.85	789.87
TOTAL	-1,030,385.41	4,057.90	20,732.72

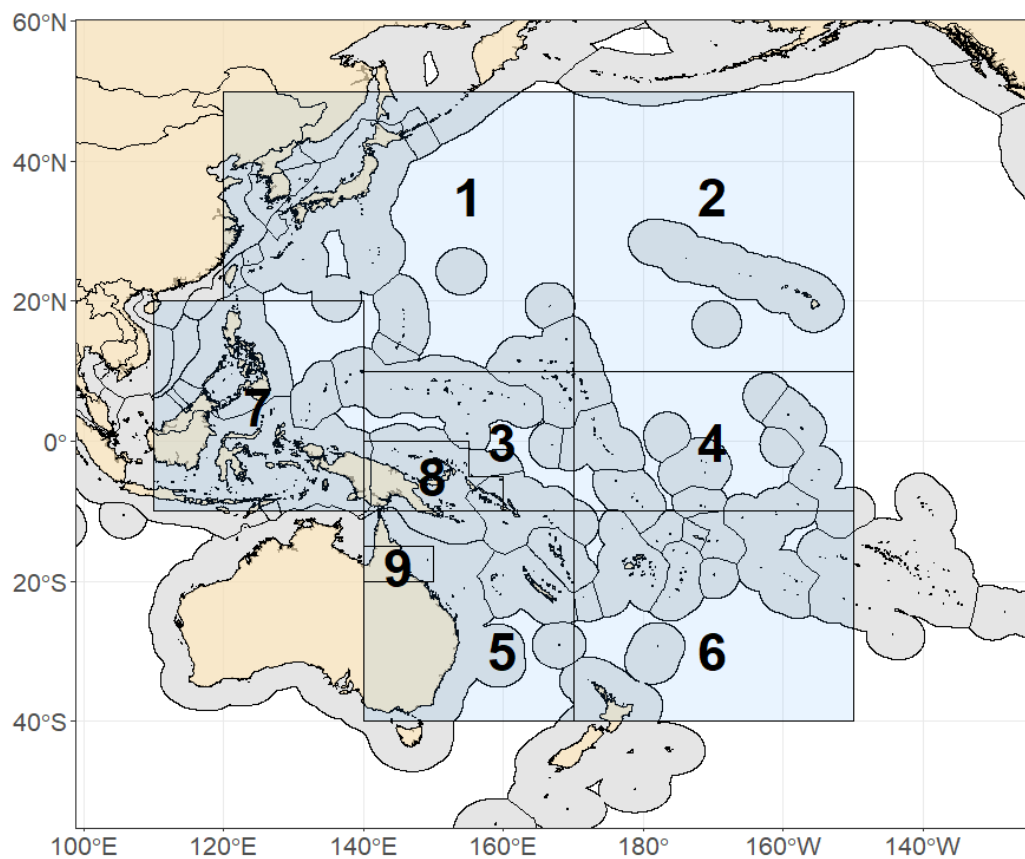


Figure 1. The nine-area model used for the 2023 bigeye tuna assessment.

