

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 focus here is on a model structure which splits the resource into areas A1E, A1W and A2+3. Given problems experienced with refining the growth rate estimates within the model fitting process because of the low OLRAC estimate for area A1E, for the purpose of this paper the extreme approach is taken. This fixes these estimates at their OLRAC values, except that area A1E is assumed to have the same growth rate as A1W. This leads to results which show reasonable fits to the data. Across a restricted range of sensitivities, the current spawning biomass depletion is estimated at 30%. Suggestions are made for aspects of the model in need of further evaluation.

Introduction

Initially, three model structures were 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

After some preliminary results were presented, the SWG decided to focus on Model 3 as the reference case model.

Model 3 candidate OMs

There appeared to be a general problem in obtaining realistic fits using the somatic growth rates for A1E as reported by OLRAC (2012). 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. Initially, three alternate OMs were developed. Of these three “Variant 1” was selected to be the most appropriate method and this method is used in all the results presented in this document.

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.

For all 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.

All OMs allow for time-varying selectivity (see Appendix for details).

Reference Case (RC) OM

The table below lists the parameter values for the RC model, and those for the three sensitivity models for which results are presented in this document.

Parameter	RC Input value	Sensitivities
σ_{sel}	7.5	
σ_R	0.8	0.4
σ_λ	1.0	0.5
w_{len}	1.0	0.1

Results

Table 1 reports the results of the RC and three sensitivities. The four models produce fairly similar estimates for B_{sp} with more variation in B_{exp} (see Appendix for definitions of spawning and exploitable biomass).

Figure 1a shows the fits to CPUE for the RC and SEN3 and Figure 1b shows the associated CPUE standardised residuals.

Figure 2a shows the RC SCI CAL residual plots for each sex and sub-area. Figure 2b is similar – but for SEN3.

Figure 3 shows B_{sp} trajectories for the RC and SEN3 both in absolute terms (top plot) and relative to pristine (bottom plot).

Figure 4 shows absolute B_{exp} trajectories for the RC and SEN3.

Figure 5a shows stock-recruit residuals for the RC and SEN3 and Figure 5b reports the proportion of total annual recruitment in each sub-area.

Figure 6 shows the growth curves which are input for these OMs for each sub-area. Note though that the models reported here fix the growth for A1E at that reported for A1W.

Figure 7a shows the RC and SEN3 selectivity functions for each sex and sub-area.

Figure 7b shows the selectivity function δ values for the RC and SEN3 (these allow for annually varying selectivity – see equation 24 in the Appendix).

Discussion

The Reference Case model considered here, and the three sensitivities to that, show little difference in terms of the results of greatest importance: the depletion estimates shown at the bottom of Table 1, which for spawning biomass for the resource as a whole are all about 0.3. The fits to the data shown in the plots all appear reasonable.

This has, however, been achieved by the rather extreme approach of fixing the Δg_{1E} parameter value equal to its larger Δg_{1W} counterpart. Further analyses will examine alternative approaches to this.

Other factors which will be considered in further analyses are:

- alternative approaches for allowing for changes over time in selectivity at length – see equation 24 (in addition to sensitivity to the value of the σ_{sel} parameter;
- alternative distributional forms for the variation over time in the recruitment distribution over areas - see equation 29 – e.g. use of a multinomial form;
- non-homoscedasticity in CPUE residuals over time – e.g. for area A1E these appear larger in the earlier compared to the more recent years; and
- alternative spatial structure models to Model 3..

References

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.

OLRAC. 2012. Non-linear growth rate estimation from mark-recapture data for South Coast rock lobster, incorporating jack-knife variance estimation and model selection. FISHERIES/2012/JUL/SWG-SCRL/12.

Table 1: Model 3 estimated parameter and $-\ln L$ values for the RC and three sensitivity analyses. Values italicised indicate the changes made for sensitivities. Note that these changes render the total and some components of the negative log likelihood non comparable. The growth parameters were either “fixed” at the OLRAC reported values, or changed as described in the text.

	RC	SEN1	SEN2	SEN3
	V1d	V1a	V1f	V1g
W_{len}	1.0	1.0	1.0	<i>0.1</i>
σ_{sel}	7.5	7.5	7.5	7.5
σ_R	0.8	<i>0.4</i>	0.8	0.8
σ_λ	1.0	1.0	<i>0.5</i>	1.0
-lnL Total	-420.53	-401.93	-405.63	-142.49
-lnl CPUE	-108.48	-89.61	-104.11	-147.92
-lnl CPUE A1E	-16.08	-15.81	-15.23	-24.13
-lnl CPUE A1W	-40.41	-39.06	-38.48	-59.73
-lnl CPUE A2+3	-51.98	-34.73	-50.40	-64.06
-ln SCI CAL	-356.55	-353.57	-350.22	-153.79
-ln SCI CAL A1E	-13.73	-14.84	-10.99	37.15
-ln SCI CAL A1W	-165.99	-162.09	-164.20	-91.15
-ln SCI CAL A2+3	-176.83	-176.64	-175.03	-99.78
CPUE A1E σ	0.378	0.381	0.388	0.298
CPUE A1W σ	0.185	0.192	0.196	0.105
CPUE A2+3 σ	0.131	0.218	0.138	0.092
SCI CAL A1E σ	0.131	0.131	0.134	0.178
SCI CAL A1W σ	0.069	0.070	0.070	0.093
SCI CAL A2+3 σ	0.069	0.069	0.070	0.089
K	2546	3 188	2571	2525
λ^{A1E}	0.102	0.106	0.1106	0.103
λ^{A1W}	0.341	0.346	0.338	0.325
λ^{A2+3}	0.557	0.548	0.556	0.571
g_{75}	3.280 fixed	3.280 fixed	3.280 fixed	3.280 fixed
κ	0.099 fixed	0.099 fixed	0.099 fixed	0.099 fixed
Δg_m	0.996 fixed	0.996 fixed	0.996 fixed	0.996 fixed
Δg_{1E}	-0.796 changed	-0.796 changed	-0.796 changed	-0.796 changed
Δg_{1W}	-0.796 fixed	-0.796 fixed	-0.796 fixed	-0.796 fixed
$B_{sp}(2011) (B_{sp}(2011)/K_{sp})$	713 (0.280)	883 (0.277)	737 (0.289)	761 (0.301)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1E	85 (0.205)	82 (0.195)	75 (0.182)	84 (0.169)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A1W	791 (0.438)	790 (0.416)	768 (0.415)	515 (0.292)
$B_{exp}(2011) (B_{exp}(2011)/K_{exp})$ A2+3	1553 (0.304)	1801 (0.265)	1673 (0.325)	1717 (0.309)

Figure 1a: RC and SEN3 (CAL down-weighted by 0.1 in $-\ln L$) OM fits to CPUE for each sub-area.

