

2012 South Coast Rock Lobster Operating models – some initial results

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Summary

Initial updated assessments are developed for the South Coast rock lobster resource incorporating the recently revised estimates of somatic growth rate by area developed by OLRAC, and fitting to area-specific CPUE and scientific catch-at-length data. The initial focus is on a model structure which splits the resource into areas A1E, A1W and A2+3. A problem arises because the slow growth rate estimate for A1E results in an unrealistically high estimate of pre-exploitation biomass, and some approaches to circumvent this are explored. The pack-category-based catch-at-length data are not consistent with these results and it is suggested that they be excluded from future model fits. Allowing selectivity at length to vary over time makes little difference to stock trajectory estimates, but scarcely improves non-random patterns in the catch-at-length residuals, so that the investigation of alternative functional forms for this variation is suggested. An alternative model structure based on areas A1, A2 and A3 yields an estimate of the current depletion of the spawning biomass which is appreciably less than in previous assessments which were based on this structure; the reasons for this need to be identified.

Introduction

Three model structures have been identified to be explored to provide the underlying operating models for the updated South Coast rock lobster assessment. These structures pertain to the spatial split of the fishing grounds and are:

Model 1: A1, A2, and A3 (as for previous operating models)

Model 2: A1E, A1W, A2 and A3 (four sub-areas)

Model 3: A1E, A1W, and A2+3

This initial investigation focuses primarily on Model 3, with brief attention also to Model 1.

1. Model 3 candidate OMs

There appears to be a general problem in obtaining realistic fits using the somatic growth rates for A1E as reported by OLRAC (FISHERIES/2012/JUL/SCRL/12). Note that this sub-area is estimated in those analyses to have much lower growth than the other two sub-areas. The assessment process returns unrealistically high K values, essentially because with a low somatic growth rate, surplus production is less and unable to account for historic catches from the region without setting the pre-exploitation abundance very high. At this stage, three alternate OMs have been developed (Variants 1, 2 and 3) to get around this problem in ways that are explained below. For these three OMs, the models are fitted, as in the recent past, to CPUE and scientific catch-at-length (SCI CAL) data from each of the three sub-areas. Pack-category catch-at-length data (PAC CAL) are not included in the likelihood for these variants (though this is examined in further variants as discussed subsequently). Furthermore, Variants 1, 2 and 3 assume time INVARIANT selectivity.

1.1 Model fitted to SCI CAL data (exclude PAC CAL data in likelihood, time invariant selectivity)

Variant 1

All five growth parameters are FIXED at the OLRAC reported values (OLRAC model 8), except for Δg_{1E} which is changed to equal the OLRAC Δg_{1W} value, i.e. growth for sub-area A1E is set equal to the higher value for A1W.

Variant 2

All five growth parameters are estimated (this estimation includes the OLRAC analysis variance-covariance matrix contribution to $-\ln L$ for the growth parameters – see Appendix for details). However, a further penalty function is added to the total $-\ln L$ to force the 1E and 1W growth parameter values closer together:

$$SG\ pen = \omega * (\Delta g_{1E} - \Delta g_{1W})^2$$

Here a value of $\omega = 40$ has been selected as it is the value at which the estimation “flips” from estimating an unrealistically high K value to a more realistic K (~ 3000-4000 mt).

Variant 3

Again all five growth parameters are estimated (including again the OLRAC analysis variance-covariance matrix contribution to $-\ln L$ for the growth parameters). A further penalty function is added to the total $-\ln L$ as follows:

$$SG\ pen = \omega * (\Delta g1E - (-0.796))^2$$

where -0.796 is the OLRAC point estimate for $\Delta g1W$, and the intent is to force the A1E growth estimate closer to this.

Here a value of $\omega = 20$ has been selected, being that at which the estimation “flips” from estimating an unrealistically high to a more realistic K .

1.2 Adding the pack category catch-at-length (PAC CAL) data to the likelihood

Variants 1, 2, and 3 are modified to include the pack-category catch-at-length data in the overall likelihood. These options are denoted as Variants 1a, 2a and 3a.

1.3 Allowing selectivity to vary over time

Variant 1 has been used to explore allowing selectivity to vary over time. The previous “MARAM method” was used to model time-varying selectivity (see Appendix for details). At first, four periods within which selectivity does change were specified – thus three extra parameters for each sex and each sub-area need to be estimated. The time periods (whose selection was based on apparent changes in the patterns of SCI CAL residuals) are:

1995-1998

1999-2002

2003-2006

2007-2010

This is denoted Variant 1b. Variant 1c extends the time-varying selectivity to include fitting selectivity parameters for each year for which CAL data are available (1995-2010).

2. Model 1 candidate OMs

2.1 Model fitted to SCI CAL data (exclude PAC CAL data in likelihood, time invariant selectivity)

Variant 1

Recall that for this model, the resource is split into three areas (A1, A2 and A3) as in the past. All five growth parameters are FIXED at the OLRAC reported values (OLRAC Model 8), except for Δg_1 which is set equal the average of the OLRAC Δg_{1E} and Δg_{1W} values.

3. Results

3.1 Model 3 Results

Table 1 reports the results of Model 3 (denoted OM3) for Variants 1, 2 and 3. The three models produce fairly different estimates for B_{sp} and B_{exp} (see Appendix for definitions of spawning and exploitable biomass). Table 2 reports results for the Variants where the PAC CAL data are included in the likelihood (Variants 1a, 2a and 3a). Table 3 reports results where the OM allows for time-varying selectivity (Variants 1b and 1c).

Figure 1a shows OM3 Variants 1-3 fits to CPUE. Figure 2b shows the associated CPUE standardised residuals. Figures 1c-e compare CPUE fits between Variants which either include or exclude PAC CAL data in the likelihood.

Figures 2a-c comprise OM3 SCI CAL residual plots for Variants 1, 2 and 3. Figure 2d shows the PAC CAL residuals plots for Variants 1, 2 and 3 (although note that the PAC CAL data are NOT included in $-\ln L$ in these cases).

Figure 2e compares OM3 SCI CAL residual plots amongst Variant 1 (no time varying selectivity), Variant 1b (four periods with different selectivity) and Variant 1c (time varying selectivity for all years with CAL data).

Figure 2f compares Variant 1 with Variant 1a model fits to 1990 and 2010 PAC CAL data. . Figure 2g compares Variant 1 with Variant 1a model fits to 1995 and 2010 SCI CAL data.

Figure 3 shows OM3 B_{sp} trajectories for Variants 1-3.

Figure 4 shows OM3 B_{exp} trajectories (relative to K_{exp}) for Variants 1-3.

Figure 5 shows OM3 stock-recruit residuals for Variants 1-3.

Figure 6a shows the growth curves which are input for OM3 for each sub-area and Figure 6b shows these for OM1. Figure 6c compares the growth curves for OM1 for the recently estimated growth parameter values recently estimated by OLRAC (“NEW”) with those used in past assessments (“OLD”).

Figure 7a shows the OM3 selectivity functions.

Figure 7b shows the selectivity function “delta” values for OM3 Variant 1c (which allows for annually varying selectivity – see equation 24 in the Appendix).

3.2 Model 1 results

Table 4a reports OM1 (Variant 1) results. Table 4b compares current B_{sp} and B_{exp} estimates for OM1 and OM3 (Variant 1), and also provides Hessian-based 95% CIs for these estimates.

Figure 8 shows the OM1 fits to CPUE data.

Figure 9 shows the OM1 SCI CAL standardised residuals.

Figure 10 shows the OM1 SCI CAL fits to data for 1995 and 2010.

4. Discussion

Adjustment of somatic growth parameter estimates: The assessment model results evidence a difficulty associated with the OLRAC estimated growth for sub-area A1E which lead to unrealistically high estimates of K – Variants 1, 2 and 3 are different approaches to address this. Is one or any of these to be preferred (note the Variant 2 leads to a rather different estimate of current depletion in terms of spawning biomass than the other two – see Figure 3).

Including PAC CAL data: Adding PAC CAL data results in a decrease of goodness-of-fit to the CPUE data (compare results in Table 2 with those in Table 1) – i.e. there is a conflict between the CPUE and PAC CAL data. Figure 2d evidences very clear consistent mismatches between PAC CAL data and model estimated values, so that we advocate exclusion of these data from the likelihood.

Time-varying selectivity: The AIC values (and the $-\ln L$ values) in Table 3 suggest that allowing for time-varying selectivity in the form considered is not justified. However a concern is that this form does not seem to allow improvement in the fits to the catch-at-length data for which the residuals manifest distinct non-random patterns (Figure 2e).

OM1 fits to data: Figure 8 shows a good fit to the CPUE data, but does not reflect the very recent downward trend in the data for area A3.

Differences in overall resource abundance between OM1 and OM3 (see Table 4b). There are definitely differences with OM3 being more optimistic and estimating current abundance (both spawning and exploitable) to be higher relative to pristine than OM1. Strangely it is that the estimates from OM3 which are much closer to those from the 2010 assessment (Johnston and Butterworth 2010) (which was based on the A1, A2, A3 sub-area split i.e. OM1 sub-area split, though different somatic growth estimates are now being used).

Possible future work

One possibility for the problems arising for OM3 with sub-area A1E are that the CPUE data for this area are much more variable for the earlier than the later years (Figure 1a), whereas the assessment method weights all these values equally; an appropriate modification to the method might be explored.

Another possible explanation for the model's difficulty related to growth rate estimates for sub-area A1E is that there is movement of lobsters of fishable size into A1E from adjacent areas, after which their growth rate decreases. Taking this possibility into account would, however, considerably increase model complexity.

The failure of the current functional form assumed for time varying selectivity to appreciably improve catch-at-length residual patterns is a concern; possibly alternative forms need investigation.

The reasons underlying the marked change in the estimated current spawning biomass depletion for OM1 compared with the previous assessment should be identified.

Reference

Johnston, S.J. and D.S. Butterworth. 2010. Updated South Coast rock lobster stock assessments for 2010 and comparisons to the 2008 and 2009 assessments. MCM/2010/APR/SWG-SCRL/04.

Table 1: OM 3 estimated parameter and $-\ln L$ values for Variants 1, 2, and 3.

	Variant 1	Variant 2	Variant 3
	Abc.tpl	Xtry6.tpl	Xsue4.tpl
	Fit to SCI CAL data	Fit to SCI CAL data	Fit to SCI CAL data
# parameters estimated	143	148	148
$-\ln L$ Total	-230.36	-165.36	-186.00
$-\ln L$ Total less var-covar and SG pen	-230.36	-188.61	-241.53
$-\ln L$ CPUE	-102.97	-116.36	-107.53
$-\ln L$ CPUE A1E	-20.06	-18.33	-18.60
$-\ln L$ CPUE A1W	-46.99	-40.82	-50.25
$-\ln L$ CPUE A2+3	-35.93	-57.06	-38.67
$-\ln$ SCI CAL	-145.02	-122.10	-152.65
$-\ln$ SCI CAL A1E	27.65	32.95	35.88
$-\ln$ SCI CAL A1W	-88.26	-76.05	-96.76
$-\ln$ SCI CAL A2+3	-84.41	-79.00	-91.76
[PAC CAL $-\ln L$ – but not included in total $-\ln L$]	26.54	31.38	30.21
CPUE A1E σ	0.336	0.354	0.351
CPUE A1W σ	0.152	0.183	0.138
CPUE A2+3 σ	0.211	0.113	0.194
SCI CAL A1E σ	0.168	0.174	0.176
SCI CAL A1W σ	0.094	0.099	0.091
SCI CAL A2+3 σ	0.035	0.095	0.091
[PAC CAL σ]	0.189	0.196	0.195
K	3 306	3 415	3 317
SG var –covar $-\ln L$	-	26.95	9.28
SG pen	-	23.25	46.24
λ^{A1E}	0.109	0.189	0.213
λ^{A1W}	0.342	0.434	0.257
λ^{A2+3}	0.549	0.377	0.529
$g75$	3.280 fixed	3.346	3.293
κ	0.099 fixed	0.104	0.111
Δgm	0.996 fixed	0.924	0.835
$\Delta g1E$	-0.796 changed	-2.805	-2.317
$\Delta g1W$	-0.796 fixed	-2.043	-0.082
$B_{sp}(2011) (B_{sp}(2011)/K_{sp})$	1017 (0.308)	1581 (0.463)	934 (0.281)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1E	118 (0.290)	270 (0.418)	271 (0.396)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1W	839 (0.440)	1641 (0.498)	655 (0.396)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A2+3	2268 (0.305)	1577 (0.315)	2386 (0.325)

Table 2: OM 3 estimated parameter and $-\ln L$ values for Variants 1a, 2a, and 3a (where the PAC_CAL data are added to likelihood).

	Variant 1a	Variant 2a	Variant 3a
	zAbc.tpl	ztry6.tpl	zsue4.tpl
	Fit to SCI CAL data and PAC CAL data	Fit to SCI CAL data and PAC CAL data	Fit to SCI CAL data and PAC CAL data
# parameters estimated	143	148	148
$-\ln L$ Total	-225.69	-158.83	-179.57
$-\ln L$ Total less var-covar and SG pen	-225.69	-210.69	-232.76
$-\ln L$ CPUE	-90.90	-80.84	-92.54
$-\ln L$ CPUE A1E	-20.10	-18.99	-18.96
$-\ln L$ CPUE A1W	-44.73	-41.68	-48.18
$-\ln L$ CPUE A2+3	-26.07	-20.17	-25.39
$-\ln$ SCI CAL	-138.08	-123.71	-142.82
$-\ln$ SCI CAL A1E	29.07	33.58	36.20
$-\ln$ SCI CAL A1W	-90.25	-84.36	-97.71
$-\ln$ SCI CAL A2+3	-76.90	-72.93	-81.30
PAC CAL $-\ln L$	-18.52	-30.42	-18.64
CPUE A1E σ	0.336	0.347	0.347
CPUE A1W σ	0.162	0.178	0.147
CPUE A2+3 σ	0.281	0.335	0.287
SCI CAL A1E σ	0.170	0.175	0.177
SCI CAL A1W σ	0.093	0.095	0.091
SCI CAL A2+3 σ	0.096	0.097	0.094
PAC CAL σ	0.132	0.120	0.132
K	3 141	3 289	3 217
SG var –covar $-\ln L$	-	21.41	6.36
SG pen	-	30.45	46.83
λ^{A1E}	0.112	0.199	0.219
λ^{A1W}	0.359	0.412	0.276
λ^{A2+3}	0.528	0.389	0.505
g75	3.280 fixed	3.34	3.27
kappa	0.099 fixed	0.105	0.108
Δg_m	0.996 fixed	0.928	0.848
Δg_{1E}	-0.796 changed	-2.733	-2.326
Δg_{1W}	-0.796 fixed	-1.861	-0.093
$B_{sp}(2011) (B_{sp}(2011)/K_{sp})$	881 (0.281)	1200 (0.365)	831 (0.258)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1E	98 (0.255)	173 (0.364)	207 (0.370)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1W	786 (0.425)	975 (0.446)	619 (0.385)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A2+3	1751 (0.263)	1528 (0.250)	1878 (0.273)

Table 3: OM 3 estimated parameter and $-\ln L$ values for Variant 1, and Variants 1b, and 1c for which selectivity varies over time.