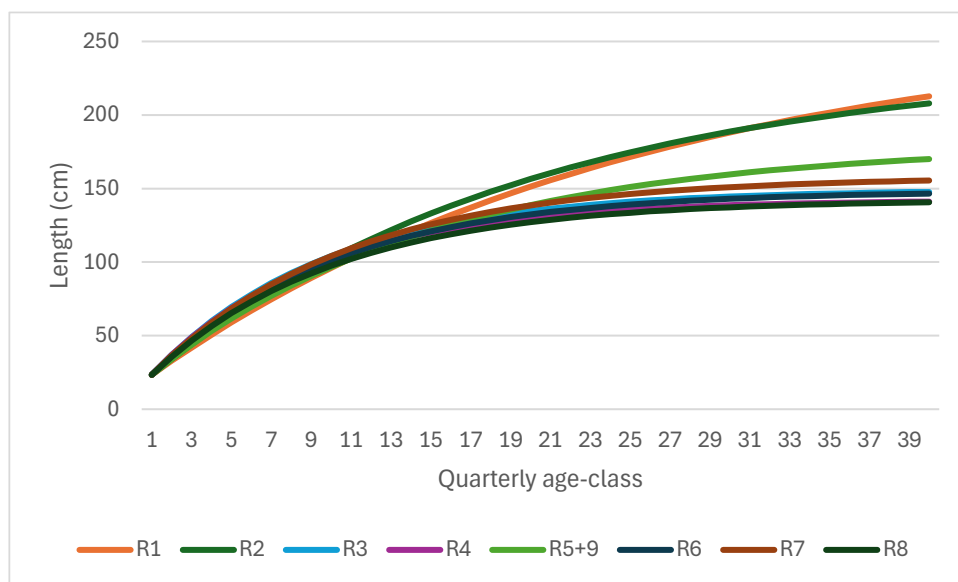


Figure 2. Estimated growth curves for each region.



Figure 3. Estimated growth curves for each region compared to the common growth curve estimated for the 2023 bigeye tuna assessment.



Figure 4. Estimated weight-at-age for each region compared to that based on the common growth curve estimated for the 2023 bigeye tuna assessment.

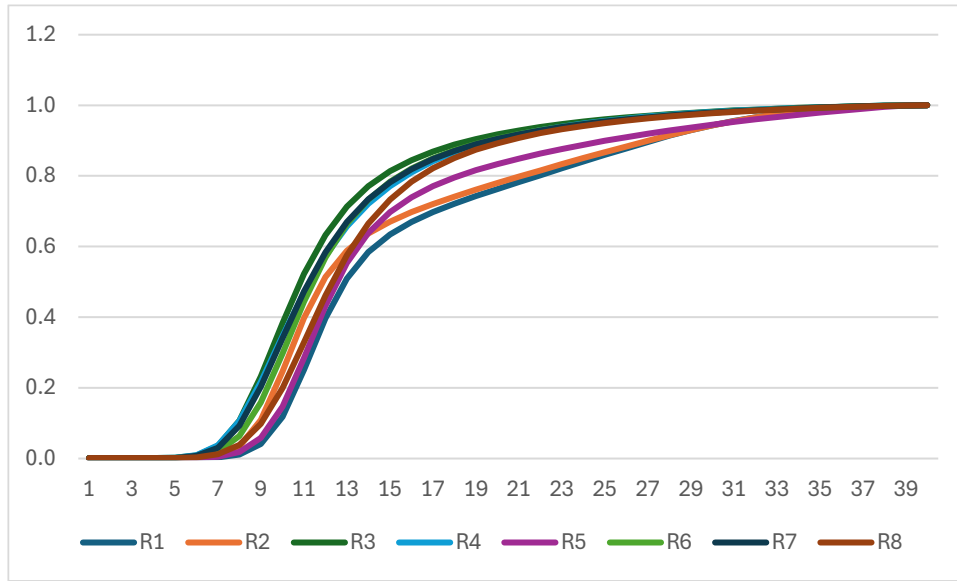


Figure 5. Estimated maturity-at-age from the individual regional models.