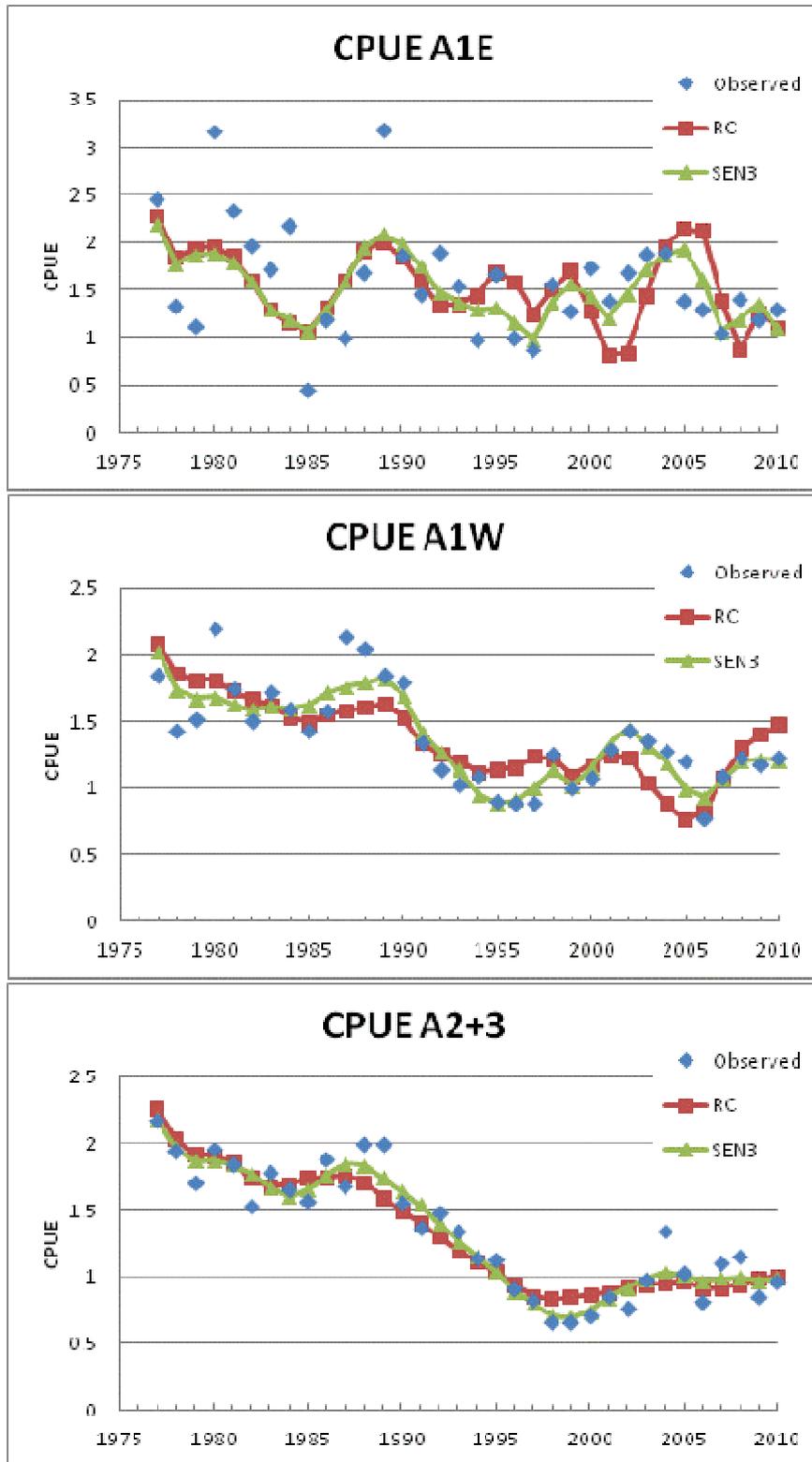


Figure 1b: RC and SEN3 (CAL down-weighted by 0.1 in $-\ln L$) standardised CPUE residuals for each sub-area.