	Variant 1	Variant 1b	Variant 1c
	Fit to SCI CAL data	Fit to SCI CAL data+4 period time varying selectivity	Fit to SCI CAL +annual time varying selectivity for 1995-2010
	Abc.tpl	V1sel4.tpl	V1selx.tpl
# parameters estimated	143	167	240
AIC	-174.72	-133.46	-3.36
$-\ln L$ Total	-230.36	-233.73	-241.68
$-\ln L$ CPUE	-102.97	-102.79	-102.62
$-\ln L$ CPUE A1E	-20.06	-20.05	-20.01
$-\ln L$ CPUE A1W	-46.99	-46.80	-47.13
$-\ln L$ CPUE A2+3	-35.93	-35.95	-35.48
$-\ln$ SCI CAL	-145.02	-151.59	-167.21
$-\ln$ SCI CAL A1E	27.65	26.99	24.67
$-\ln$ SCI CAL A1W	-88.26	-90.37	-93.86
$-\ln$ SCI CAL A2+3	-84.41	-88.21	-98.02
[PAC CAL $-\ln L$ – but not included in total $-\ln L$]	26.54	26.78	28.29
CPUE A1E σ	0.336	0.336	0.337
CPUE A1W σ	0.152	0.153	0.152
CPUE A2+3 σ	0.211	0.211	0.214
SCI CAL A1E σ	0.168	0.167	0.165
SCI CAL A1W σ	0.094	0.093	0.092
SCI CAL A2+3 σ	0.035	0.092	0.089
[PAC CAL σ]	0.189	0.189	0.191
K	3 306	3 304	3 293
λ^{A1E}	0.109	0.109	0.109
λ^{A1W}	0.342	0.342	0.342
λ^{A2+3}	0.549	0.549	0.548
g_{75}	3.280 fixed	3.280 fixed	3.280 fixed
κ	0.099 fixed	0.099 fixed	0.099 fixed
Δg_m	0.996 fixed	0.996 fixed	0.996 fixed
Δg_{1E}	-0.7906 changed	-0.796 changed	-0.796 changed
Δg_{1W}	-0.796 fixed	-0.796 fixed	-0.796 fixed
$B_{sp}(2011) (B_{sp}(2011)/K_{sp})$	1017 (0.308)	1016 (0.308)	1105 (0.305)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1E	118 (0.290)	117 (0.287)	117 (0.285)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1W	839 (0.440)	834 (0.427)	830 (0.436)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A2+3	2268 (0.305)	2264 (0.304)	2243 (0.307)

Table 4a: OM 1 estimated parameter and $-\ln L$ values for Variant 1.

	Variant 1
	Xmod1fix.tpl
	Fit to SCI CAL data
# parameters estimated	143
$-\ln L$ Total	-201.41
$-\ln L$ CPUE	-139.90
$-\ln L$ CPUE A1	-59.83
$-\ln L$ CPUE A2	-51.26
$-\ln L$ CPUE A3	-28.81
$-\ln$ SCI CAL	-82.39
$-\ln$ SCI CAL A1	-49.55
$-\ln$ SCI CAL A2	-15.01
$-\ln$ SCI CAL A3	-17.83
[PAC CAL $-\ln L$ – but not included in total $-\ln L$]	24.05
CPUE A1 σ	0.104
CPUE A2 σ	0.134
CPUE A3 σ	0.260
SCI CAL A1 σ	0.103
SCI CAL A2 σ	0.115
SCI CAL A3 σ	0.107
[PAC CAL σ]	0.185
K	3283
λ^{A1}	0.503
λ^{A2}	0.327
λ^{A3}	0.170
g_{75}	3.079 fixed
κ	0.097 fixed
Δg_m	0.968 fixed
Δg_1	-1.609 fixed
Δg_3	0.292 fixed
$B_{sp}(2011) (B_{sp}(2011)/K_{sp})$	548 (0.167)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1	427 (0.172)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A2	457 (0.167)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A3	426 (0.174)

Table 4b: Comparison of total biomass statistics for OM1 and OM3 (Variant 1 in each case– i.e. both fixed growth parameters). Hessian-based 95% CIs are given in parentheses.

	OM1	OM3
$B_{sp}(2011)$	548 (392-703)	1017 (768-1266)
$B_{sp}(2011)/K_{sp}$	0.167 (0.120-0.214)	0.308 (0.242-0.374)
$B_{exp}(2011)$	1312 (1025-1598)	3226 (2556-3896)
$B_{exp}(2011)/K_{exp}$	0.171 (0.140-0.202)	0.331 (0.278-0.384)

Table 5a: Operating Model 3 - Growth curve G75 values (mm) estimated for each Variant, as well as the input OLRAC-Model 7 estimated values.

	OLRAC	Variant 1	Variant 2	Variant 3
A1Em	1.44	4.39	1.47	1.81
A1Ef	0.44	2.49	0.54	0.98
A1Wm	3.48	3.48	2.22	4.05
A1Wf	2.49	2.49	1.30	3.21
A23m	4.28	4.28	4.27	4.13
A23f	3.28	3.28	3.35	3.29

Table 2b: Operating Model 3 - Growth curve L_{∞} values (mm) estimated for each Variant, as well as the input OLRAC-Model 7 estimated values.

	OLRAC	Variant 1	Variant 2	Variant 3
A1Em	89.51	110.21	89.09	91.32
A1Ef	79.44	100.15	80.20	83.79
A1Wm	110.15	110.15	96.41	111.45
A1Wf	100.09	100.09	87.52	103.93
A23m	118.19	118.19	116.06	112.19
A23f	108.13	108.13	107.17	104.67

Table 2c: Operating Model 1 - Growth curve G75 values (mm) which are set equal to the OLRAC-Model 8 estimated values (A1 is taken as the average of A1E and A1W).

	OLRAC	Variant 1
A1m	2.44	2.44
A1f	1.47	1.47
A2m	4.05	4.05
A2f	3.08	3.08
A3m	4.34	4.34
A3f	3.37	3.37

Table 2d: Operating Model 3 - Growth curve L_{∞} values (mm) which are fixed on input to equal as the OLRAC-Model 7 estimated values.

	OLRAC	Variant 1
A1m	100.13	100.13
A1f	90.15	90.15
A2m	116.72	116.72
A2f	106.74	106.74
A3m	119.73	119.73
A3f	109.75	109.75

Figure 1a: OM3 fits to CPUE for each sub-area for Variants 1, 2 and 3.

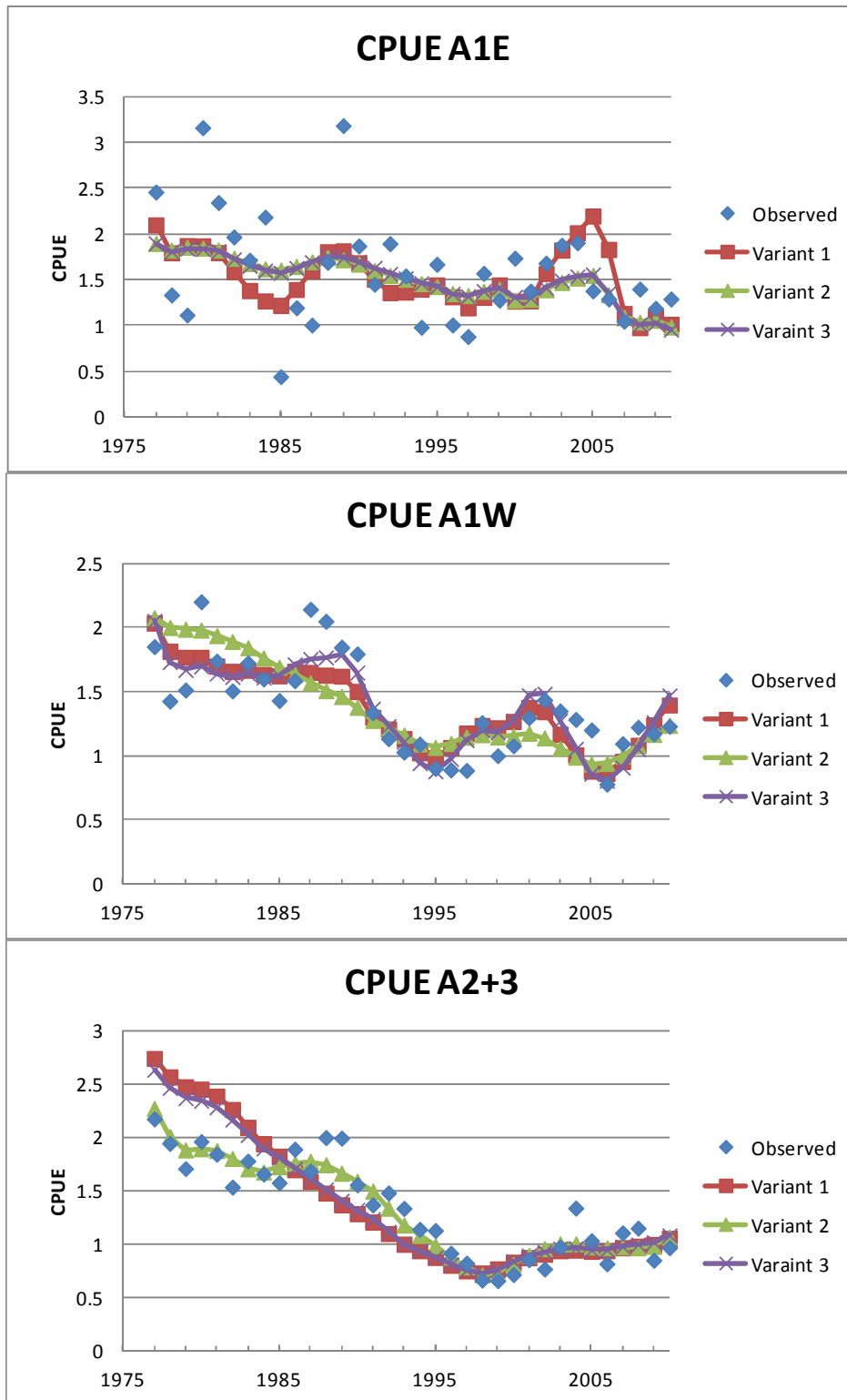


Figure 1b: Standardised CPUE residuals for each sub-area for OM3 fits for Variants 1, 2 and 3.

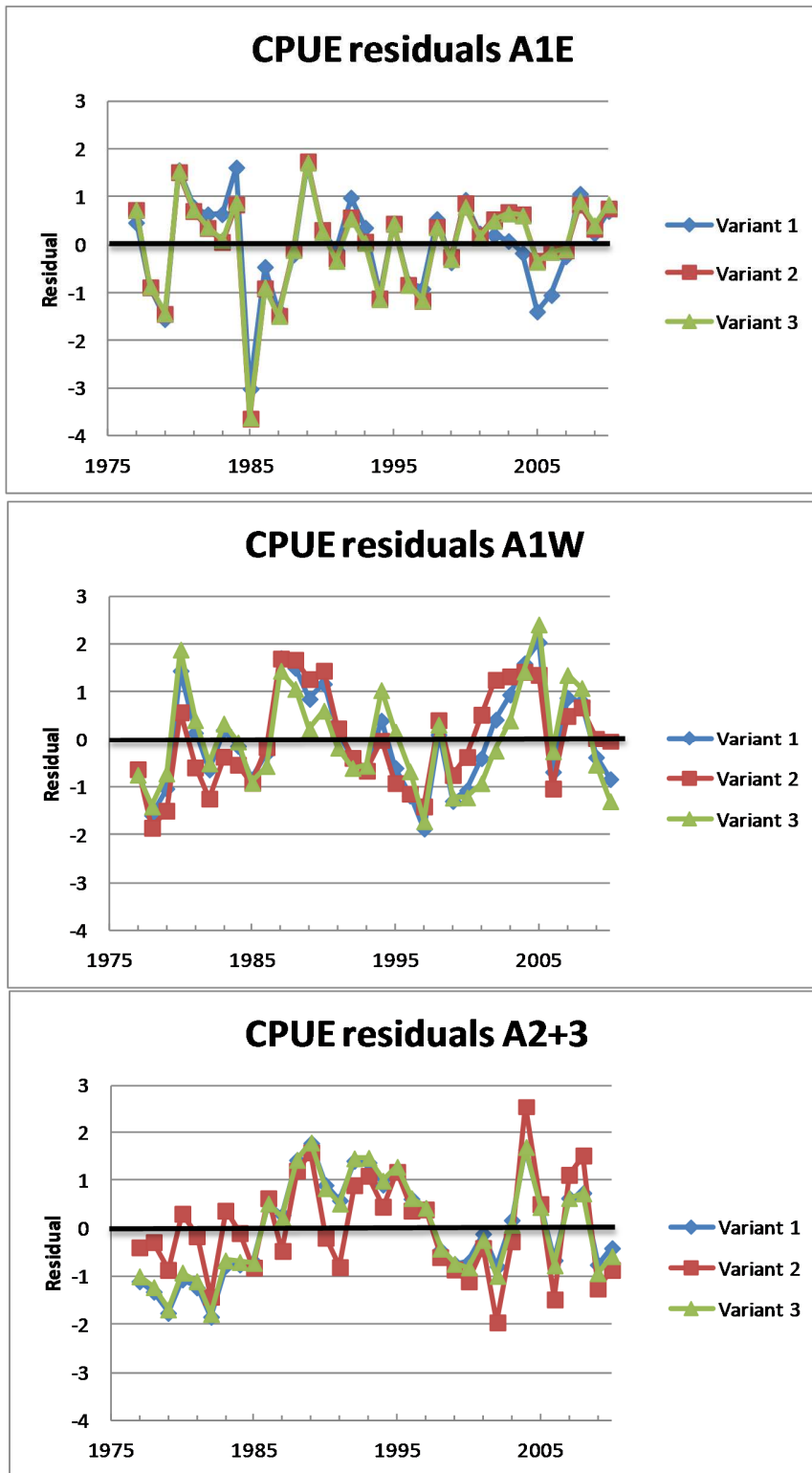


Figure 1c: Comparison of CPUE fits for Variant 1 and Variant 1a (i.e. exclude or include PAC CAL data in likelihood) for OM3.

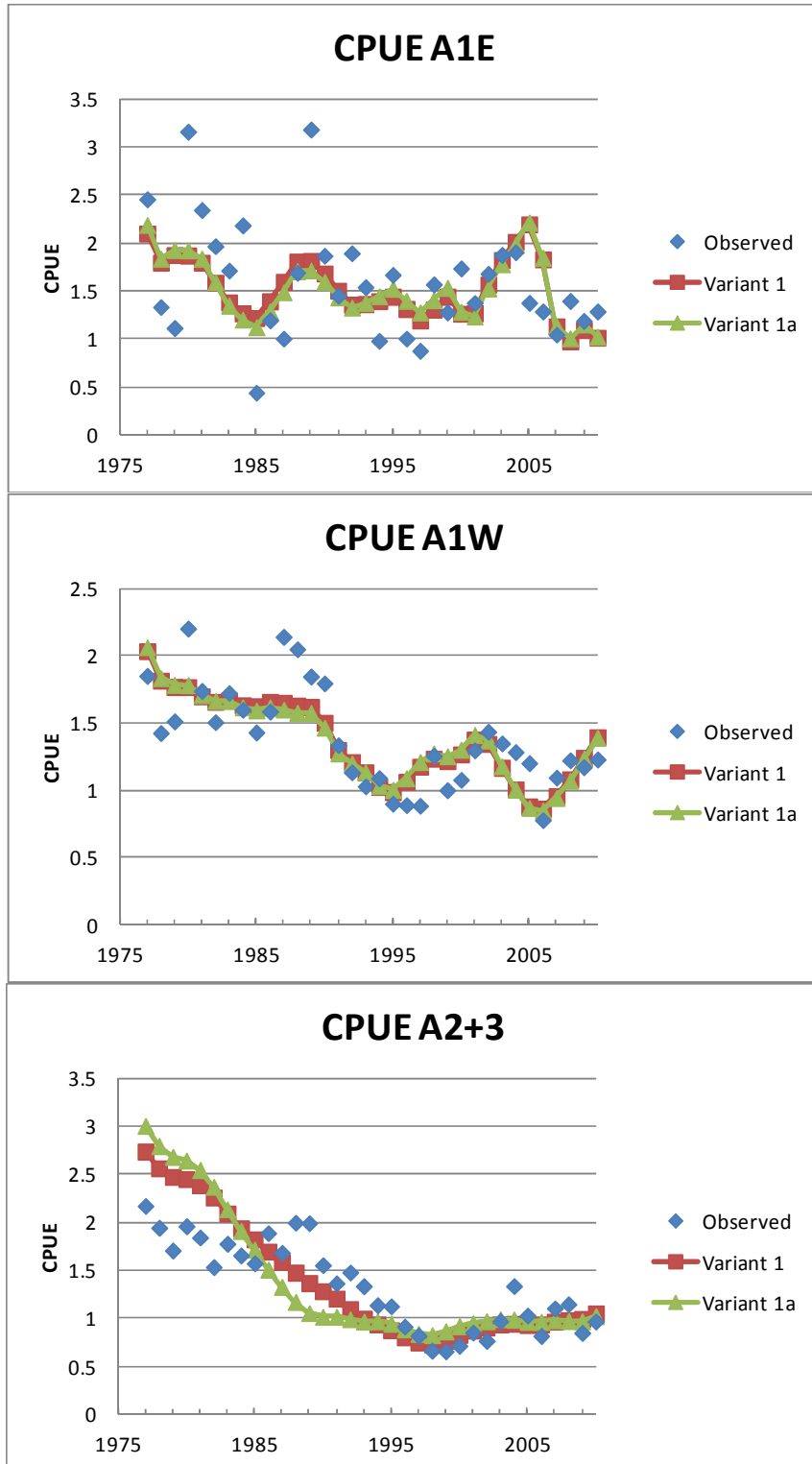


Figure 1d: Comparison of CPUE fits for Variant 2 and Variant 2a (i.e. exclude or include PAC CAL data in likelihood) for OM3.