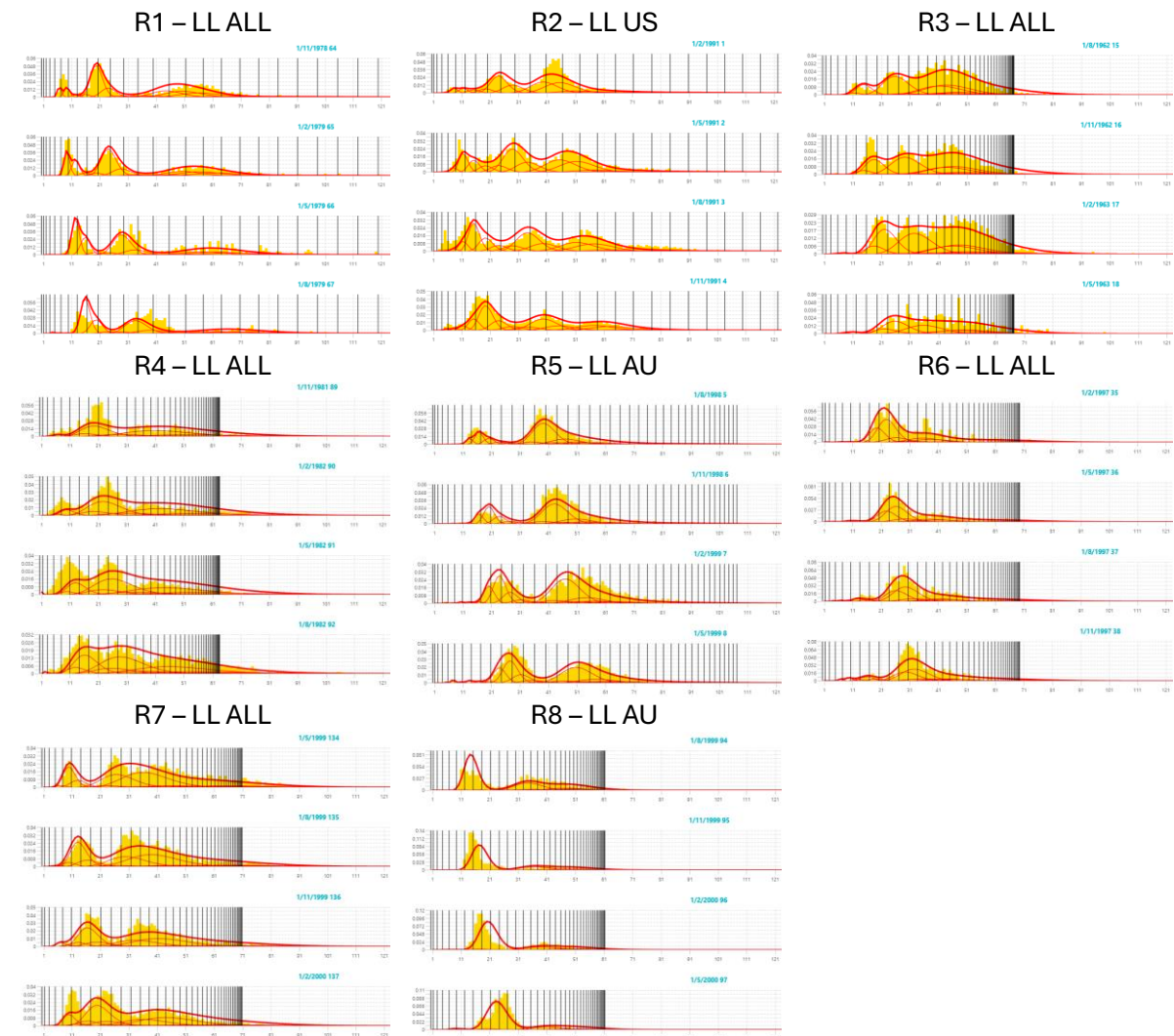


Figure 6. Examples of individual region model fits to weight-frequency data. The vertical bars in each plot represent the estimated quarterly weight-at-age.