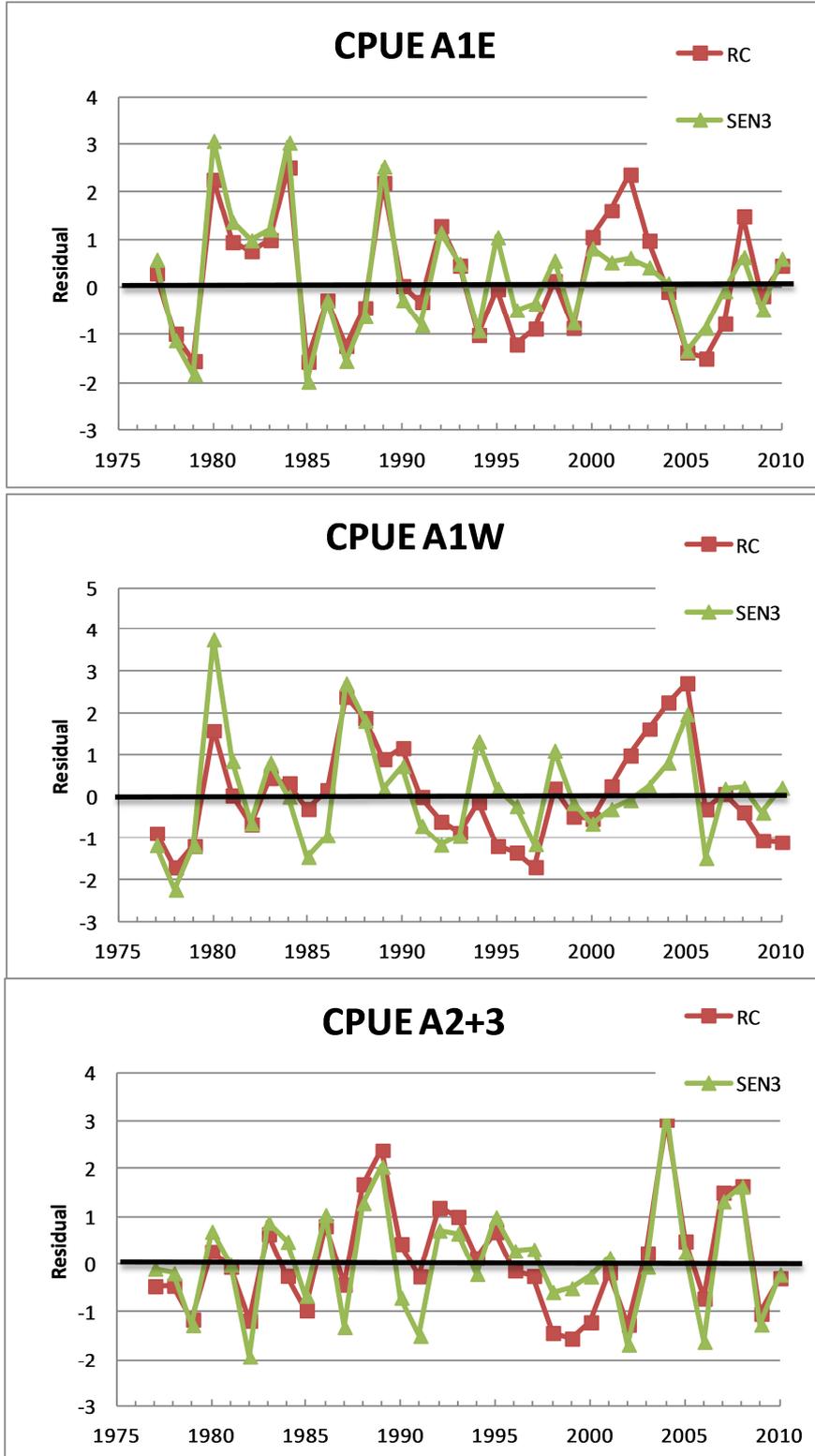


Figure 2a: RC CAL standardised residuals.

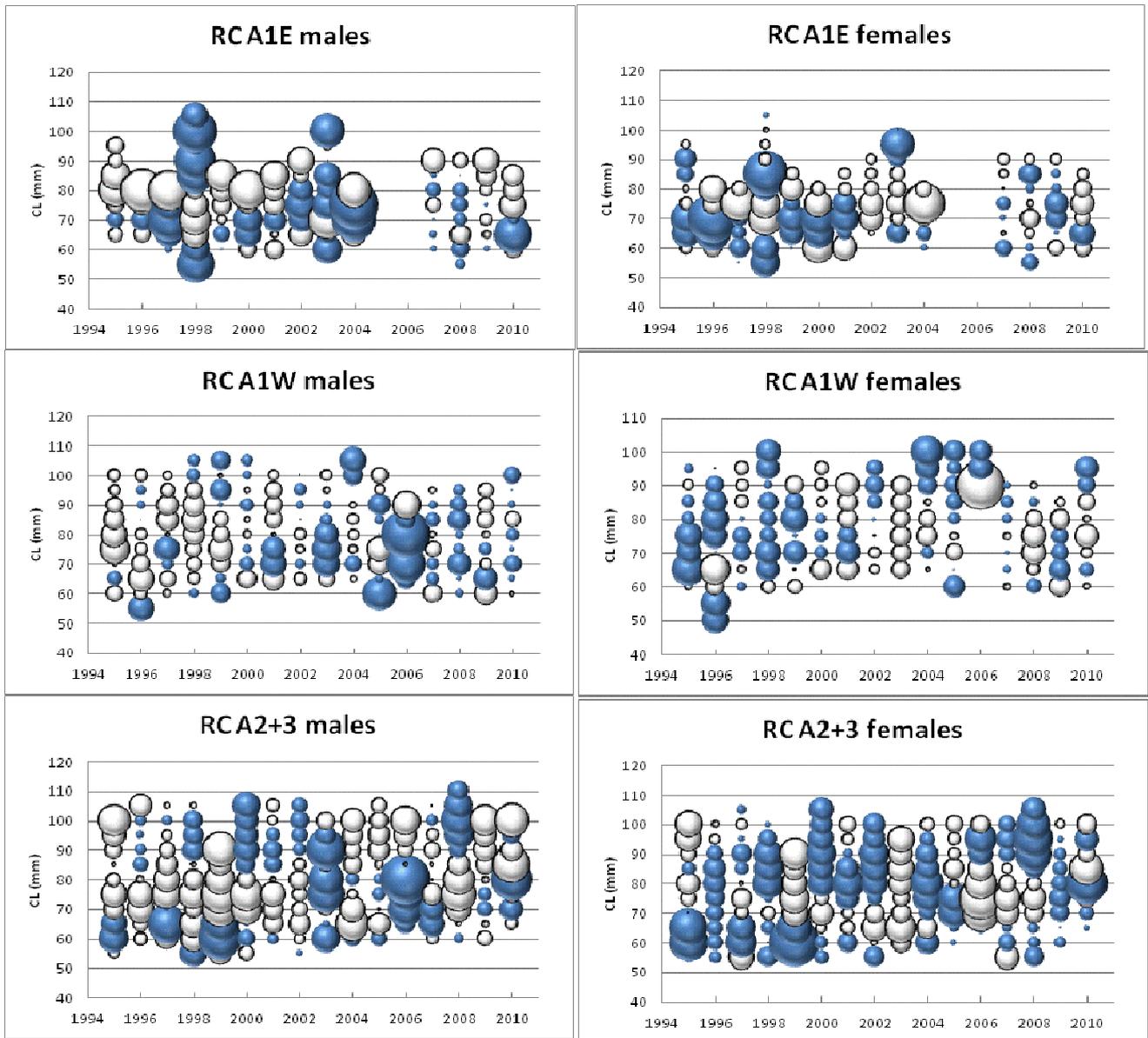


Figure 2b: SEN3 CAL standardised residuals.