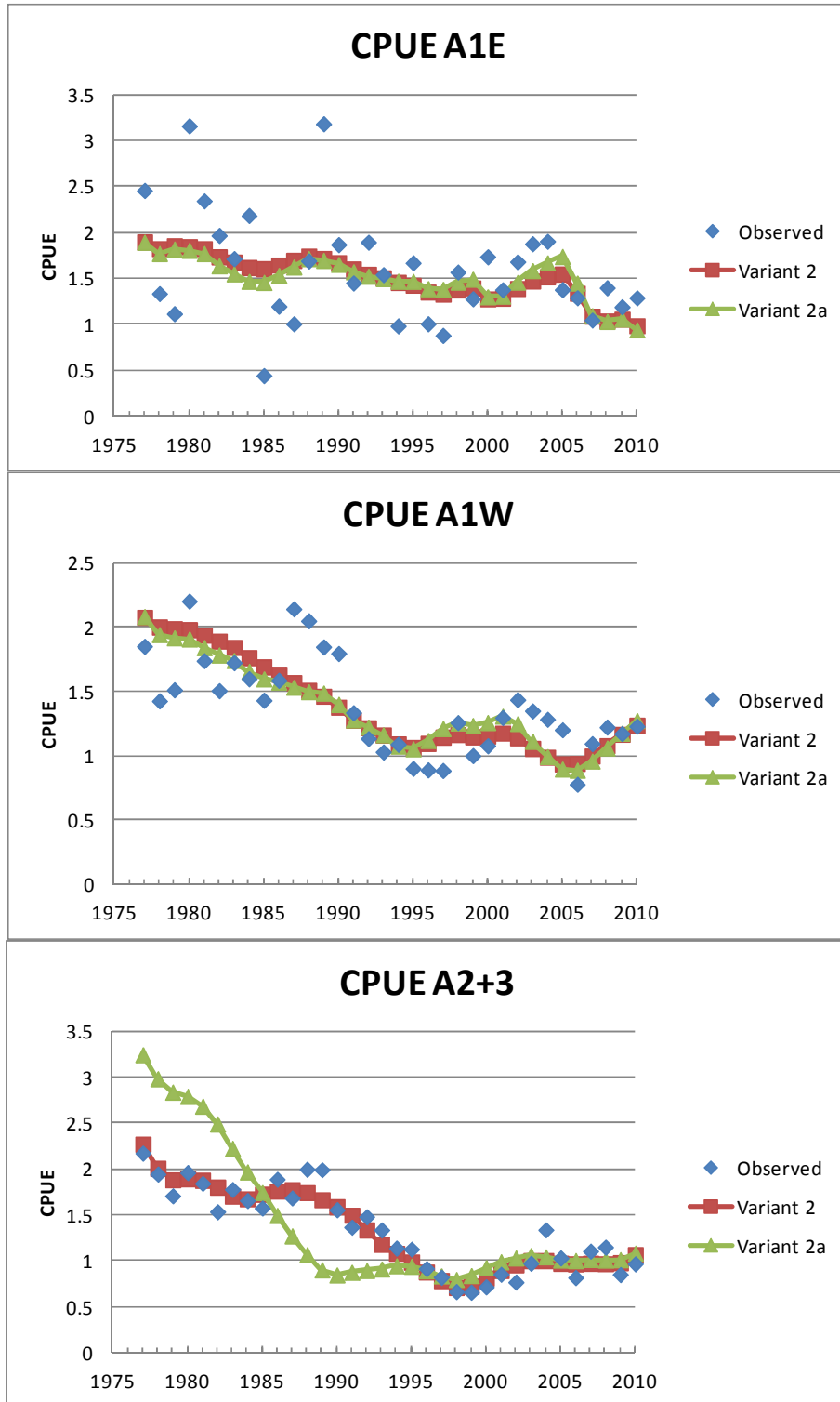


Figure 1e: Comparison of CPUE fits for Variant 3 and Variant 3a (i.e. exclude or include PAC CAL data in likelihood) for OM3.

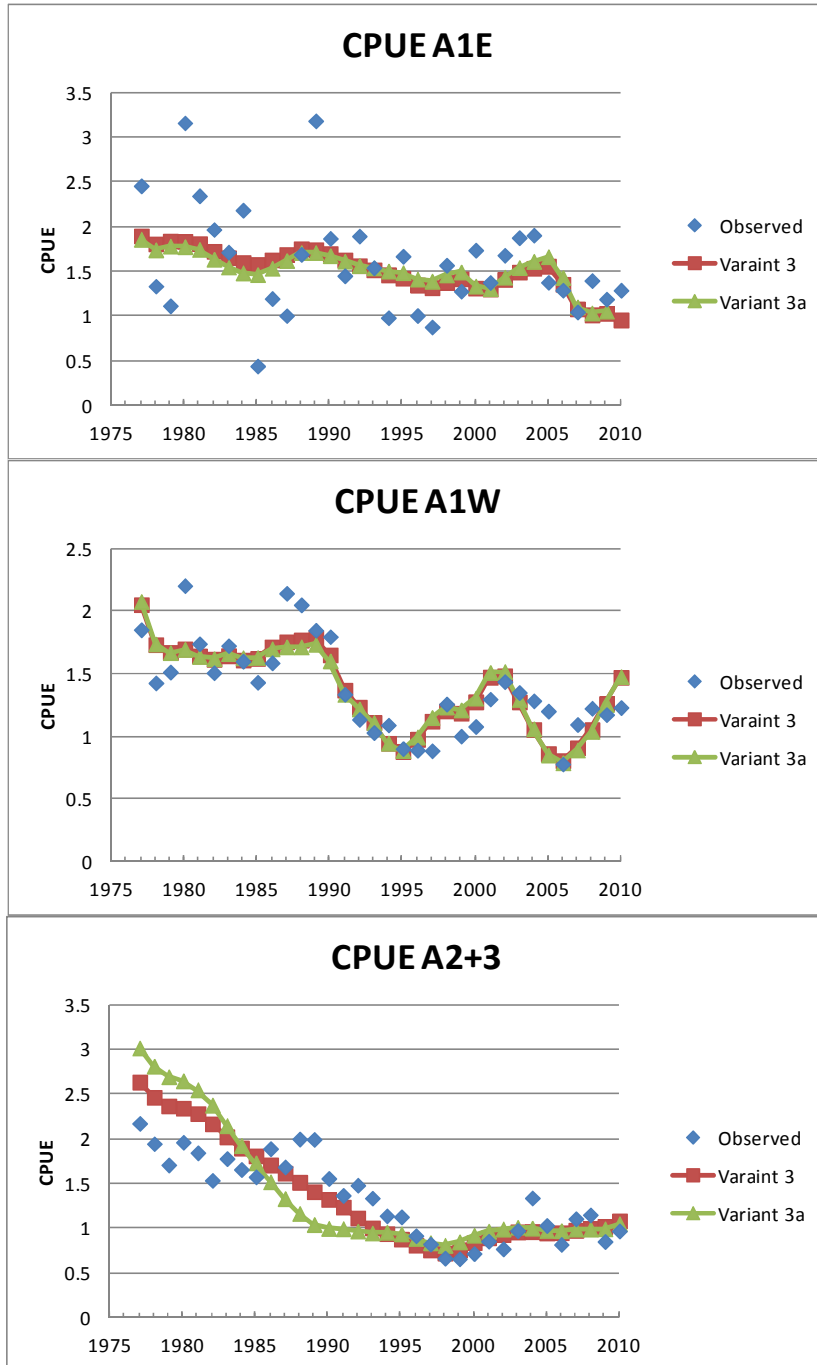


Figure 2a: OM3 Variant 1 SCI CAL standardised residuals.

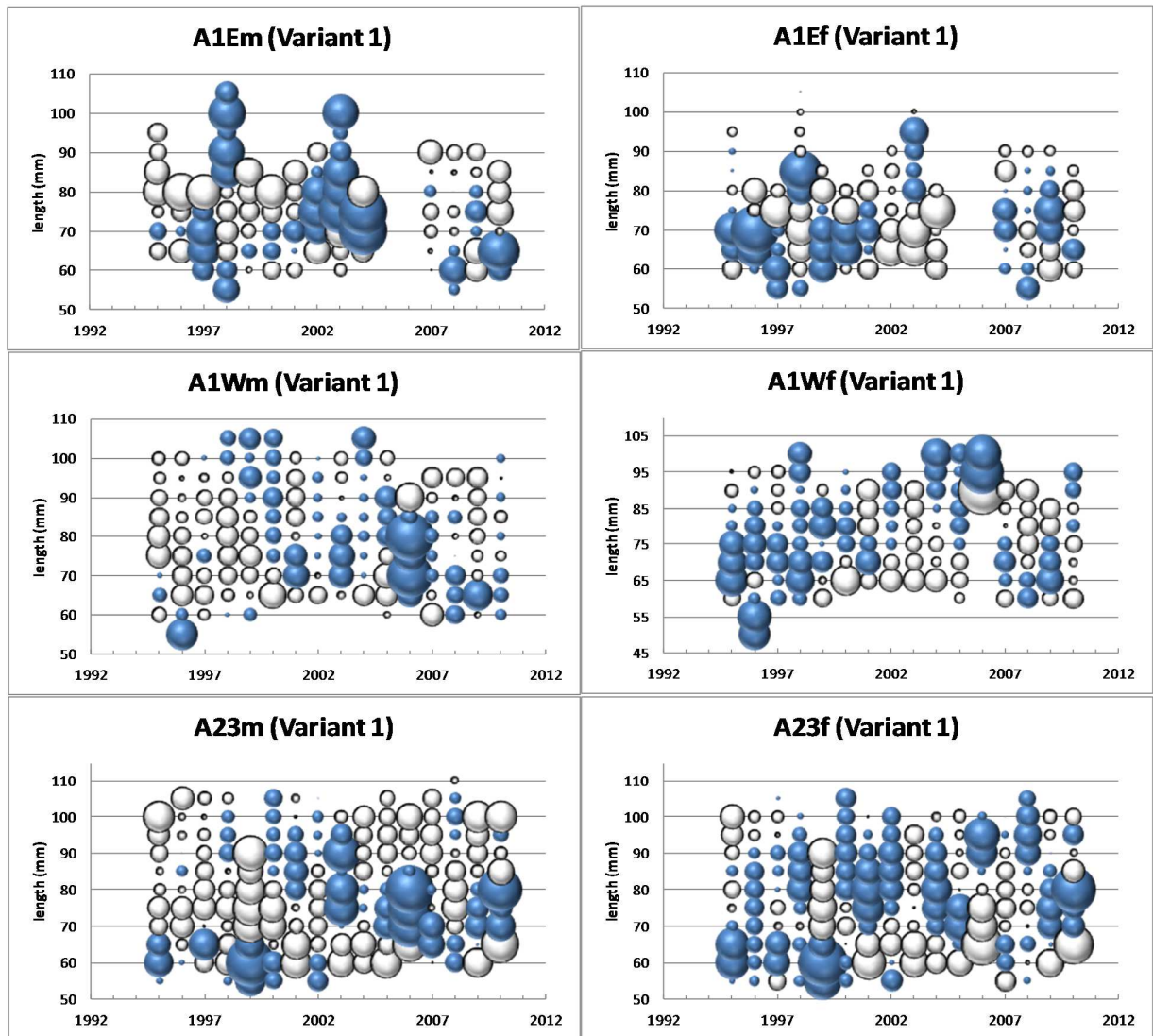


Figure 2b: OM3 Variant 2 SCI CAL standardised residuals.

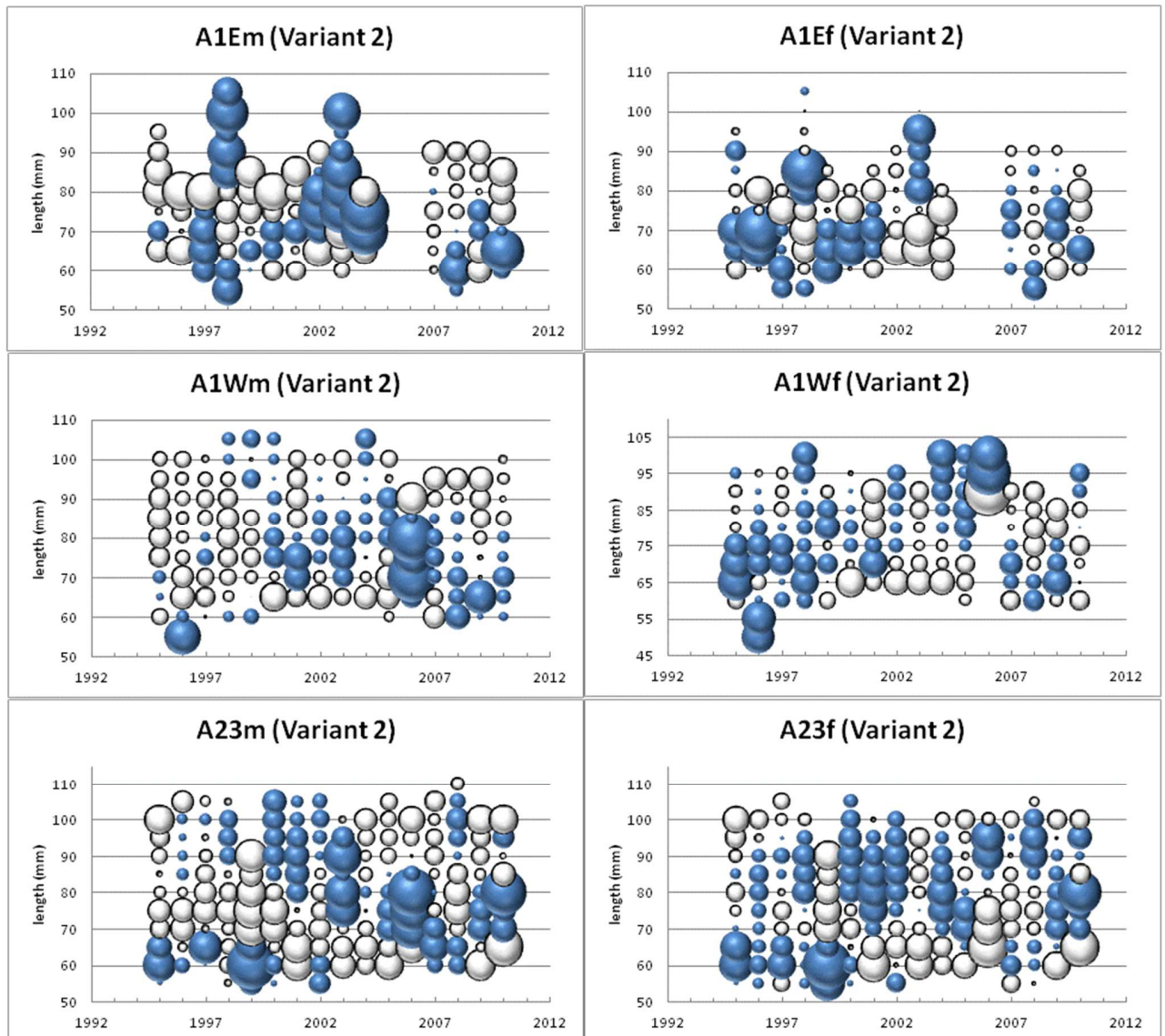


Figure 2c: OM3 Variant 3 SCI CAL standardised residuals.