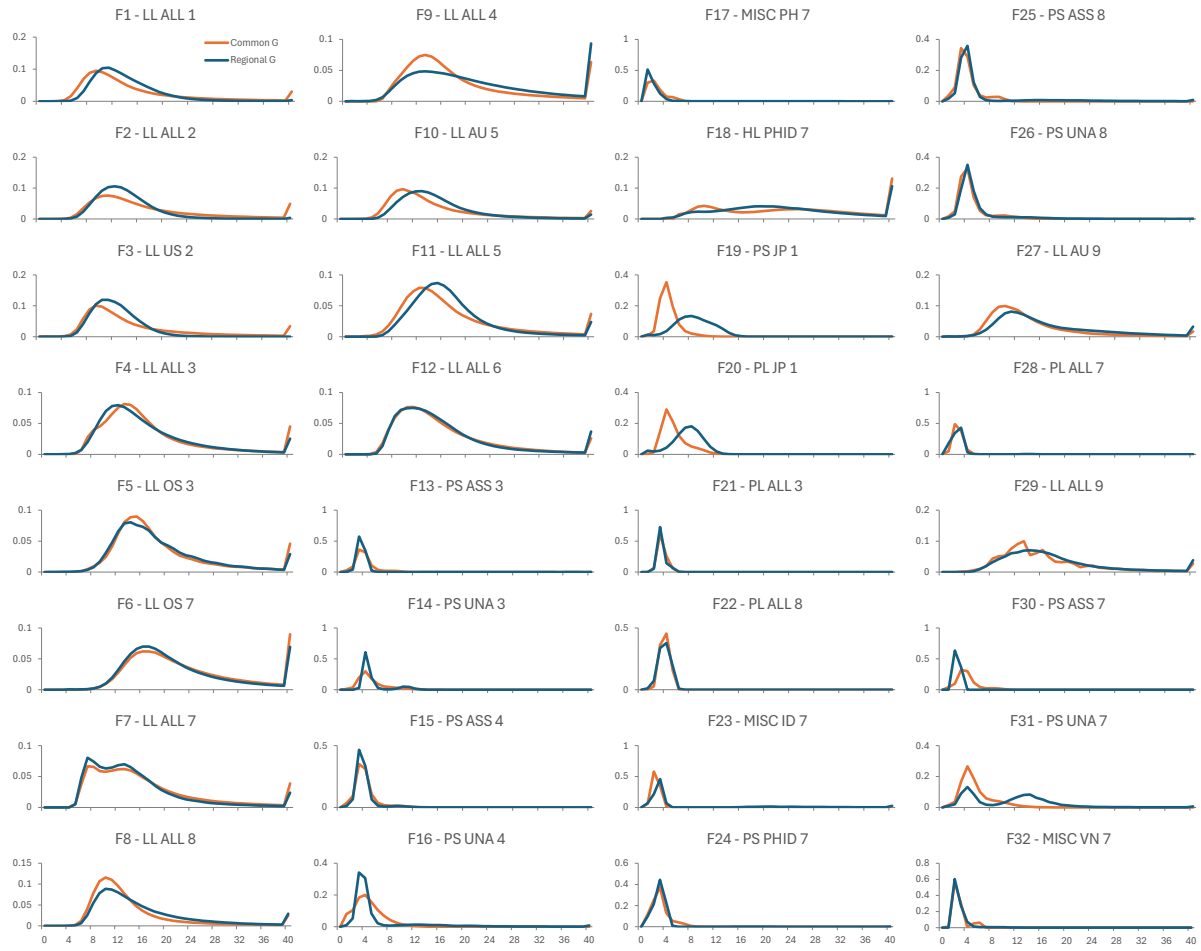


Figure 7. Catch-at-age data summed over all time periods (plotted as proportions) for the control (common growth) model (orange) and the regional growth model (blue).