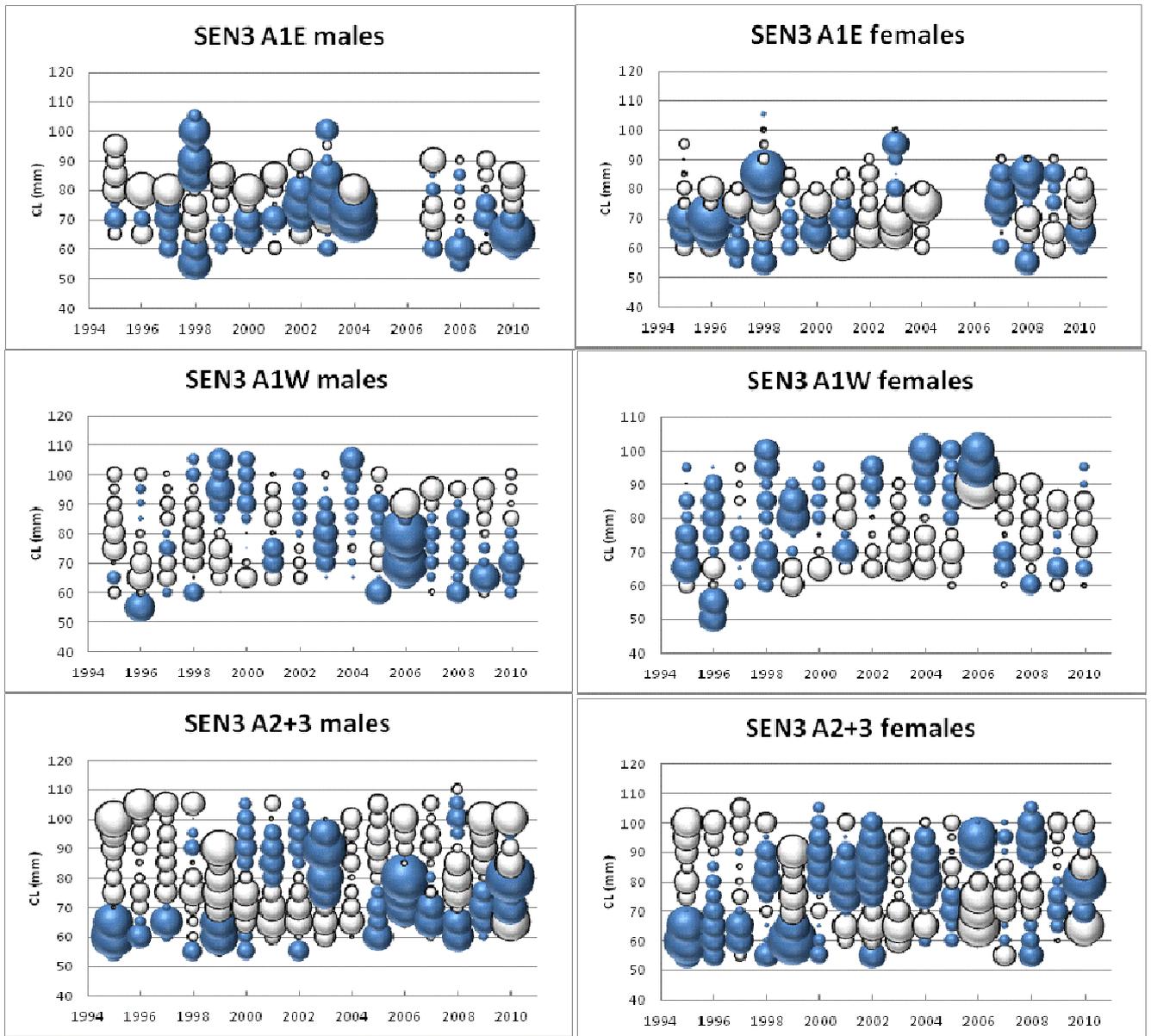


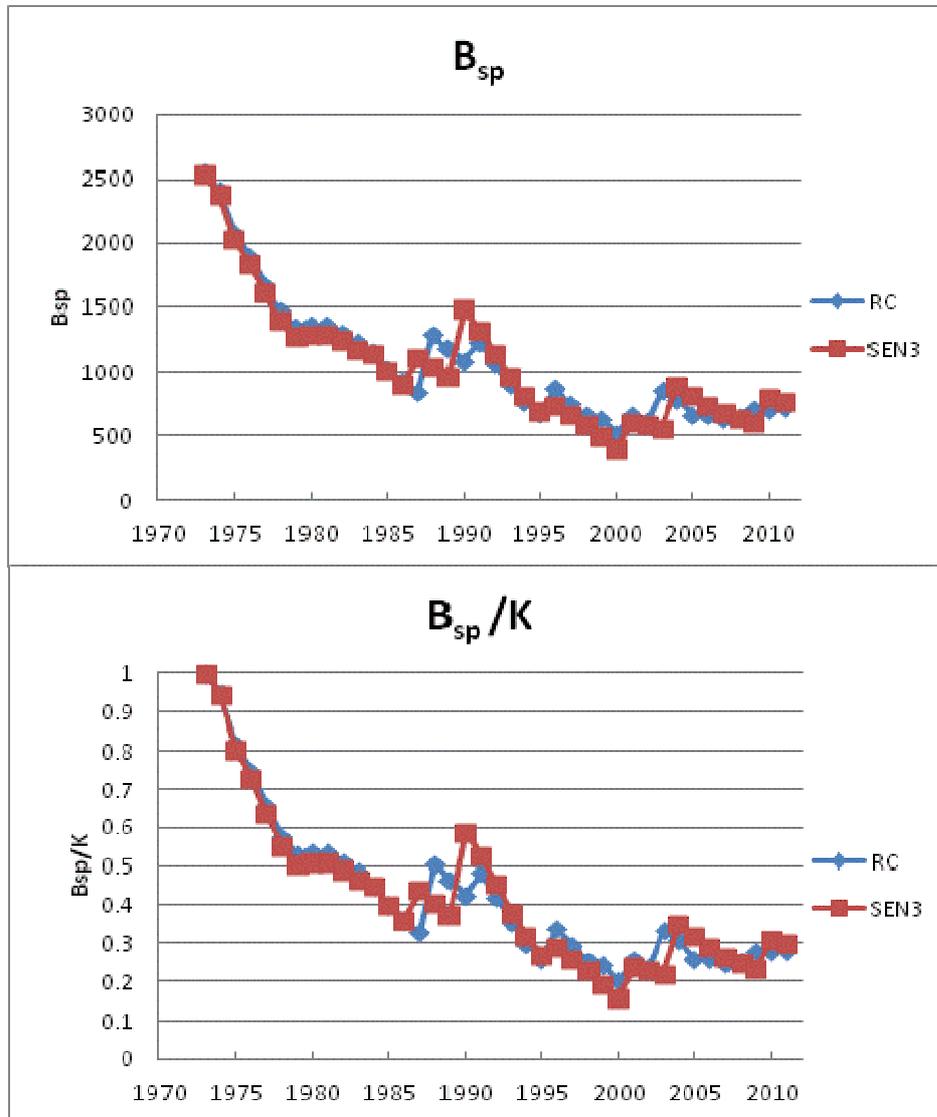
Figure 3: B_{sp} and B_{sp}/K trajectories for the RC and SEN3.

Figure 4: B_{exp} Trajectories for each sub-area for the RC and SEN3.