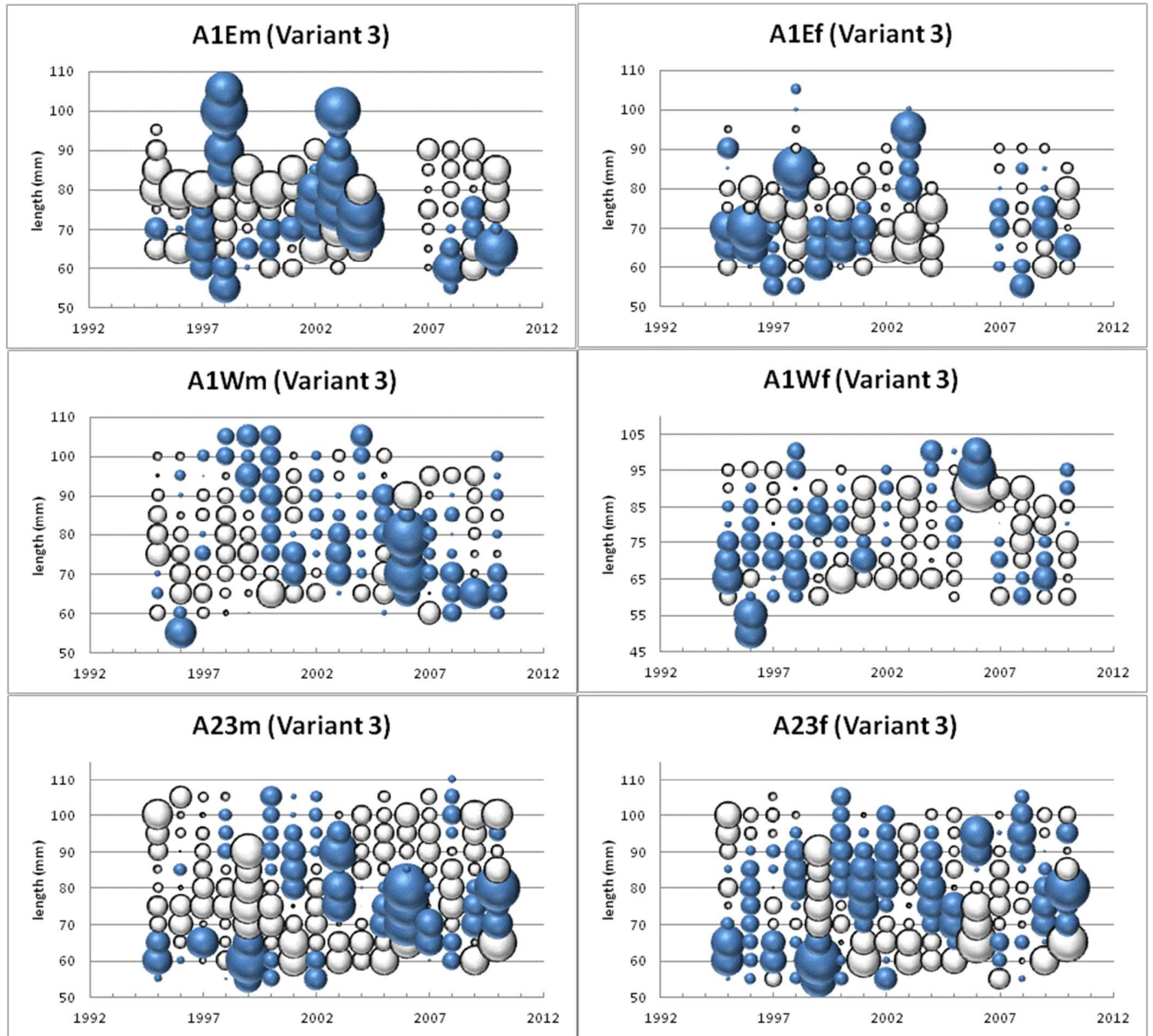


Figure 2d: Comparison for OM3 of Variants 1, 2 and 3 with Variants 1a, 2a and 2b respectively of the PAC CAL standardised residuals. Note that the PAC_CAL data are taken into account only for the second set of models.

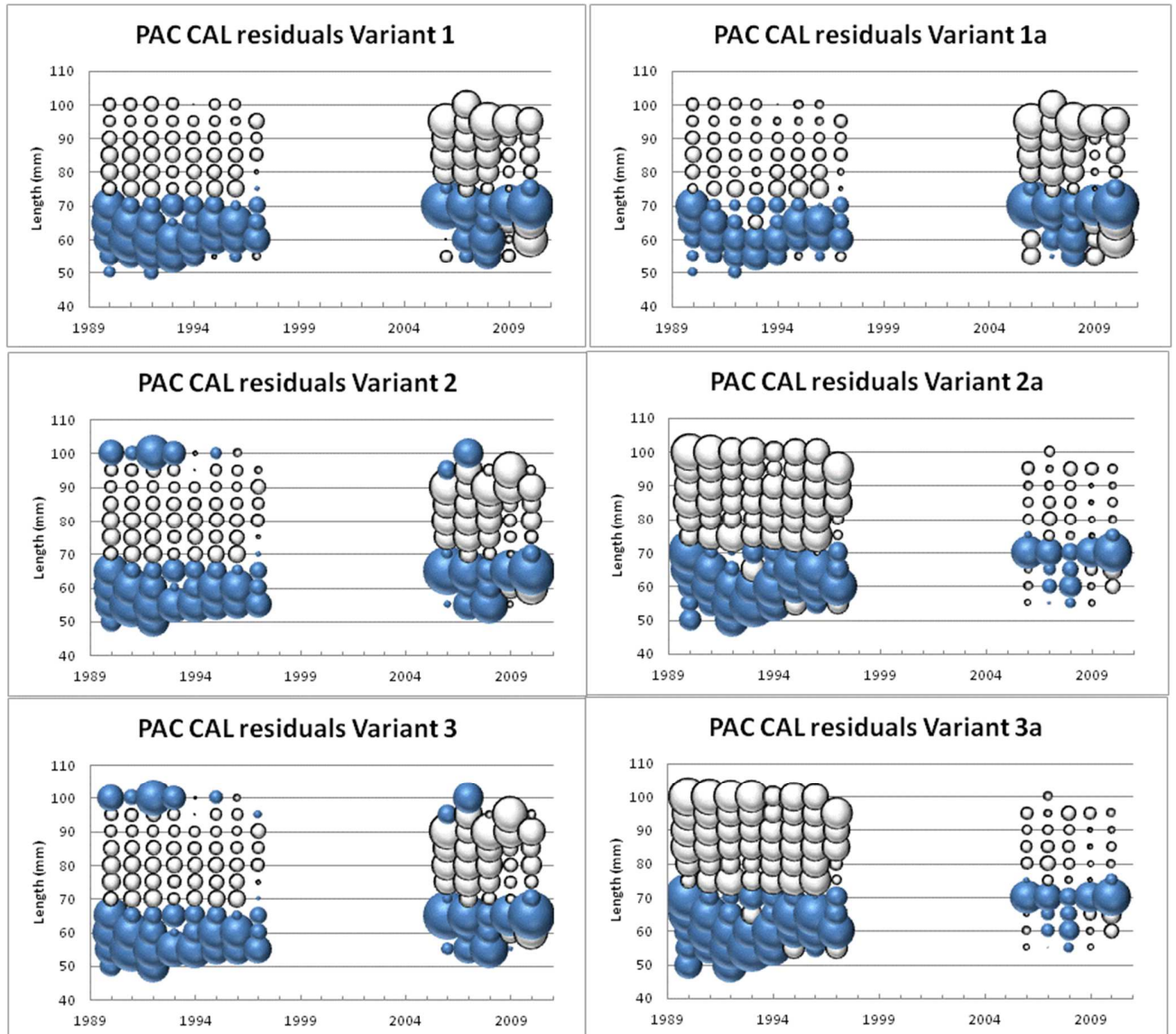


Figure 2e: Comparison for OM3 Variants 1 (no time varying selectivity), 1b (four periods with different selectivities) and 1c (selectivity varying annually) of SCI CAL standardised residuals.

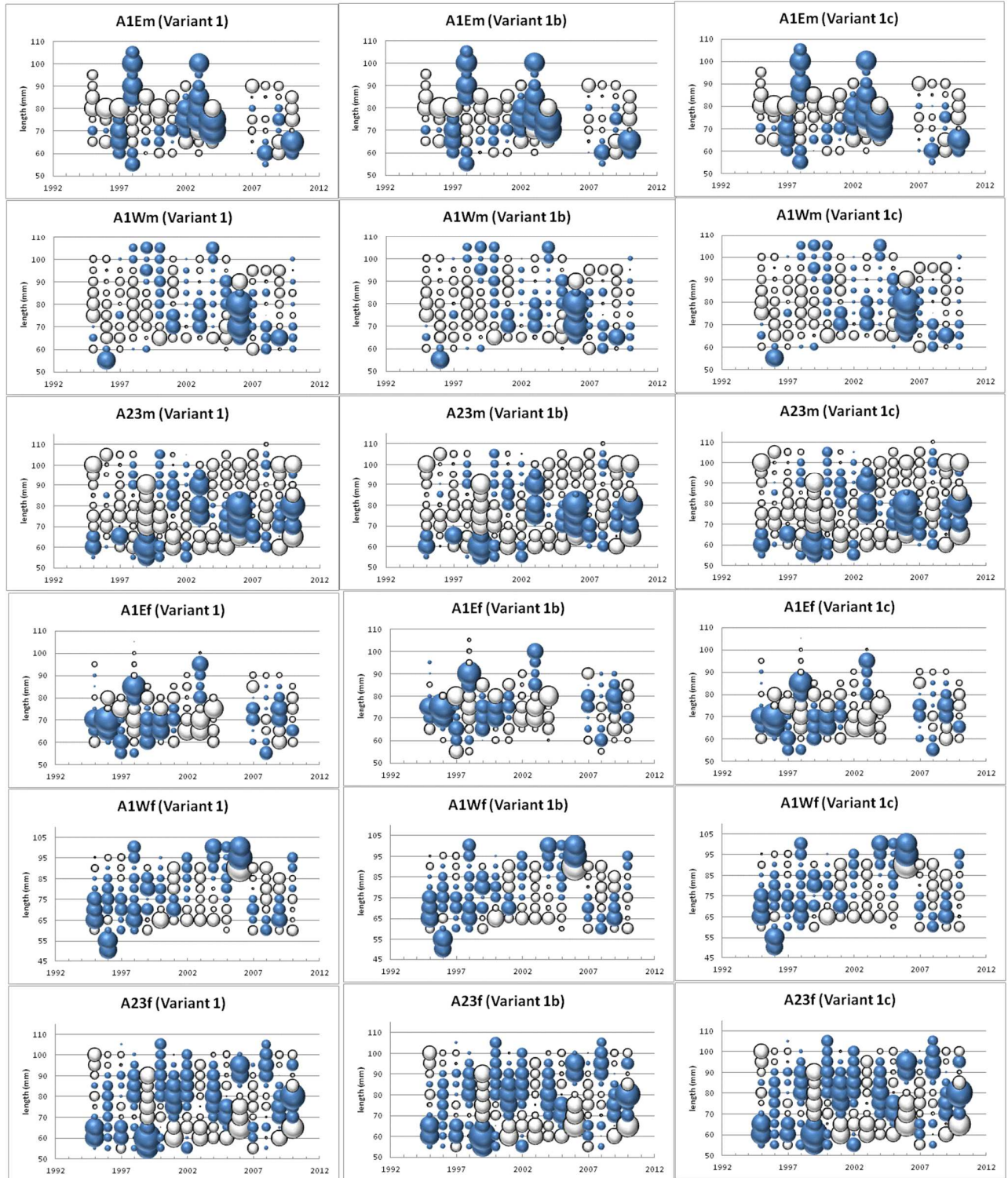


Figure 2f: Comparison of PAC CAL fits for OM3 Variant 1 (PAC CAL data not part of likelihood) and Variant 1a (PAC CAL data part of likelihood) for 1990 and 2010.

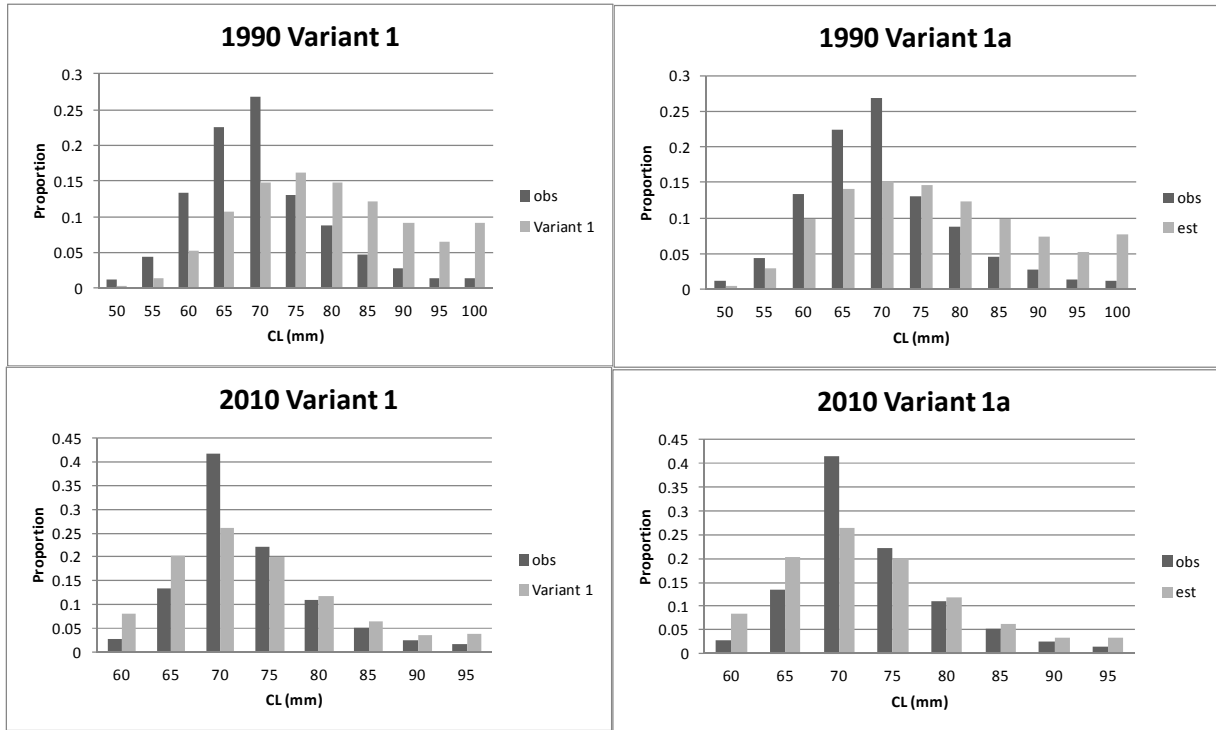


Figure 2g: Comparison of SCI CAL fits for OM3 Variant 1 (PAC CAL not part of likelihood) and Variant 1a (PAC CAL part of likelihood) for 1995 and 2010.

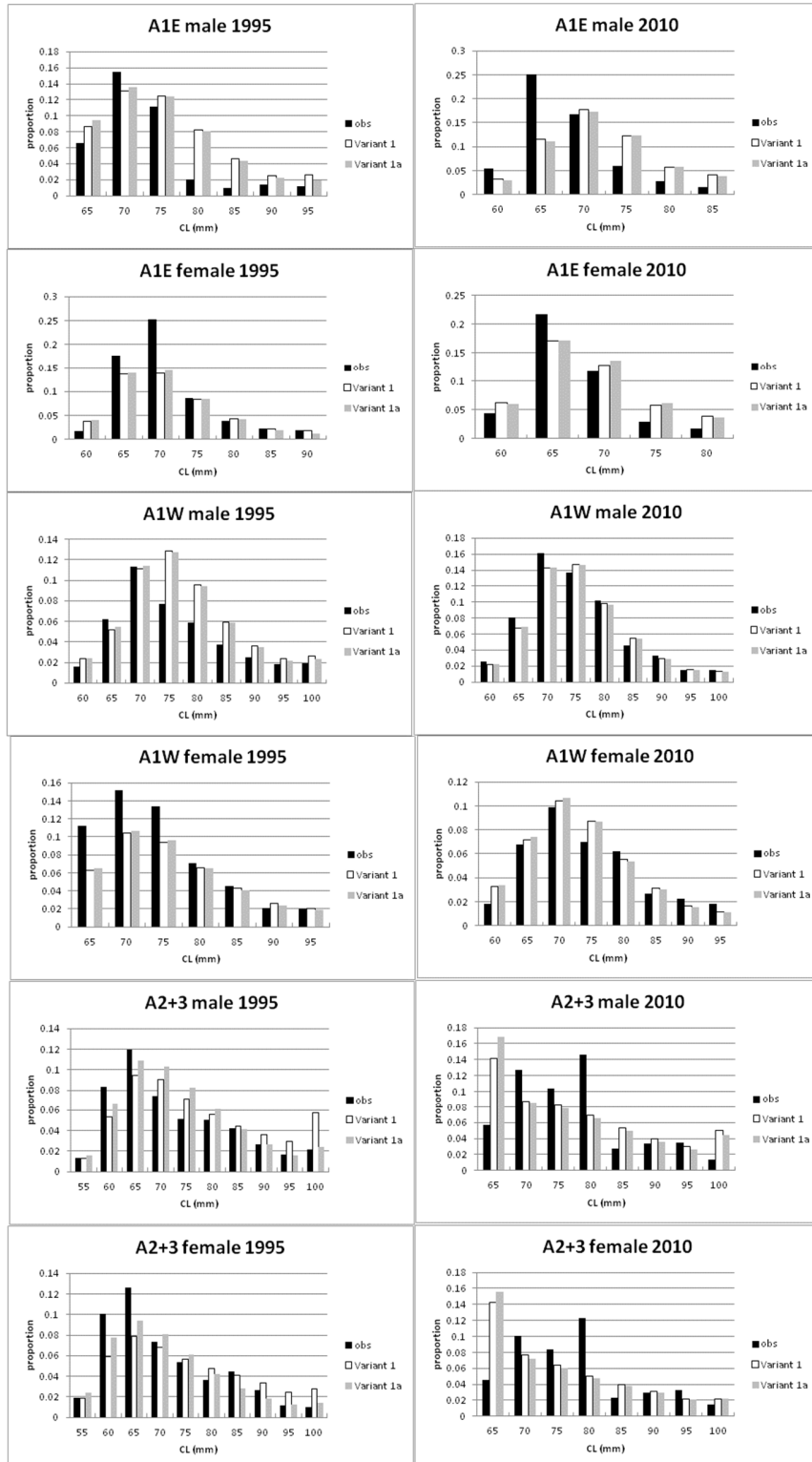


Figure 3: B_{sp} trajectories for OM3 Variants 1, 2 and 3.