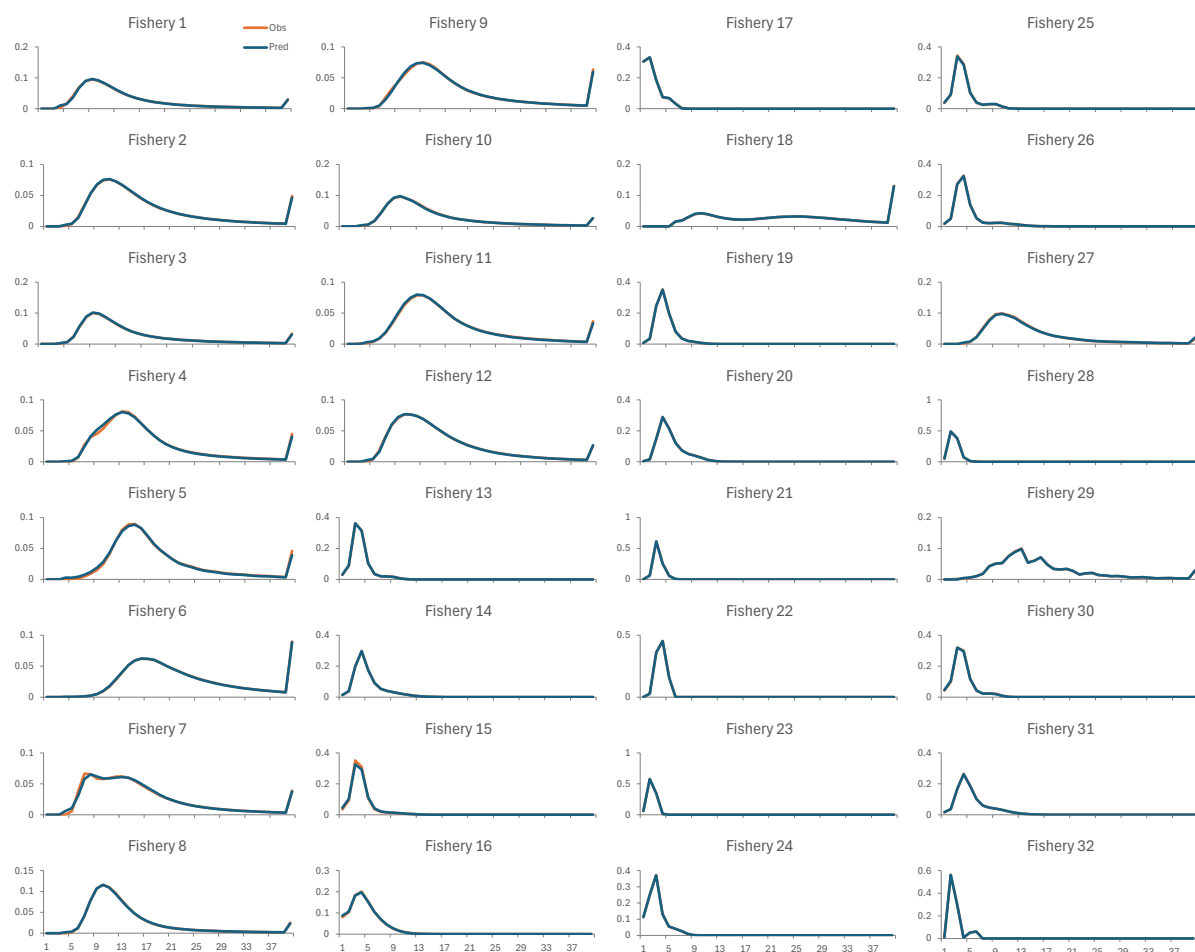


Figure 8. Observed (orange) and predicted (blue) average catch-at-age proportions in the control (common growth) model.