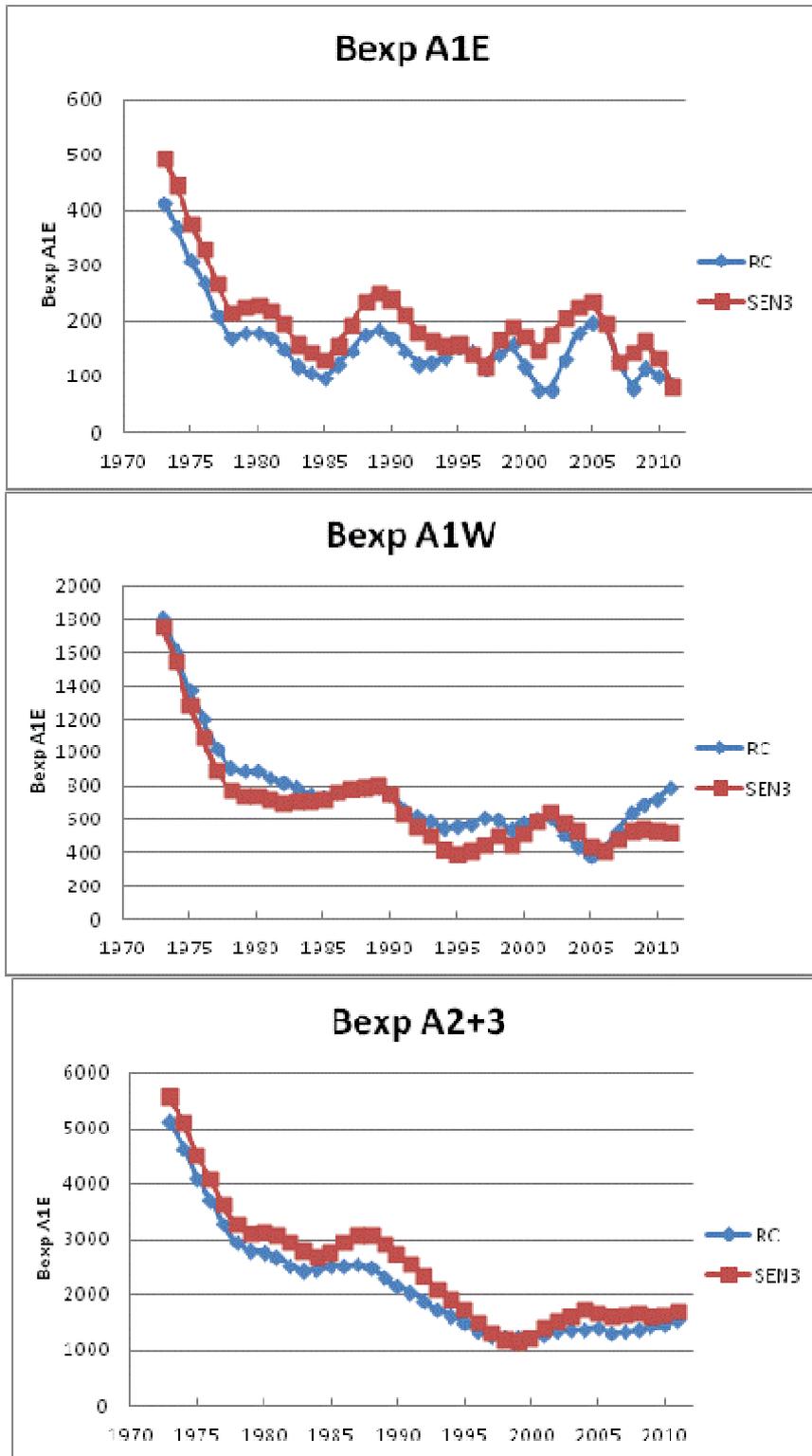


Figure 5a: Stock recruit residuals for the RC and SEN3.

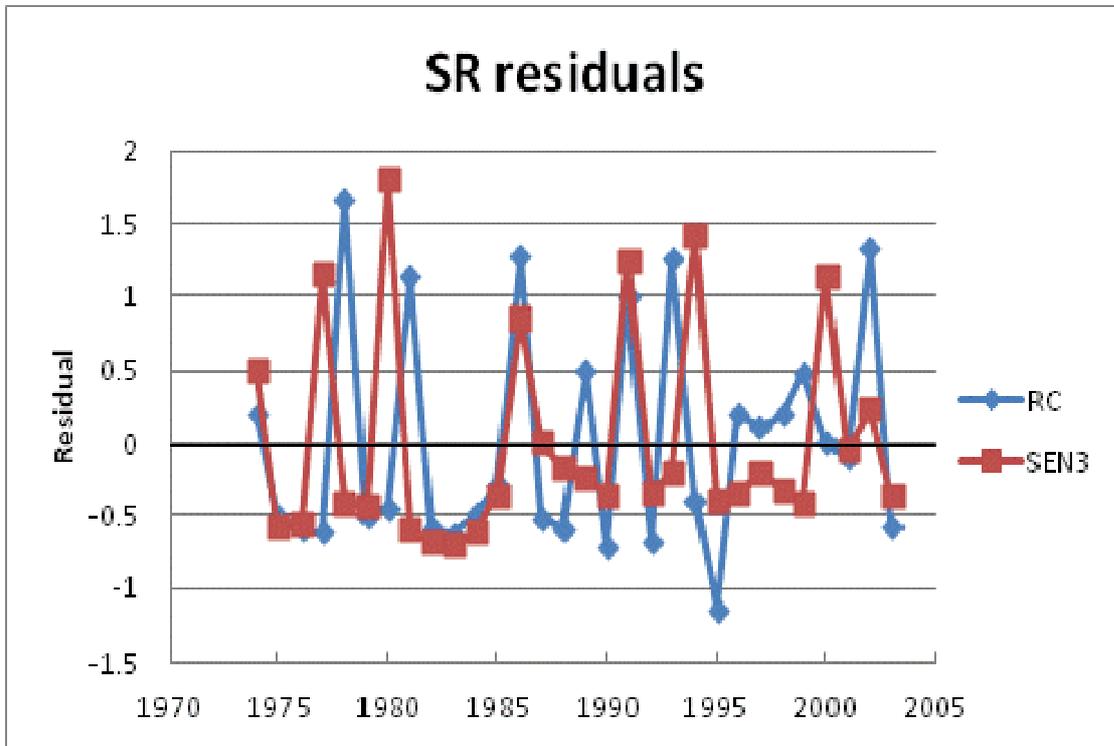


Figure 5b: Proportion of total annual recruitment for each sub-area.