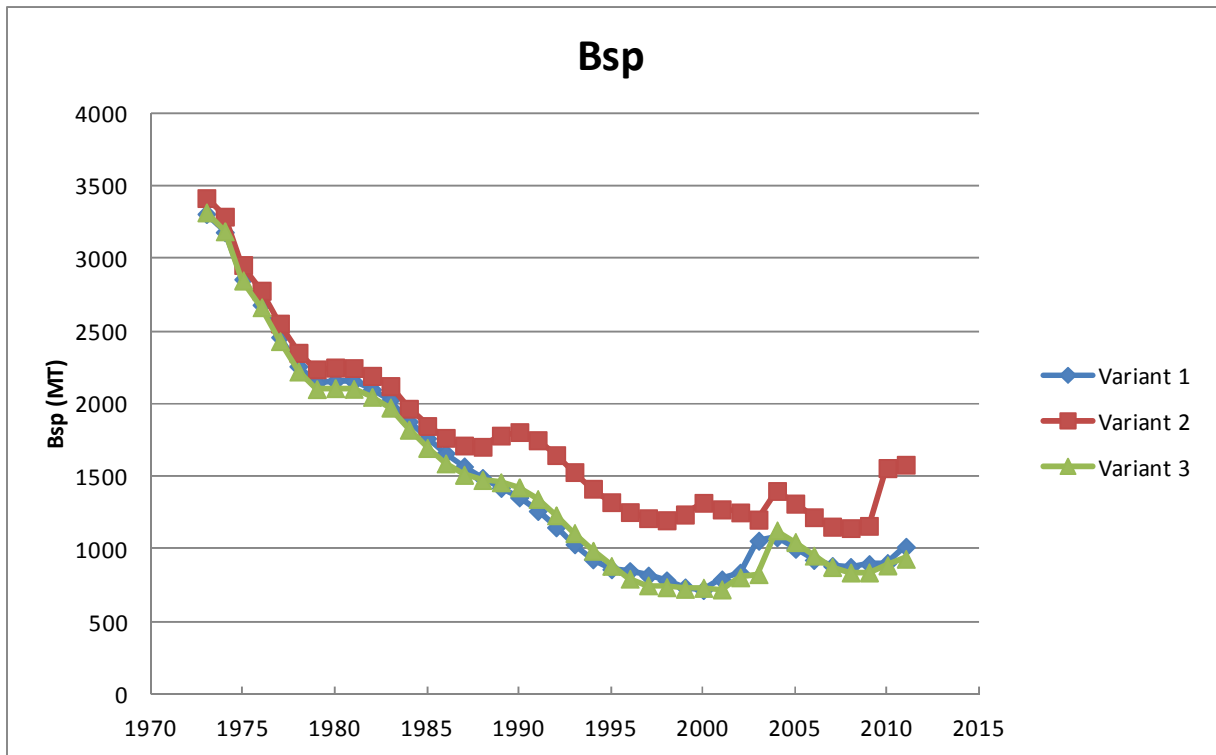


Figure 4: B_{exp} trajectories for each sub-area for OM3 Variants 1, 2 and 3.

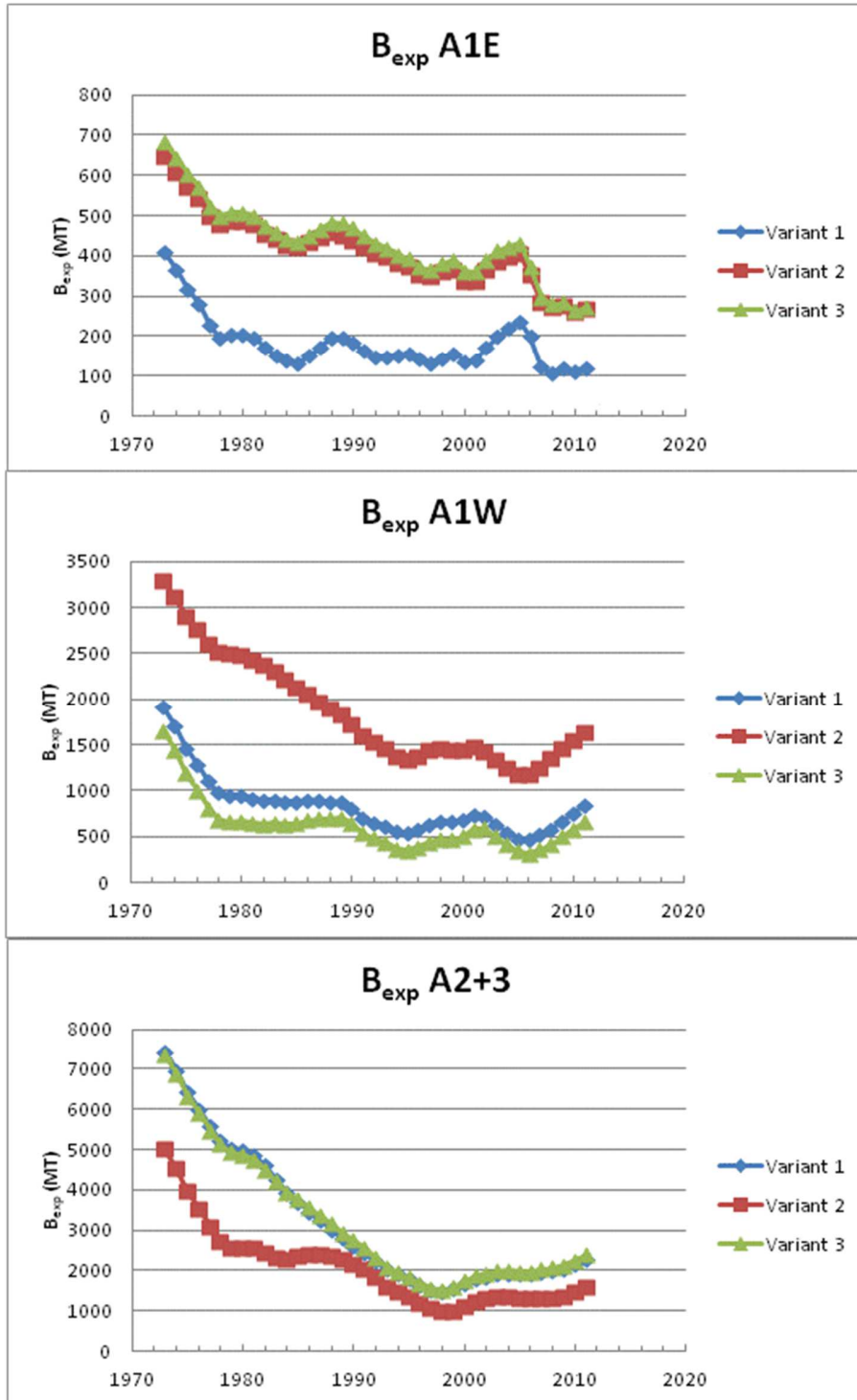


Figure 5: Stock recruit residuals for OM3 Variants 1, 2 and 3.

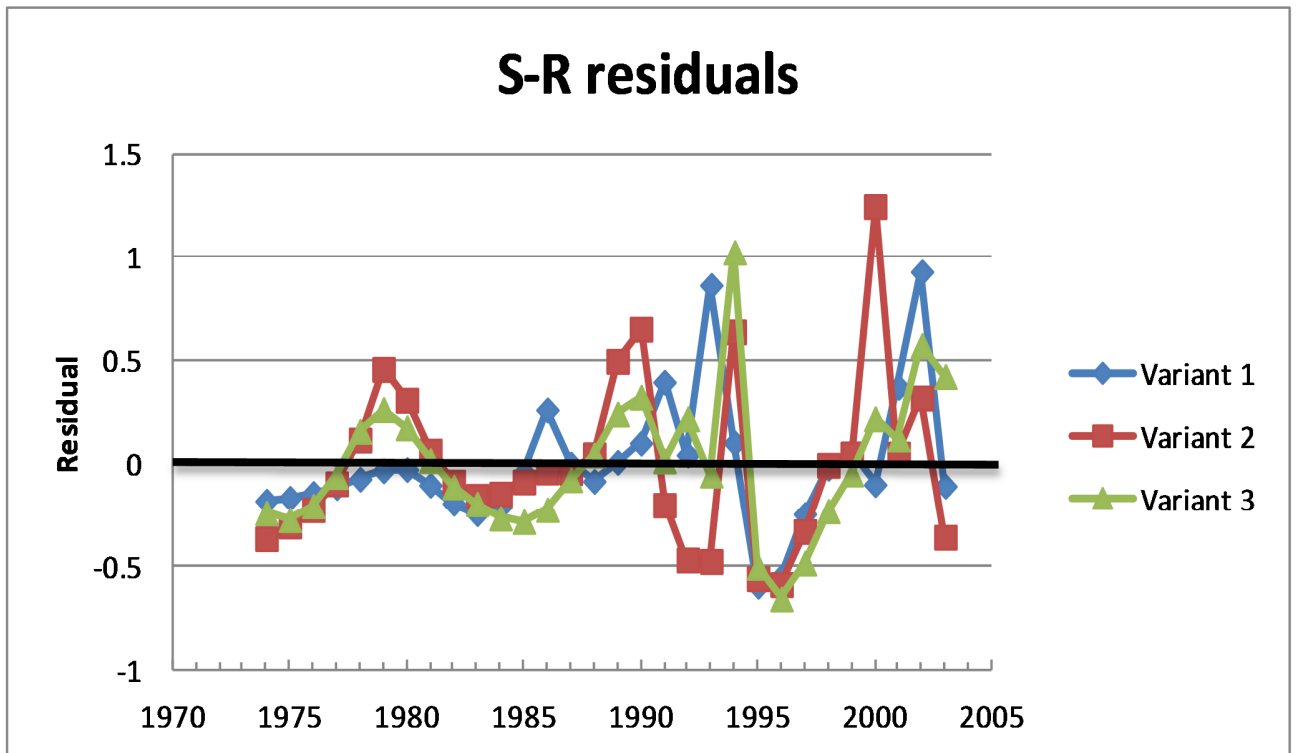


Figure 6a: Somatic growth curves as estimated by OLRAC-Model 7 and used for input to OM 3.

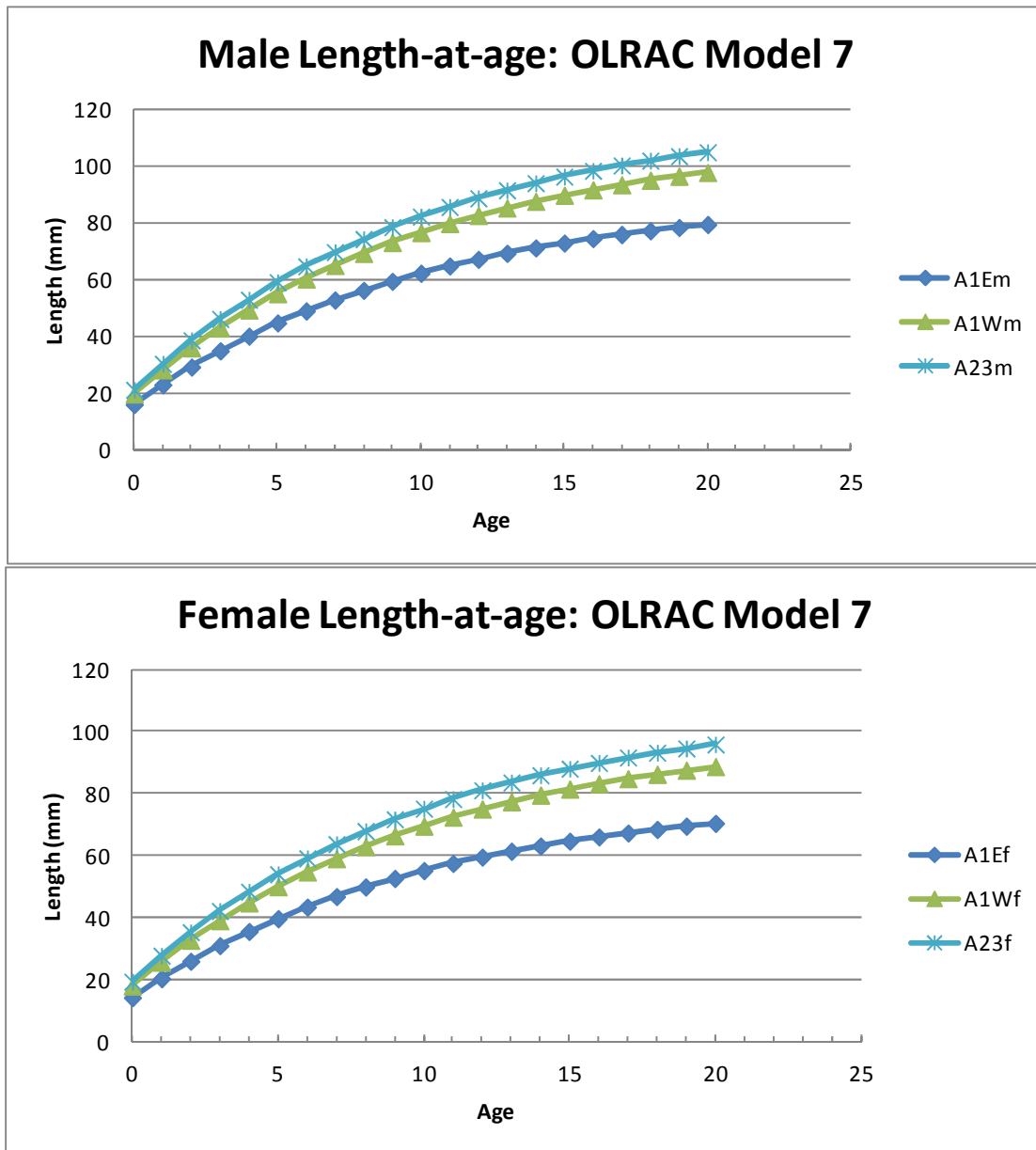


Figure 6b: Somatic growth curves as estimated by OLRAC Model 8 which are used for input to OM 1.