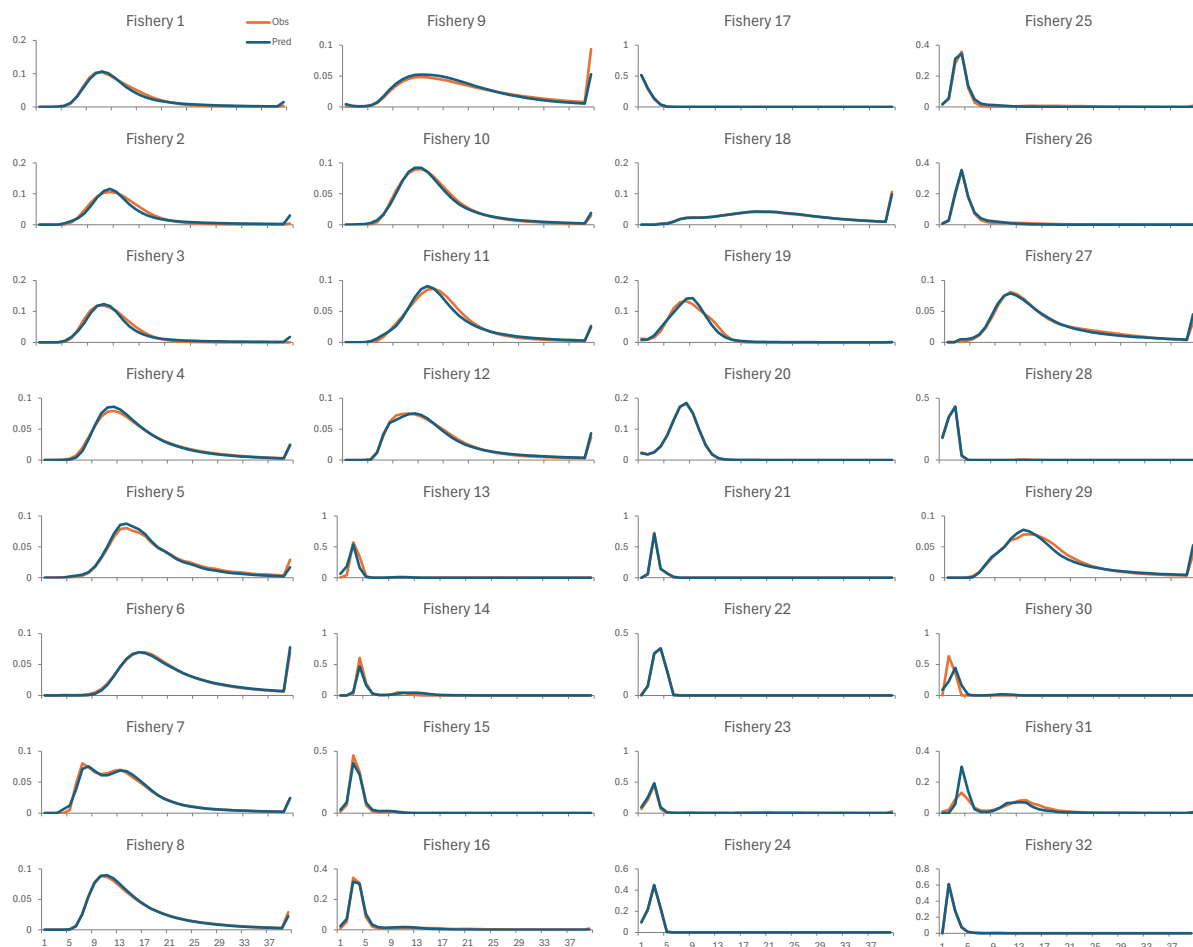


Figure 9. Observed (orange) and predicted (blue) average catch-at-age proportions in the regional growth model.