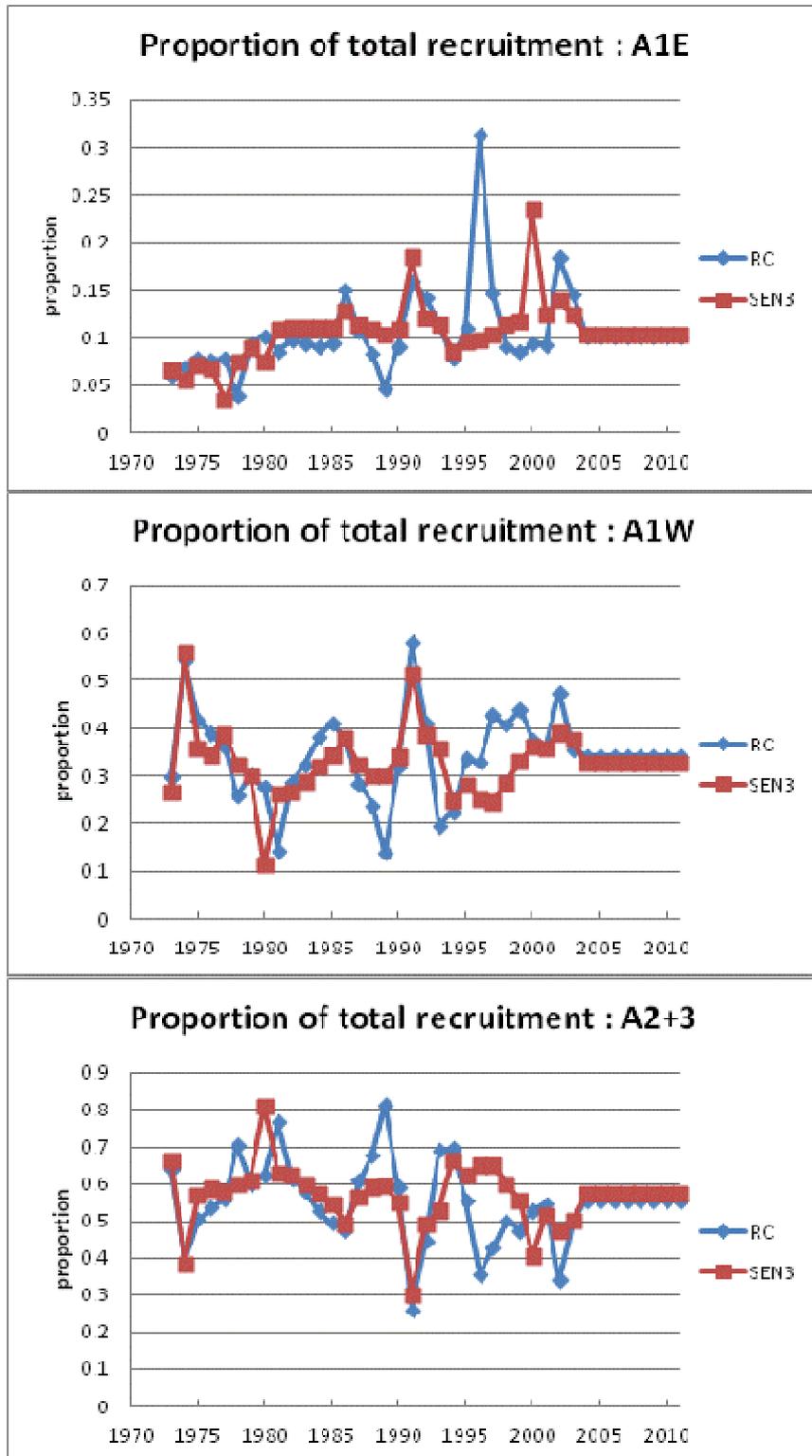


Figure 6: Somatic growth curves as estimated by OLRAC-Model 7 and used for input to the OMs.

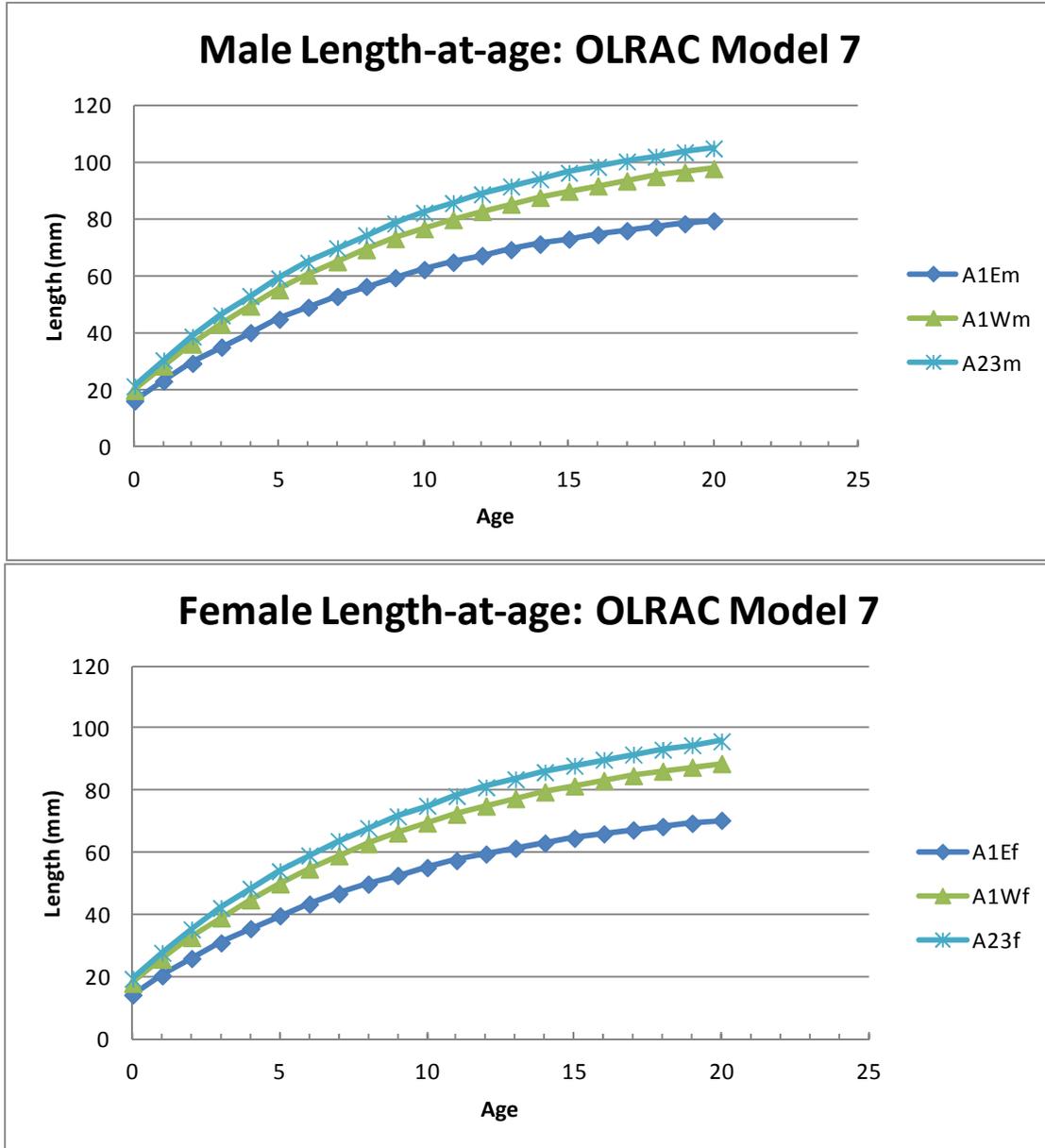


Figure 7a: Selectivity functions for each sub-area for the RC and SEN3 – functions shown for 1973.