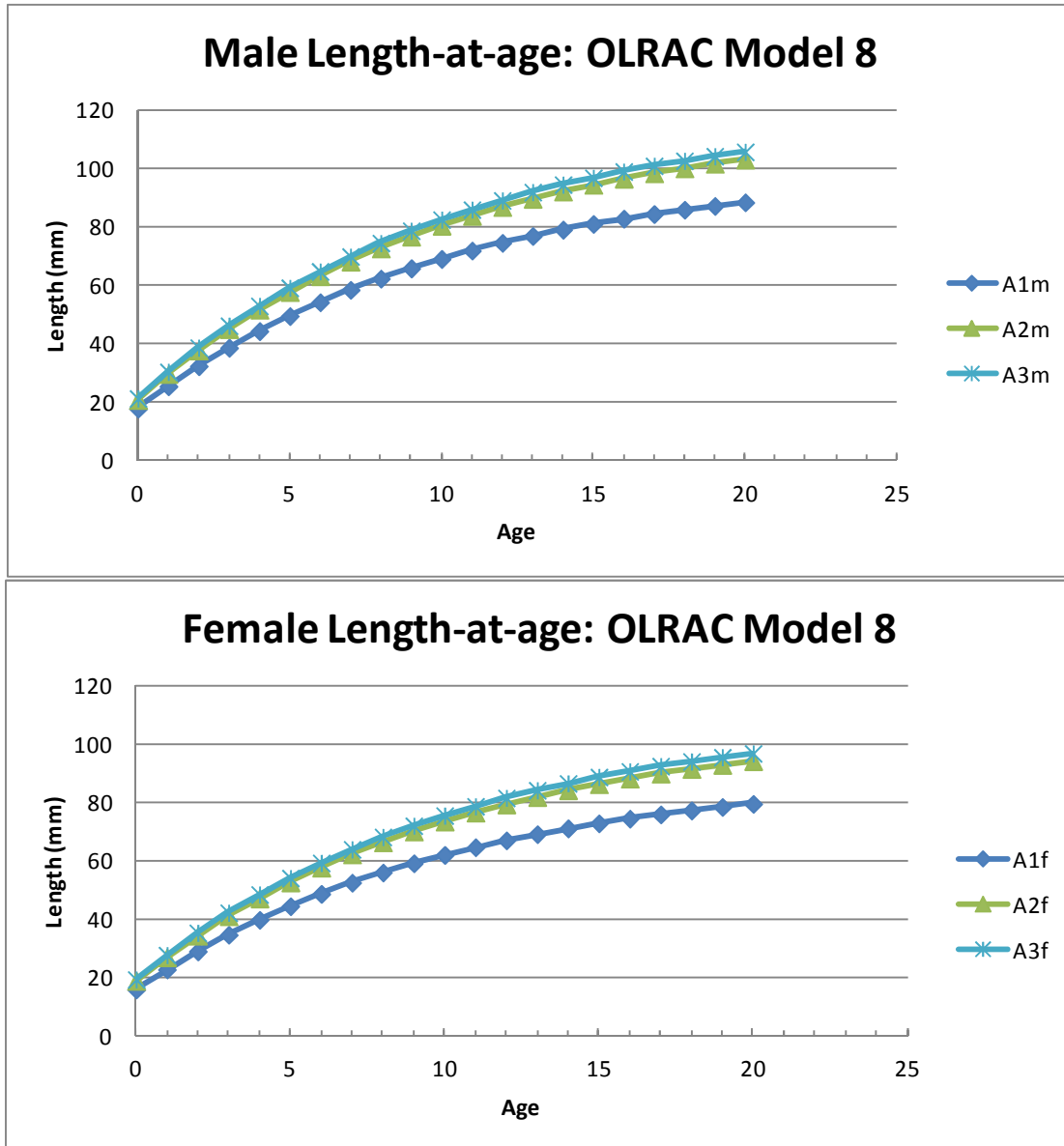


Figure 6c: Comparison of-growth curves for OM1 (A1, A2, A3) – the values recently estimated by OLRAC (“NEW”) and the values used in past assessments (“OLD”).

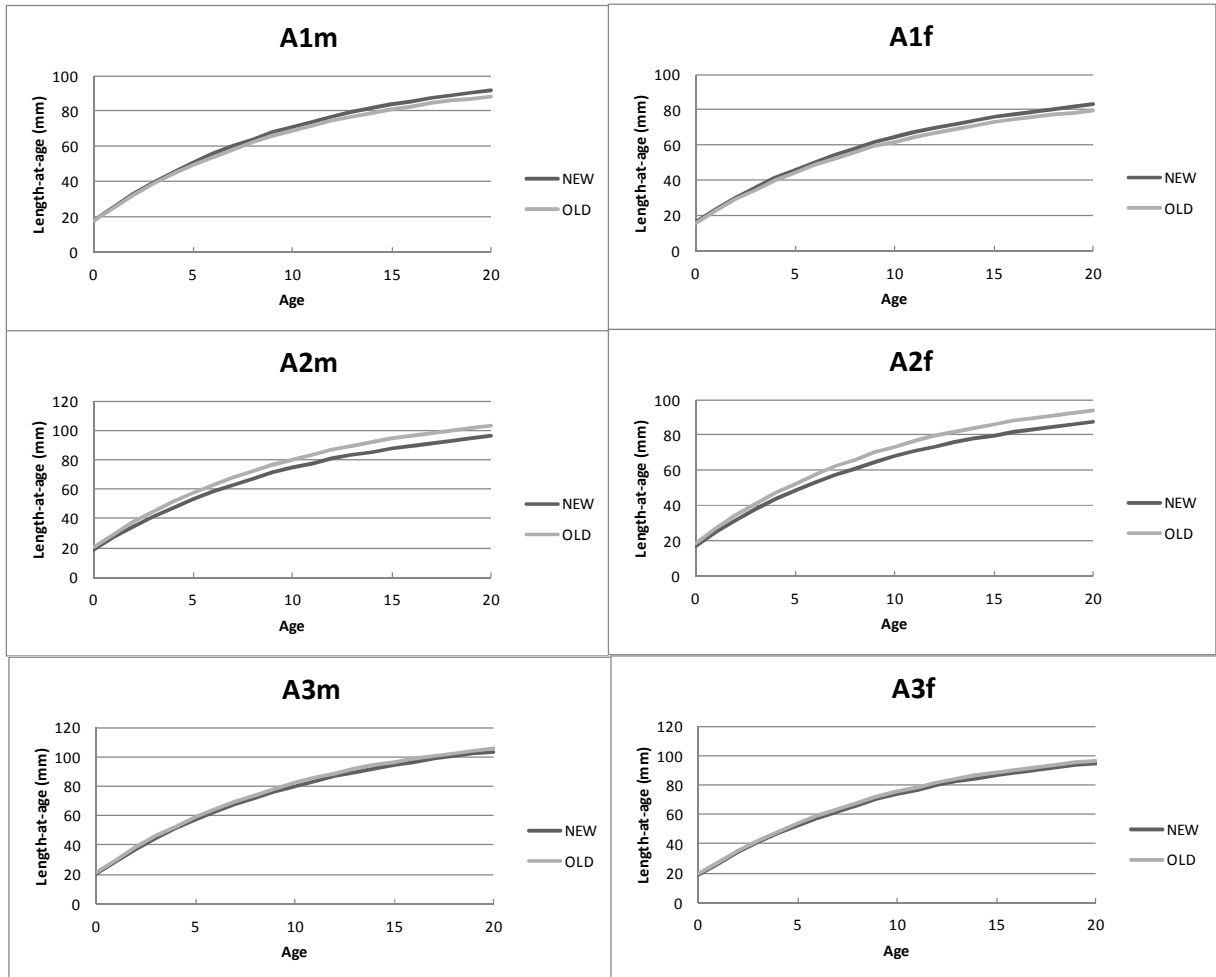


Figure 7a: Selectivity functions for each Variant for OM3.

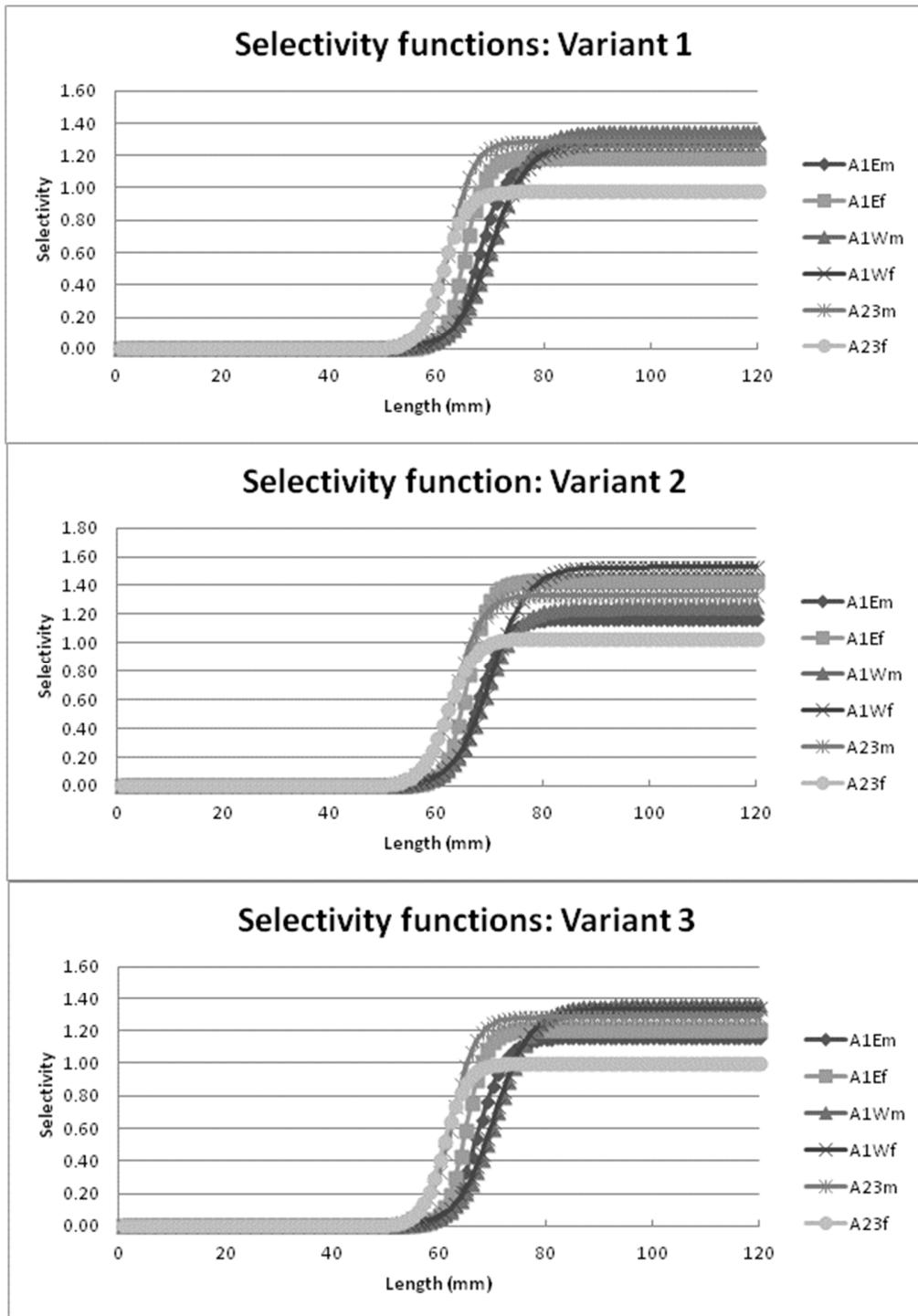


Figure 7b: Selectivity “delta” values (see equation 24) estimated for OM3 Variant 1c.

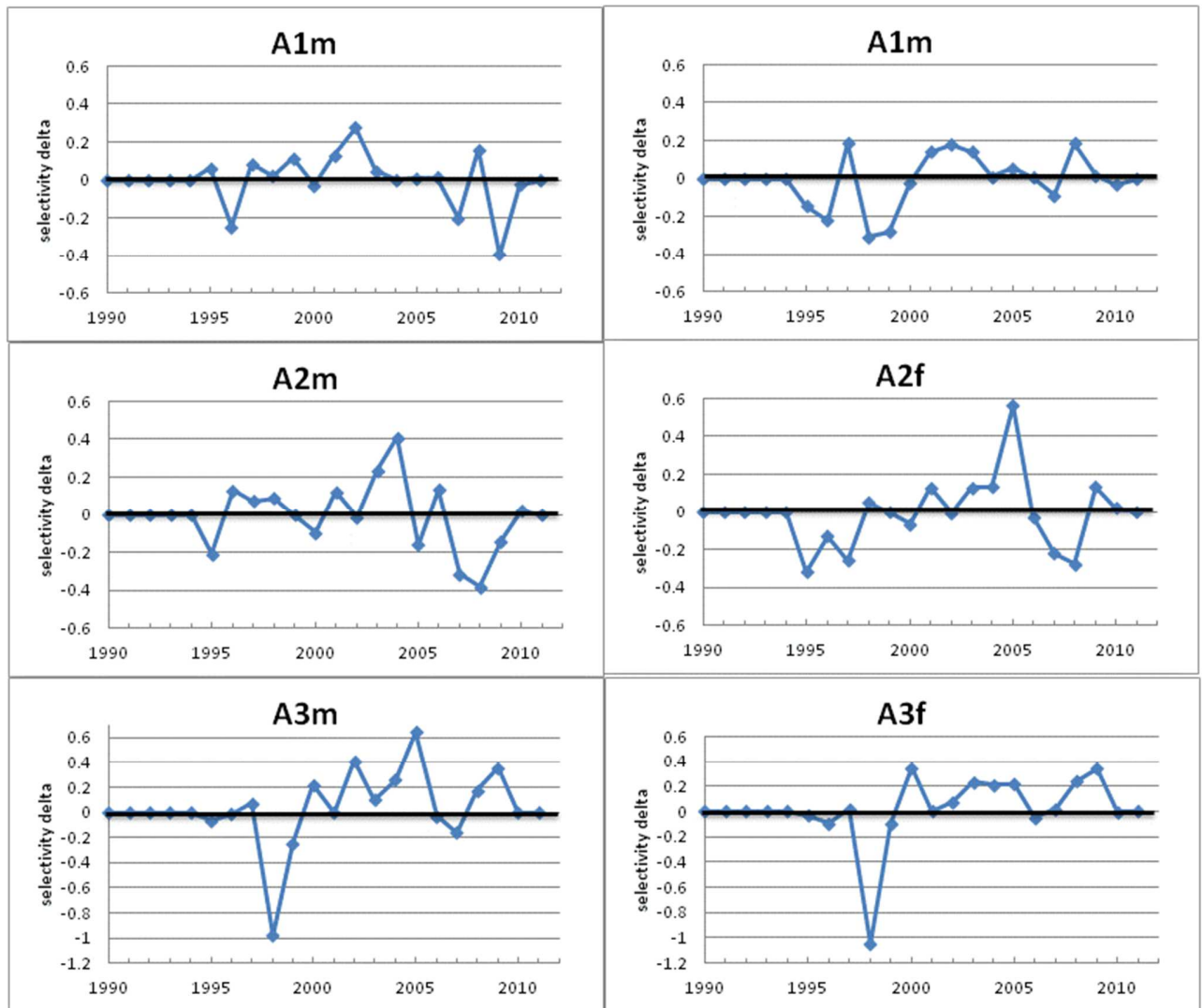


Figure 8: OM 1 Variant 1 fits to CPUE.