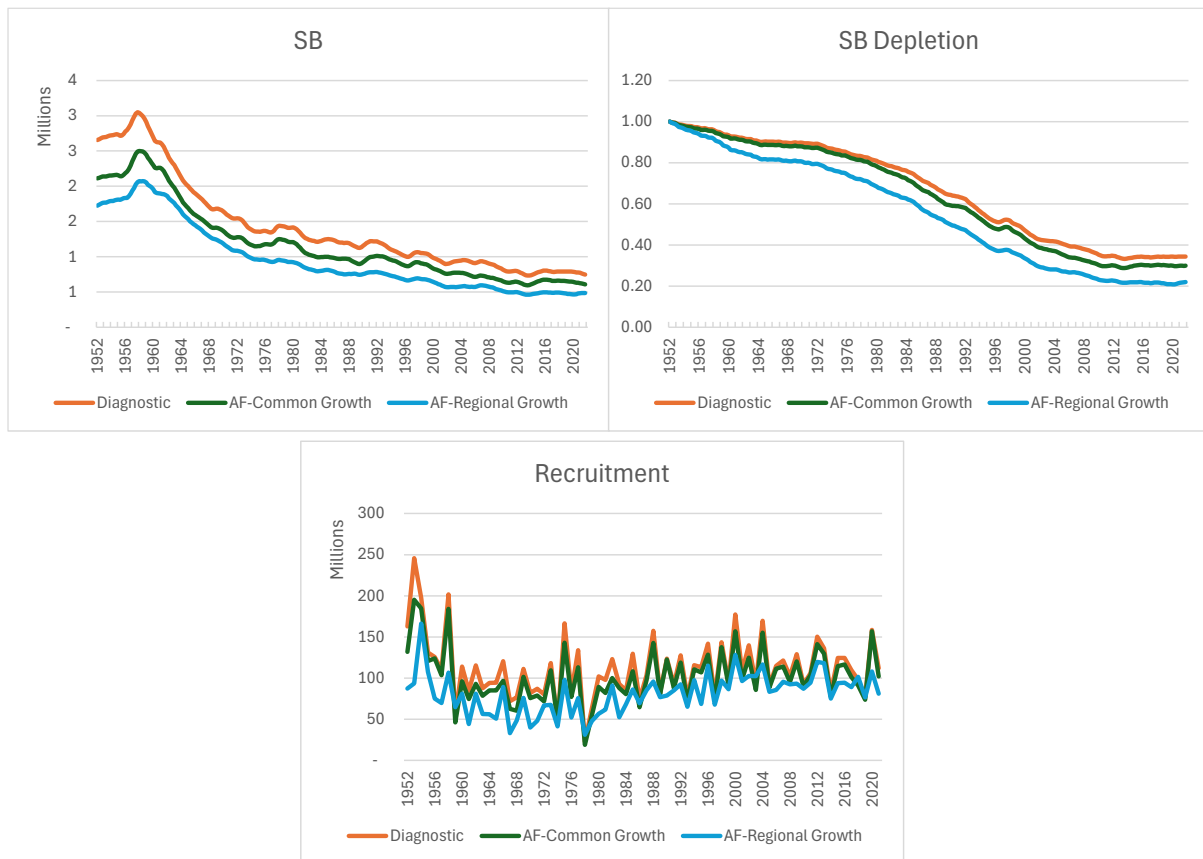


Figure 10. Estimates of spawning biomass (SB), SB depletion and recruitment from the 2023 diagnostic case model, the control (common growth) model and the regional growth model.

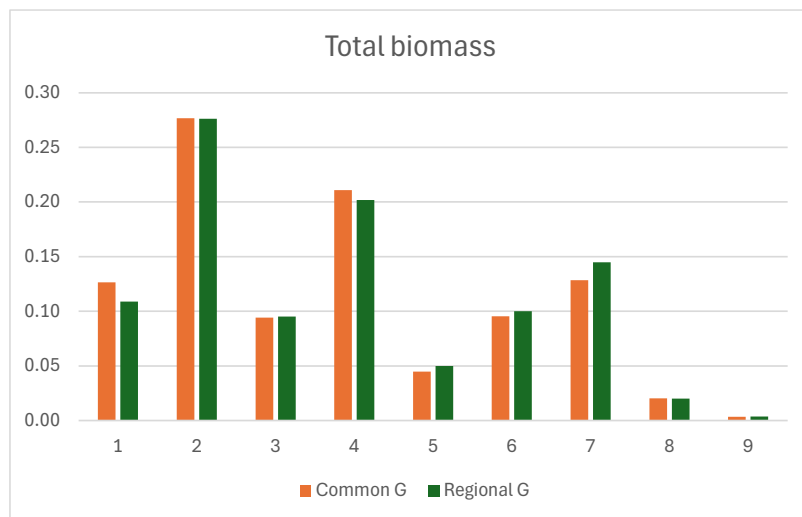
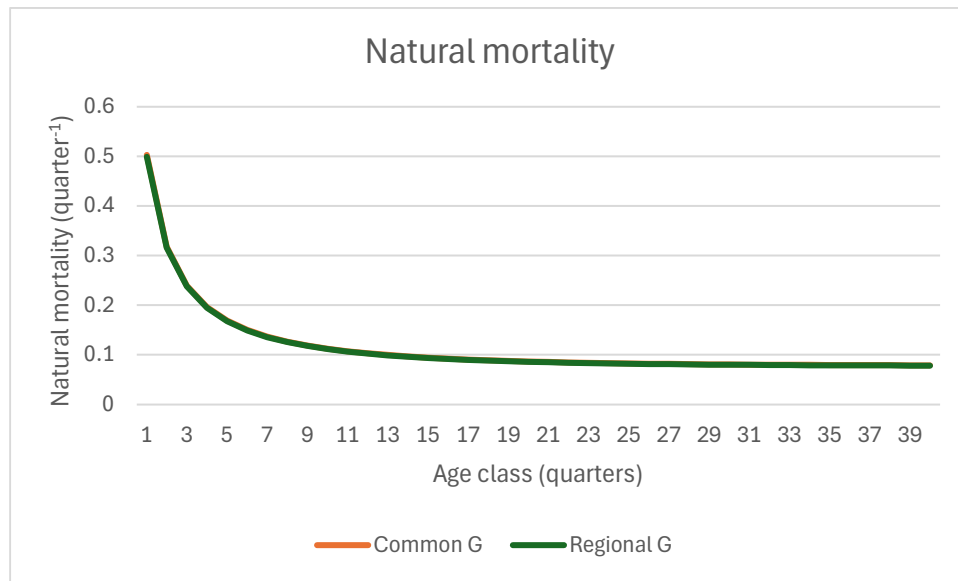


Figure 11. Estimates of spawning biomass by region and for all regions combined for the control (common growth) and regional growth models.