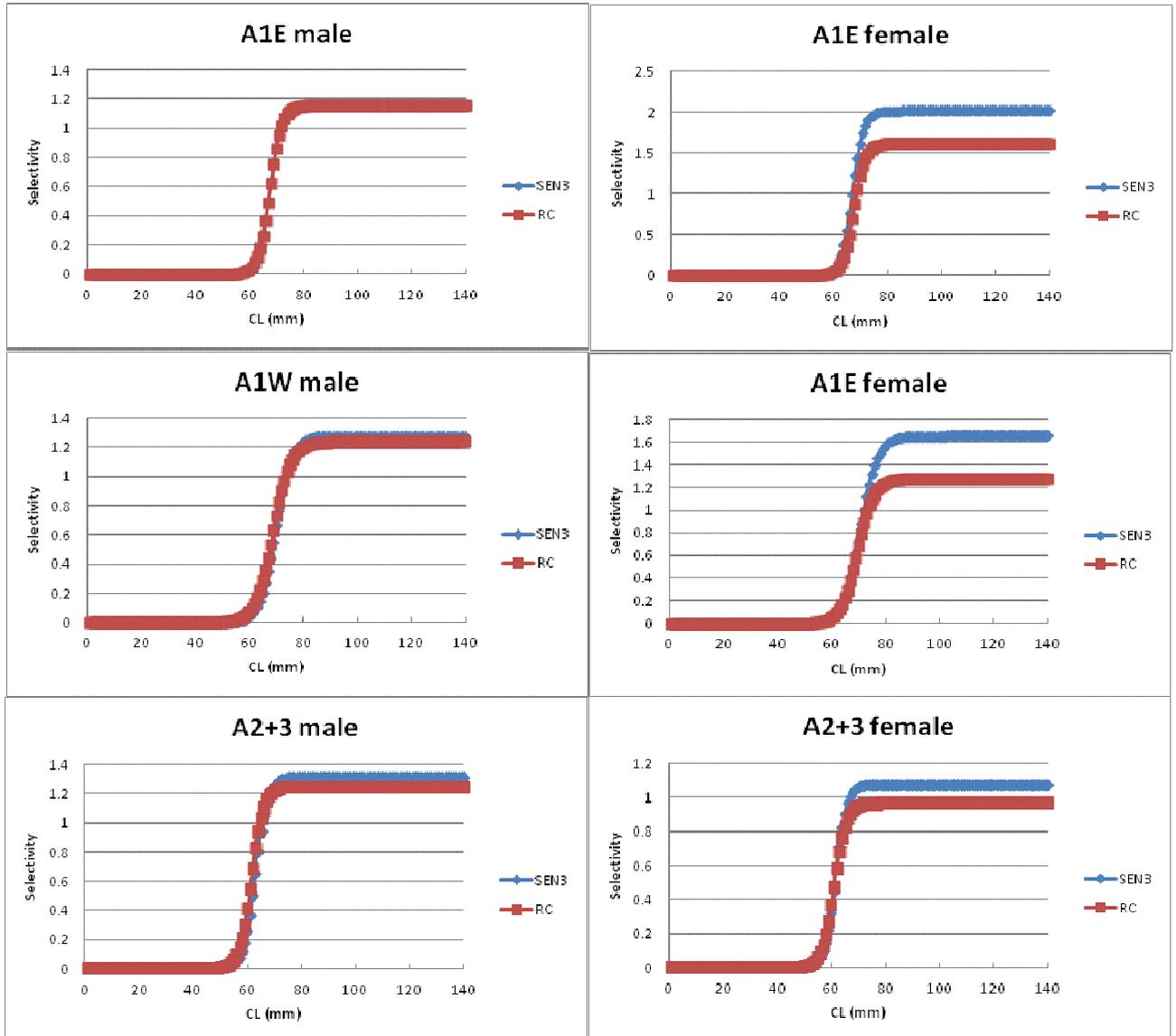
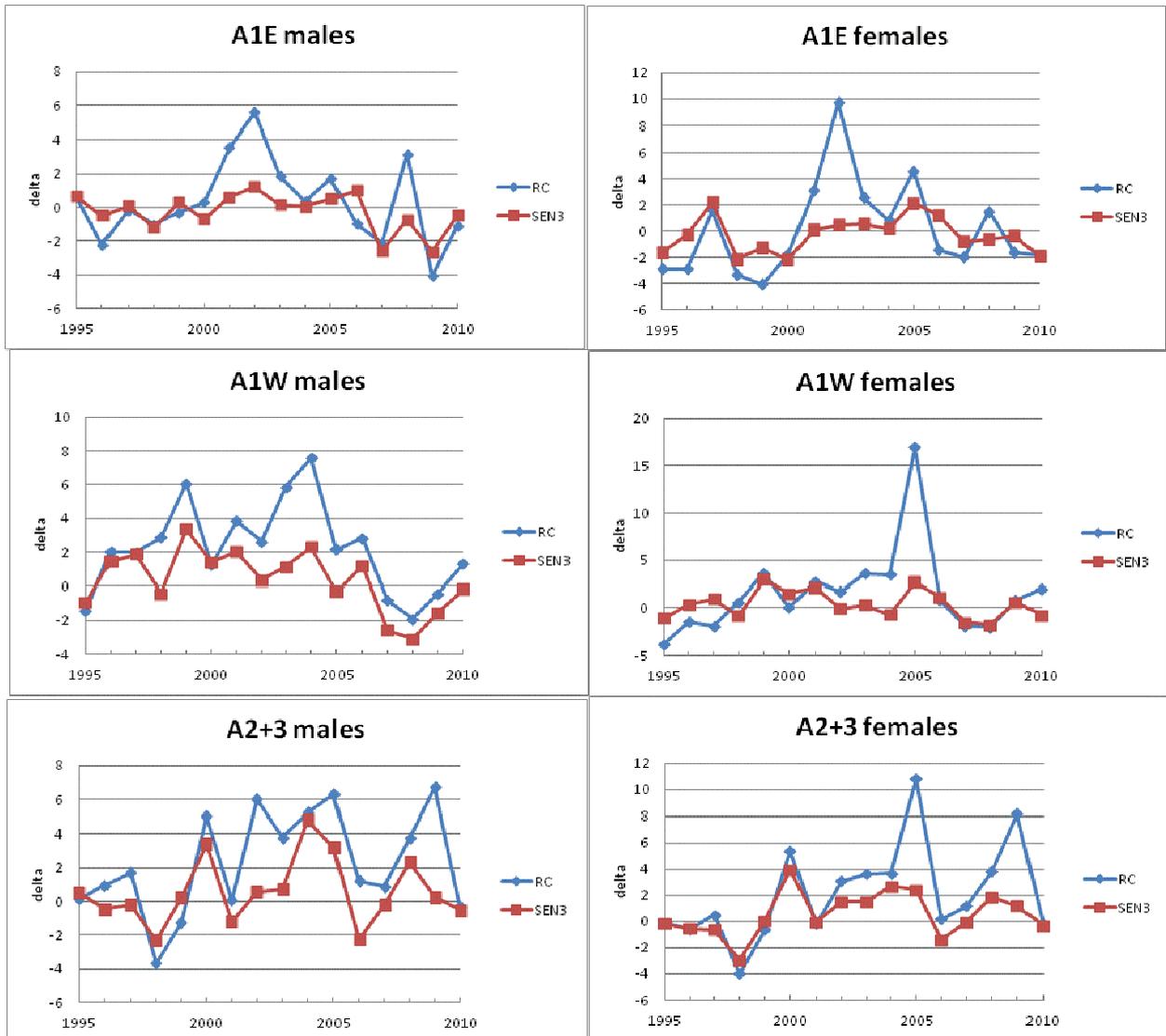


Figure 7b: Selectivity δ values (see equation 24) estimated for the RC and SEN3.