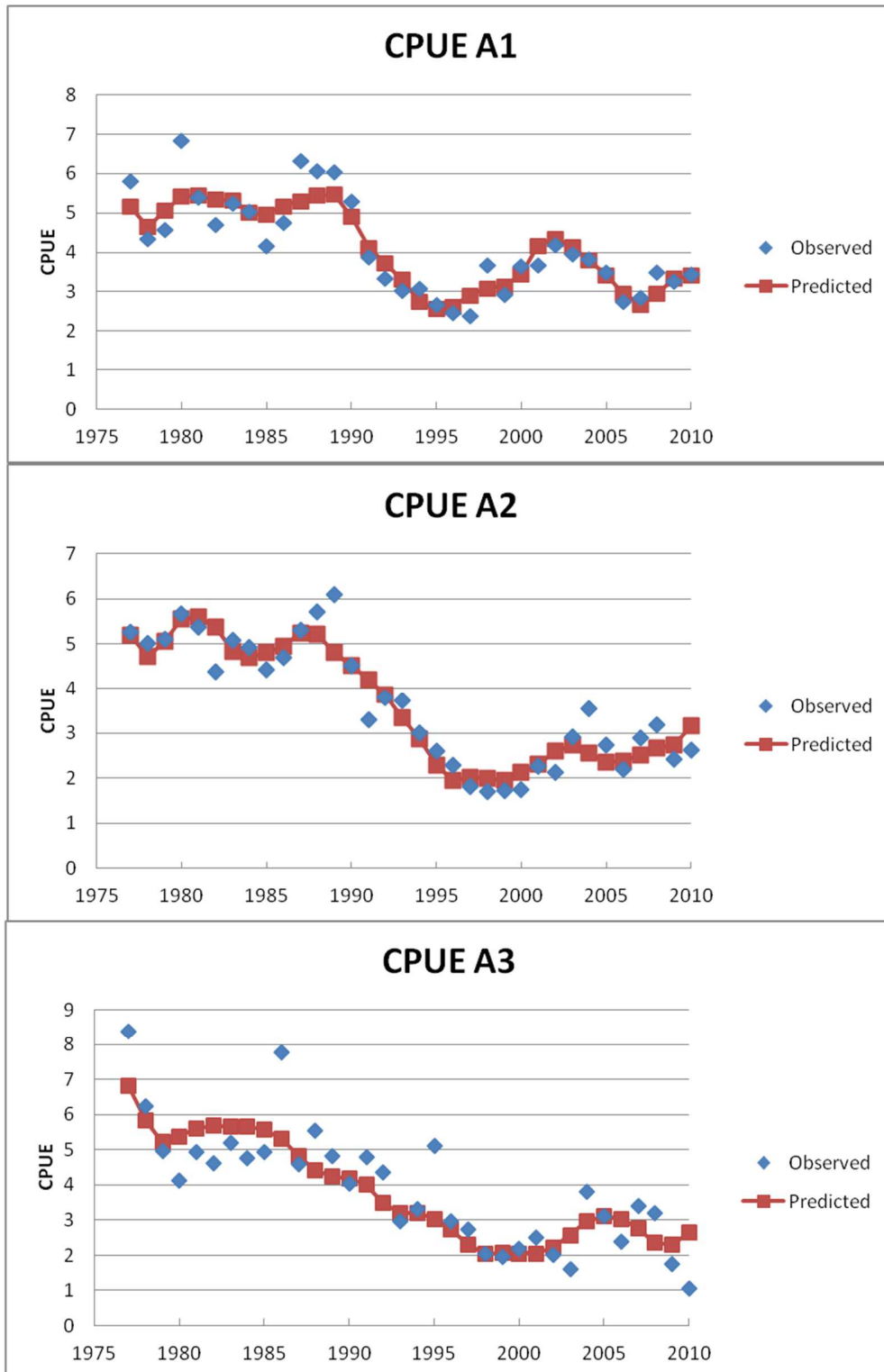


Figure 9: OM1 Variant 1 SCI CAL standardised residuals.

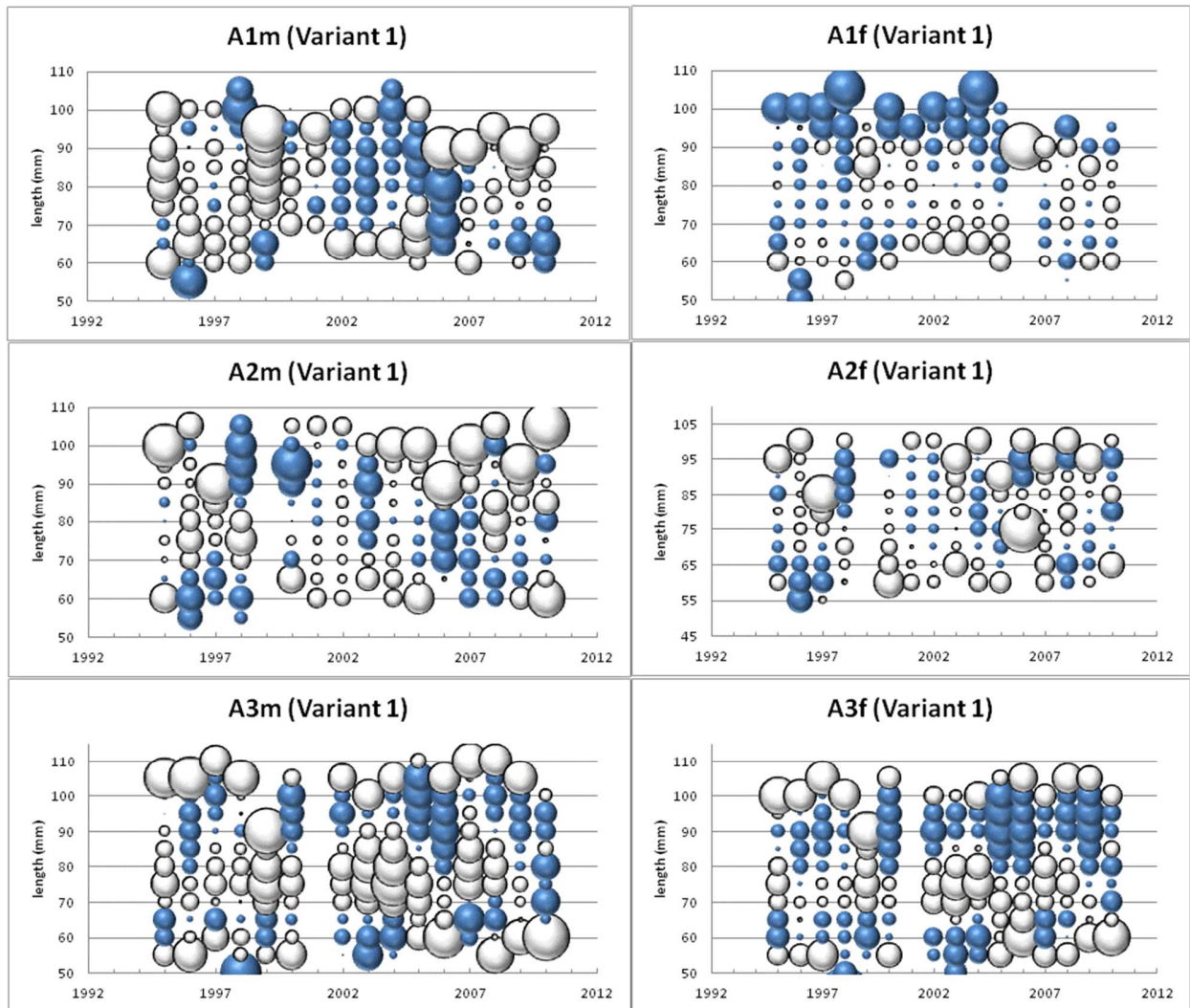
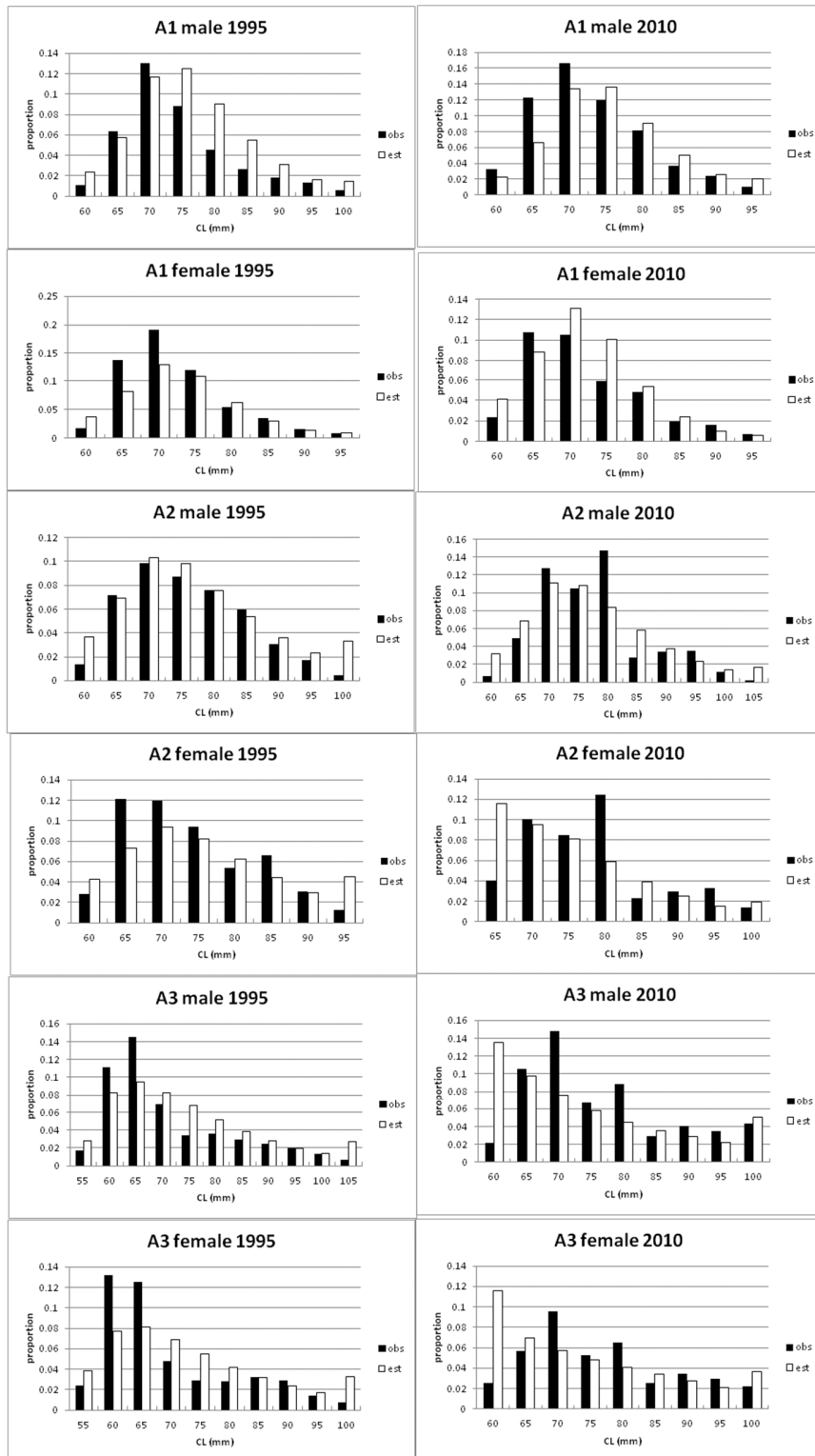


Figure 10: OM1 Variant 1 SCI CAL fits to 1995 and 2010 data.



Appendix

The Age-Structured Production Model for the South Coast rock lobster population

The south coast rock lobster resource is modelled using an age-structured-production-model (ASPM) which fits to catch-at-length data directly. The model is sex-disaggregated (*m/f*) and area-disaggregated. Population equations have been modified from Baranov form to Pope's approximation. This reduces the number of estimable parameters, and speeded runtime of the program.

Note that the model estimates annual variability in the proportion of recruitment (age 0 lobsters) to each area each year. Though formally there is not inter-area movement after this recruitment, in effect this means that there is allowance for such movement, but only for ages less than those which the fishery exploits.

1. The population model

The resource dynamics are modelled by the equations:

$$N_{y+1,0}^{m,A} = \lambda^A R_{y+1} \quad (1)$$

$$N_{y+1,0}^{f,A} = \lambda^A R_{y+1} \quad (2)$$

$$N_{y+1,a+1}^{m,A} = \sum_l [\bar{N}_{y,a,l}^{m,A} e^{-M^m/2} - \bar{C}_{y,a,l}^{m,A}] e^{-M^m/2} \quad (3)$$

$$N_{y+1,a+1}^{f,A} = \sum_l [\bar{N}_{y,a,l}^{f,A} e^{-M^f/2} - \bar{C}_{y,a,l}^{f,A}] e^{-M^f/2} \quad (4)$$

$$N_{y+1,p}^{m,A} = \sum_l [\bar{N}_{y,p-1,l}^{m,A} e^{-M^m/2} - \bar{C}_{y,p-1,l}^{m,A}] e^{-M^m/2} + \sum_l [\bar{N}_{y,p,l}^{m,A} e^{-M^m/2} - \bar{C}_{y,p,l}^{m,A}] e^{-M^m/2} \quad (5)$$

$$N_{y+1,p}^{f,A} = \sum_l [\bar{N}_{y,p-1,l}^{f,A} e^{-M^f/2} - \bar{C}_{y,p-1,l}^{f,A}] e^{-M^f/2} + \sum_l [\bar{N}_{y,p,l}^{f,A} e^{-M^f/2} - \bar{C}_{y,p,l}^{f,A}] e^{-M^f/2} \quad (6)$$

where

$N_{y,a}^{m/f,A}$ is the number of male or female (m/f) lobsters of age a at the start of year y in area A ,

$\bar{N}_{y,a,l}^{m/f,A}$ is the number of male or female (m/f) lobsters of age a of length l at the start of year y in area A (see equation 15),

$M^{m/f}$ denotes the natural mortality rate for male or female (m/f) lobsters which is assumed to be constant for all a (and here identical for male and female lobsters). Note that this value is fixed at 0.10 in this model.

$\bar{C}_{y,a,l}^{m/f,A}$ is the catch of male or female (m/f) lobsters of age a of length l in year y in area A , and

p is the maximum age considered (taken to be a plus-group).

Note: $\sum_A \lambda^A = 1$ and that $0 < \lambda^A < 1$. The model makes the assumption there is no cross-boundary movement after recruitment.

The number of recruits of age 0, of each sex, at the start of year y is related to the spawner stock size by a stock-recruitment relationship:

$$R_y = \frac{\alpha B_y^{sp}}{\beta + (B_y^{sp})^\gamma} e^{\zeta_y} \quad (7)$$

where

α, β and γ are spawner biomass-recruitment parameters ($\gamma=1$ for a Beverton-Holt relationship),

ζ_y reflects fluctuation about the expected (median) recruitment for year y , and

B_y^{sp} is the spawner biomass at the start of year y , given by:

$$B_y^{sp} = \sum_{a=1}^p f_a \sum_A [w_a^{f,A} N_{y,a}^{f,A}] \quad (8)$$

where $w_a^{f,A}$ is the begin-year mass of female lobsters at age a in area A , and f_a is the proportion of lobster of age a that are mature.

In order to work with estimable parameters that are more meaningful biologically, the stock-recruit relationship is re-parameterised in terms of the pre-exploitation equilibrium female spawning biomass, K^{sp} , and the “steepness” of the stock-recruit relationship (recruitment at $B^{sp} = 0.2K^{sp}$ as a fraction of recruitment at $B^{sp} = K^{sp}$):

$$\alpha = \frac{4hR_1}{5h-1} \quad (9)$$

and

$$\beta = \frac{(K^{sp}(1-h))}{5h-1} \quad (10)$$

where

$$R_1 = K^{sp} / \left\{ \sum_A \lambda^A \left[\sum_{a=1}^{p-1} f_a w_a^{f,A} e^{-\sum_{a'=0}^{a-1} M_{a'}^f} + f_p w_p^{f,A} \frac{e^{-\sum_{a'=0}^{p-1} M_{a'}^f}}{1 - e^{-M_p^f}} \right] \right\} \quad (11)$$

The total catch by mass in year y for area A is given by:

$$C_y^A = \sum_{m/f} \sum_a \sum_l \bar{C}_{y,a,l}^{m/f,A} \quad (12)$$

where

$$\bar{C}_{y,a,l}^{m,A} = w_{a+\frac{1}{2}}^{m,A} \bar{N}_{y,a,l}^{m,A} S_l^{m,A} F_y^A \quad (13)$$

$$\bar{C}_{y,a,l}^{f,A} = w_{a+\frac{1}{2}}^{f,A} \bar{N}_{y,a,l}^{f,A} S_l^{f,A} \mu^A F_y^A \quad (14)$$

where $w_l^{m/f,A}$ denotes the mass of a m/f lobster at length l in area A , and where

$S_l^{m/f,A}$ is the length-specific selectivity for male/female lobsters in area A ,

F_y^A is the fully selected fishing mortality in year y for lobsters in area A , and which is constrained to be ≤ 0.80 ,

μ^A is the relative female selectivity scaling parameter for area A , and

$$\bar{N}_{y,a,l}^{m/f,A} = N_{y,a}^{m/f,A} Q_{a,l}^{m/f,A} \quad (15)$$

where $Q_{a,l}^{m/f,A}$ is the proportion of fish of age a that fall in the length group l for the sex and area concerned (thus $\sum_l Q_{a,l}^{m/f,A} = 1$ for all ages a).