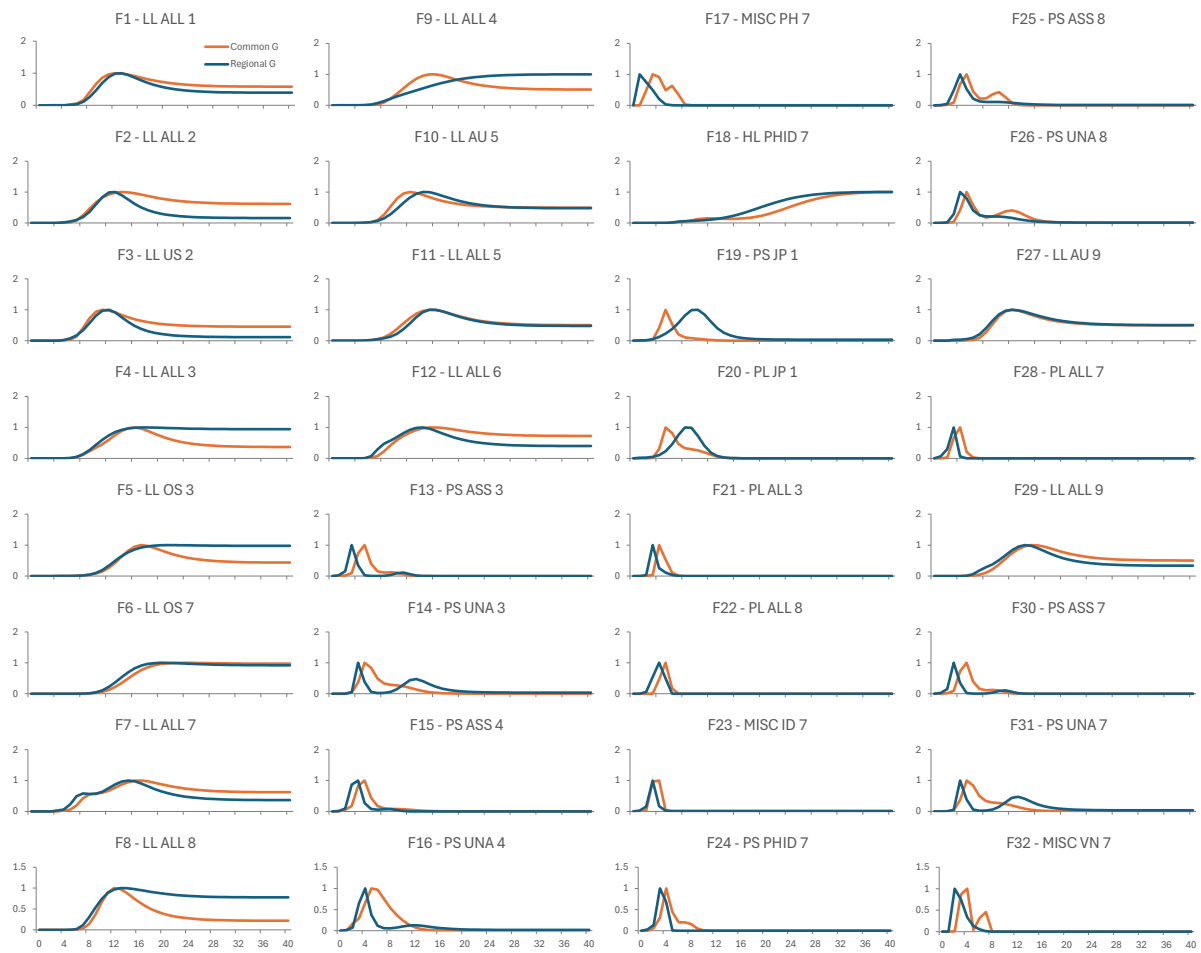


Figure 12. Estimates of spawning biomass depletion by region and for all regions combined for the control (common growth) and regional growth models.

Appendix 1 Selection of demographic parameter comparisons from the control (common growth) and regional growth models.



Selectivity-at-age



Likelihood profile