The matrix Q is calculated under the assumption that length-at-age is normally distributed about a mean given by the von Bertalanffy equation (Brandão *et al.*, 2002), i.e.:

$$l_a \sim N^* \left[l_{\infty}^{m/f,A} \left(1 - e^{-\kappa(a-t_0)} \right); \theta_a^2 \right] \quad (16)$$

where

N^* is the normal distribution truncated at ± 3 standard deviations, and
 θ_a is the standard deviation of length-at-age a , which is modelled to be proportional to the expected length-at-age a , i.e.:

$$\theta_a = \beta^* l_{\infty}^{m/f,A} \left(1 - e^{-\kappa(a-t_0)} \right) \quad (17)$$

with β^* a parameter estimated in the model fitting process.

The model estimate of mid-year exploitable biomass is given by:

$$\hat{B}_y^A = \hat{B}_y^{m,A} + \hat{B}_y^{f,A} \quad (18)$$

where

$$\hat{B}_y^{f,A} = \sum_a \sum_l \mu^A S_l^{f,A} \left[w_{a+\frac{1}{2}}^{f,A} \bar{N}_{y,a,l}^{f,A} e^{-M^f/2} \right] \quad (19)$$

$$\hat{B}_y^{m,A} = \sum_a \sum_l S_l^{m,A} \left[w_{a+\frac{1}{2}}^{m,A} \bar{N}_{y,a,l}^{m,A} e^{-M^m/2} \right] \quad (20)$$

and where

μ^A is an area-specific factor that scales female relative to male catchability; and

\hat{B}_y^A is the total (male plus female) model estimate of mid-year exploitable biomass for year y in area A .

Fishing proportion:

$$F_y^A = \frac{C_y^{obs,A}}{B_y^A} \quad (21)$$

1.1 Catch-at-length proportions

$$\hat{P}_{y,l}^{m,A} = \frac{\sum_a \bar{C}_{y,a,l}^{m,A}}{\sum_l \sum_{m,f} \sum_a \bar{C}_{y,a,l}^{m/f,A}} \quad (22)$$

$$\hat{P}_{y,l}^{f,A} = \frac{\sum_a \bar{C}_{y,a,l}^{f,A}}{\sum_l \sum_{m,f} \sum_a \bar{C}_{y,a,l}^{m/f,A}} \quad (23)$$

where $\hat{P}_{y,l}^{m/f,A}$ is the estimated proportion of catch in area A of m/f lobsters in length class l in year y (note that the total proportions of male plus female lobsters will thus equal 1.0 in any given year and area).

1.2 Time varying selectivity-at-length function

The selectivity function (which depends on length) may be allowed to vary over the time period for which catch-at-age data are available (1995-2010). To effect this, the form of the selectivity function is generalised to:

$$S_{y,l}^{m/f,A} = \frac{1}{1 + e^{-\ln 19(l - (l_{50}^{m/f,A} + \delta_y^{m/f,A}) / \Delta^{m/f,A})}} \quad (24)$$

The estimable parameters are thus:

- $l_{50}^{m/f,A}$ (the expected length at 50% selectivity), and
- $\Delta^{m/f,A}$ and for $y = 1995-2010$

Note:

- the expected length at 95% selectivity ($l_{95}^{m/f,A}$) is given by $l_{50}^{m/f,A} + \Delta^{m/f,A}$,
- $\delta_y^{m/f,A}$ for pre-1995 and 2010+ = 0.

An extra term is added to the negative log likelihood to limit the extent to which the $\delta_y^{m/f,A}$ differ from zero – see section 2.6.

An issue to be taken into account is that for equation (24), if $\delta_y^{m/f,A}$ decreases, this means that selectivity is increasing on younger lobsters; however given that the model fitting procedure assumes that:

$$C\hat{P}UE_y = q \sum_l w_l S_{l,a} N_{l,a} e^{-M/2} \quad (25)$$

this situation seems implausible, in that an enhanced CPUE would result even if there was not any increase in abundance.

Presumably enhanced catches of younger animals are achieved by spatially redistributing effort on a scale finer than captured by the GLM standardisation of the CPUE. A standard method to adjust for this, while maintaining a constant catchability coefficient q , is to renormalise the selectivity function in some way:

$$S_{y,l}^{m/f,A} \rightarrow S_{y,l}^{*,m/f,A} = S_{y,l}^{m/f,A} / X_y^{m/f,A} \quad (26)$$

where here as a simple initial approach we have chosen:

$$X_y^{m/f,A} = \sum_{l_1^{m/f,A}}^{l_2^{m/f,A}} \frac{S_{y,l}^{m/f,A}}{l_2^{m/f,A} - l_1^{m/f,A} + 1} \quad (27)$$

i.e., normalising selectivity by its average over a certain length range, so that now if $\delta_y^{m/f,A}$ decreases, the $S_{y,l}^{*,m/f,A}$ will decrease for large l to compensate for the effort spread to locations where younger animals are found associated with the increase for smaller l .

The values of $l_1^{m/f,A}$ and $l_2^{m/f,A}$ have been fixed at the following values to ensure that the ranges associated with these l values cover the greater part of these distributions. [Note that for the moment, these values remain the same as were used for previous OM1 type assessments.]

m/f	OM1 A	OM3 A	$l_1^{m/f,A}$	$l_2^{m/f,A}$
M	1	1E	65mm	90mm
F	1	1E	65mm	90mm
M	2	1W	65mm	90mm
F	2	1W	65mm	90mm
M	3	2+3	55mm	90mm
f	3	2+3	55mm	90mm

1.3 Time varying recruitment distribution over areas

The model is further expanded to allow for recruitment distributions which vary over time for each of the three areas as follows:

Without time-varying recruitment:

$$R_y^A = \lambda^A R_y \quad \text{see equation (1)}$$

Now instead:

$$R_y^A = \lambda_y^{*,A} R_y \quad (28)$$

where

$$\lambda_y^{*,A} = \frac{\lambda^A e^{\varepsilon_{A,y}}}{\sum_A \lambda^A e^{\varepsilon_{A,y}}} \quad (29)$$

and

$$\varepsilon_{A,y} \sim N(0, \sigma_\varepsilon^2); \quad \sigma_\varepsilon = 0.05.$$

The $\varepsilon_{A,y}$ are thus further estimable parameters. An additional term is also added to the $-\ln L$ function (see section 2.5 below).

2. The likelihood function

The model is fitted to CPUE and catch-at-length (male and female separately) data from each of the three areas to estimate the model parameters. Contributions by each of these to the negative log-likelihood ($-\ln L$), and the various additional penalties added are as follows.

2.1 Relative abundance data (CPUE)

The likelihood is calculated assuming that the observed abundance index is log-normally distributed about its expected (median) value:

$$CPUE_y^A = q^A B_y^A e^{\varepsilon_y^A} \text{ or } \varepsilon_y^A = \ln(CPUE_y^A) - \ln(q^A B_y^A) \quad (30)$$

where

$CPUE_y^A$ is the CPUE abundance index for year y in area A ,

B_y^A is the model estimate of mid-year exploitable biomass for year y in area A

given by equation 18,

q^A is the constant of proportionality (catchability coefficient) for area A , and

ε_y^A from $N(0, (\sigma^A)^2)$.

The contribution of the abundance data to the negative of the log-likelihood function (after removal of constants) is given by:

$$-\ln L = \sum_A \sum_y \left[(\varepsilon_y^A)^2 / 2(\sigma^A)^2 + \ln(\sigma^A) \right] \quad (31)$$

where

σ^A is the residual standard deviation estimated in the fitting procedure by its maximum likelihood value:

$$\hat{\sigma}^A = \sqrt{1/n \sum_y (\ln CPUE_y^A - \ln \hat{q}^A \hat{B}_y^A)^2} \quad (32)$$

where

n is the number of data points in the CPUE series, and

q^A is the catchability coefficient, estimated by its maximum likelihood value:

$$\ln \hat{q}^A = 1/n \sum_y \left(\ln CPUE_y^A - \ln \hat{B}_y^A \right) \quad (33)$$

2.2 Catches-at-length (from Rademeyer 2003)

The following term is added to the negative log-likelihood:

$$-\ell_n L^{\text{length}} = w_{len} \sum_A \sum_y \sum_l \sum_{m/f} \left[\ln \left(\sigma_{len}^A / \sqrt{p_{y,l}^{m/f,A}} \right) + p_{y,l}^{m/f,A} \left(\ln p_{y,l}^{m/f,A} - \ln \hat{p}_{y,l}^{m/f,A} \right)^2 / 2 \left(\sigma_{len}^A \right)^2 \right] \quad (34)$$

where

$p_{y,l}^{m/f,A}$ is the observed proportion of m/f lobsters (by number) in length group l in the catch in year y in area A , and

σ_{len}^A is the standard deviation associated with the length-at-age data in area A , which is estimated in the fitting procedure by:

$$\hat{\sigma}_{len}^A = \sqrt{ \sum_{m/f} \sum_y \sum_l p_{y,l}^{m/f,A} \left(\ln p_{y,l}^{m/f,A} - \ln \hat{p}_{y,l}^{m/f,A} \right)^2 / \sum_{m/f} \sum_y \sum_l 1 } \quad (35)$$

Equation (31) makes the assumption that proportion-at-length data are log-normally distributed about their model-predicted values. The associated variance is taken to be inversely proportional to $p_{y,l}^{m/f,A}$ to downweight contributions from observed small proportions which will correspond to small predicted sample sizes.

2.3 Length-at-age

The model estimates the L_∞ parameters of the growth curve (and hence weight-at-age functions – see equation 16) for male and female lobsters for each area, as well as the κ and t_0 parameters, by adding a number of penalties to the likelihood function as follows:

$$-\ln L = -\ln L + \sum_{m/f} \sum_A \frac{1}{2\sigma_{growth}^2} \left(\frac{\hat{L}_\infty^{m/f,A}}{L_\infty^{m/f,A,obs}} - 1 \right)^2 + \frac{1}{2\sigma_{growth}^2} \left(\frac{\hat{\kappa}}{\kappa^{obs}} - 1 \right)^2 + \frac{1}{2\sigma_{growth}^2} \left(\frac{\hat{t}_0}{t_0^{obs}} - 1 \right)^2 \quad (36)$$

where σ_{growth} is set equal to 0.05.

2.4 Stock-recruitment function residuals

The assumption that these residuals are log-normally distributed and could be serially correlated defines a corresponding joint prior distribution. This can be equivalently regarded as a penalty function added to the log-likelihood, which for fixed serial correlation ρ is given by:

$$-\ln L = -\ln L + \sum_{y=y1}^{y2} \left[\frac{\zeta_y - \rho \zeta_{y-1}}{\sqrt{1-\rho^2}} \right]^2 / 2\sigma_R^2 \quad (37)$$

where

$\zeta_y = \rho \tau_{y-1} + \sqrt{1-\rho^2} \varepsilon_y$ is the recruitment residual for year y (see equation 7), which is estimated for years $y1$ to $y2$ if $\rho = 0$, or $y1+1$ to $y2$ if $\rho > 0$,

$$\varepsilon_y \sim N(0, \sigma_R^2),$$

σ_R is the standard deviation of the log-residuals, which is input, and

ρ is their serial correlation coefficient, which is input.

Note that here (as in previous assessments), ρ is set equal to zero, i.e. the recruitment residuals are assumed uncorrelated, and σ_R is set equal to 0.4. Because of the absence of informative age data for a longer period, recruitment residuals are estimated for years 1974 to 2003 only.

2.5 Time varying recruitment parameters

The following term is added to the $-\ln L$ term to constrain the size of these terms (i.e. to fit to genuine difference rather than to noise):

$$-\ln L = -\ln L + \sum_A \sum_{y=1973}^{y=2004} \left(\frac{\varepsilon_{A,y}^2}{\sigma_R^2} \right) \quad (38)$$

2.6 Time varying selectivity (if applicable)

An extra term is added to the likelihood function in order to smooth the extent of change in the selectivity, as follows:

$$-\ln L \rightarrow -\ln L + \sum_{m/f} \sum_A \sum_{y=1995}^{y=2010} \left(\frac{\delta_y^{m/f,A}}{\sigma_{sel}} \right)^2 \quad (39)$$

where the σ_{sel} is input (a value of 0.75 was found to provide reasonable performance in previous assessments).

2.7 Somatic growth parameters – multivariate -lnL

The growth parameters constitute a vector \mathbf{x} . The probability density for a vector \mathbf{x} is:

$$f_{\mathbf{x}}(x_1, \dots, x_k) = \frac{1}{(2\pi)^{k/2} |\Sigma|^{1/2}} \exp \left(-\frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^T \Sigma^{-1} (\mathbf{x} - \boldsymbol{\mu}) \right)$$

where Σ is the variance covariance matrix (as provided by OLRAC), and the vector $\boldsymbol{\mu}$ contains the means (as provided by OLRAC). The log-likelihood is

$$\ln(L) = -\frac{k}{2} \ln(2\pi) - \frac{1}{2} \ln |\Sigma| - \frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^T \Sigma^{-1} (\mathbf{x} - \boldsymbol{\mu})$$

The first two terms are constants, omitting the first of these gives -LLF

$$-\text{LLF} = + \frac{1}{2} \ln |\Sigma| + \frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^T \Sigma^{-1} (\mathbf{x} - \boldsymbol{\mu})$$

3. Further Model parameters

Natural mortality: Natural mortality $M^{m/f}$ for male and female lobsters is assumed to be the same (M) for all age classes and both sexes, and is fixed here at 0.10 yr⁻¹.

Age-at-maturity: The proportion of lobsters of age a that are mature is approximated by $f_a = 1$ for $a > 9$ years (i.e. $f_a = 0$ for $a = 0, \dots, 9$).

Minimum age: Age 0.

Maximum age: $p = 20$, and is taken as a plus-group.

Minimum length: length 1mm.

Maximum length: 180mm, what is taken as a plus-group.

Mass-at-age: The mass $w_a^{m/f,A}$ of a m/f lobster at age a in area A is given by:

$$w_a^{m/f,A} = \alpha \left[\hat{L}_{\infty}^{m/f,A} \left(1 - e^{-\hat{k}(a-\hat{t}_0)} \right) \right]^{\beta} \quad (40)$$

where the values used for the growth parameters are shown in Table 5.

Mass-at-length:

$$w_l^{m/f,A} = \alpha l^{\beta} \quad (41)$$

where the values of α and β are 0.0007 and 2.846 respectively (and are assumed constant for male and female lobsters and across areas).

Stock-recruitment relationship: The shape parameter, γ , is fixed to 1, corresponding to a Beverton-Holt form.

4. The Bayesian approach

The Bayesian method entails updating prior distributions for model parameters according to the respective likelihoods of the associated population model fits to the CPUE, catch-at-age and tag-recapture data, to provide posterior distributions for these parameters and other model quantities.

The catchability coefficients (q^A) and the standard deviations associated with the CPUE and catch-at-length data (σ^A and σ_{len}^A) are estimated in the fitting procedure by their maximum likelihood values, rather than integrating over these three parameters as well. This is adequately accurate given reasonably large sample sizes (Walters and Ludwig 1994, Geromont and Butterworth 1995).

Modes of posteriors, obtained by finding the maximum of the product of the likelihood and the priors, are then estimated rather than performing a full Bayesian integration, due to the time intensiveness of the latter.

4.1 Priors

The following prior distributions are assumed:

h $N(0.95, SD^2)$ with $SD=0.2$, where the normal distribution is truncated at $h = 1$.

$I_{50}^{m/f,A}$: $U[1, 140]$ mm

$\Delta^{m/f,A}$ $U[1, 100]$ mm

μ^A $U[0,3]$

β^* $U[0,1]$ (from equation 19)

$F_y^{m/f,A}$: $U[0,0.8]$

SR residuals ζ_y : $N(0, \sigma_R^2)$ where $\sigma_R = 0.4$, bounded by $[-5, 5]$

λ^A $U[0,1]$

4.2 Estimable parameters (for Variant 1 – fixed somatic growth parameters)

Parameter	What is it	Which equation	Number of parameters
K^{sp}	Pristine female spawning biomass	11	1
h	Steepness parameter of SR function	9,10	1
$l_{50}^{m/f,A}$	Selectivity function parameter	24	6
$\Delta_{95}^{m/f,A}$	Selectivity function parameter	24	6
μ^A	Relative female selectivity scaling parameters	14	3
β^*	Parameter of length-at-age distribution	17	1
λ^A	Area specific recruitment proportion	1	2 ($\lambda^3 = 1 - \lambda^1 - \lambda^2$)
$\varepsilon_{A,y}$	Time varying recruitment distribution	29	93
ζ_y	Stock recruit residuals	7	30
TOTAL			143

References

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