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 so speeds 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:

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

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

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

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

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

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

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.

Growth rate model

Growth is assumed to be both sex and area dependent. The κ (slope) parameter of the length increment versus length relationship is area-independent, but the intercepts vary with area.

Thus the annual growth of a 75mm male lobster from each area is given by

$$g75^{m,1E} = g75 + \Delta g1E + \Delta gm$$

$$g75^{m,1W} = g75 + \Delta g1W + \Delta gm$$

$$g75^{m,2+3} = g75 + \Delta gm$$

and, the annual growth rate of a 75mm female lobster from each area is given by:

$$g75^{f,1E} = g75 + \Delta g1E$$

$$g75^{f,1W} = g75 + \Delta g1W$$

$$g75^{f,2+3} = g75.$$

[It follows that $l_{\infty}^{m/f,A} = 75.0 + \left(\frac{g75^{m/f,A}}{\kappa}\right)$.]

Using growth Model 8 of OLRAC's SCRL12 document, the five somatic growth rate parameters are:

	Estimates
g75	3.280 mm
κ	0.099 yr ⁻¹
Δg_m	0.996 mm
Δg_{1E}	-2.840 mm
Δg_{1W}	-0.790 mm

To put these parameter values into perspective, the above values result in l_{∞} (mm) and g75 (mm) values as reported below.

	l_{∞} (mm)	g75 (mm)
A1Em	89.51	1.44
A1Ef	79.44	0.44
A1Wm	110.15	3.48
A1Wf	100.09	2.48
A2+3m	118.19	4.28
A2+3f	108.13	3.28

[Note for A1Em there is a catch-at-length data maximum plus group of 105+mm, and for A1Ef one of 95+mm.]

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

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

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

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 .

The overall fishing proportion is:

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

1.1 Catch-at-length proportions

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

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

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	area	$l_1^{m/f,A}$	$l_2^{m/f,A}$
<i>m</i>	1E	65mm	90mm
<i>f</i>	1E	65mm	90mm
<i>m</i>	1W	65mm	90mm
<i>f</i>	1W	65mm	90mm
<i>m</i>	2+3	55mm	90mm
<i>f</i>	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

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

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

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

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

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:

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

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 down-weight contributions from observed small proportions which will correspond to small predicted sample sizes.

The RC model fixes $w_{\text{len}} = 1.0$ (i.e. gives equal weight to the CAL data as to the CPUE data).

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:

$$-\ln L = -\ln L + \sum_{y=y_1}^{y_2} \left[\frac{\zeta_y - \rho \zeta_{y-1}}{\sqrt{1 - \rho^2}} \right]^2 / 2\sigma_R^2 \quad (36)$$

where

$\zeta_y = \rho\tau_{y-1} + \sqrt{1-\rho^2}\eta_y$ 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 $\rho > 0$,

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

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 0.8. 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 distribution parameters

The following term is added to the $-\ln L$ term to constrain the size of these terms in equation 29(i.e. to fit to genuine difference rather than to noise):

$$-\ln L = -\ln L + \sum_A \sum_{y=1973}^{y=2004} \left(\frac{\varepsilon_{A,y}^2}{\sigma_\lambda^2} \right) \quad (37)$$

where $\sigma_\lambda=1.0$.

2.6 Time varying selectivity

An extra term is added to the likelihood function in order to smooth the extent of change in the selectivity in equation 24, as follows:

$$-\ln L \rightarrow -\ln L + \sum_{m/f} \sum_A \sum_{y=1995}^{y=2010} \left(\frac{\delta_y^{m/f,A}}{\sigma_{sel}} \right)^2 \quad (38)$$

where the σ_{sel} is input (a value of 7.5 is used, having provided reasonable performance in previous assessments).

2.7 Somatic growth parameters – within model estimation

The RC model considered in the main text fixes these parameters as input. A variant allows these input values to be updated in the model fitting process.

The growth parameters constitute a vector \mathbf{x} . The following contribution is then added to the negative log-likelihood in the assessment:

$$-\ln L^c = \frac{1}{2} \ln |\Sigma| + \frac{1}{2} (\mathbf{x} - \boldsymbol{\mu})^T \Sigma^{-1} (\mathbf{x} - \boldsymbol{\mu}) \quad (39)$$

where the parameters $g75$, κ , Δgm , $\Delta g1E$ and $\Delta g1w$ are components of the vector \mathbf{x} ,

Σ is the variance covariance matrix (as provided by OLRAC(2012)), and

$\boldsymbol{\mu}$ is a vector which contains the estimates (as provided by OLRAC(2012)).

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:

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

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 (units gm and mm) 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 $h = 1$.

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

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

$$\mu^A \quad U[0,3]$$

$$\beta^* \quad U[0,1] \text{ (from equation 19)}$$

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

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

$$\lambda^A \quad U[0,1]$$

4.2 Fixed inputs for the Reference case

Parameter	Equation	RC Input value	Sensitivities
σ_{sel}	38	7.5	
σ_R	36	0.8	0.4
σ_λ	37	1.0	0.5
w_{len}	34	1.0	0.1

4.3 Estimable 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 ($\lambda^3 = 1 - \lambda^1 - \lambda^2$)
$\mathcal{E}_{A,y}$	Time varying recruitment distribution	29	93
ζ_y	Stock recruit residuals	7	30
$\delta_y^{m/f,A}$	Time varying selectivity	24, 38	2 x 3 x 16=96
TOTAL			239

References

Brandão A., Butterworth D.S., Watkins B.P. and Staveres L. 2002. An updated assessment of the toothfish (*Dissostichus eleginoides*) resource in the Prince Edward Island vicinity and extensions taking commercial catch-at-length data into account. Unpublished report, CCAMLR. WG/FSA/02-76. 23pp.

Geromont, H.F. and D.S. Butterworth. 1995. Interpretation of South coast rock lobster catch and CPUE data by a Bayesian assessment: methodology summary. MCM document, WG/03/95/SCL3.

Rademeyer, R. 2003. Assessment of and Management Procedures for the Hake stocks off Southern Africa. MSc. Thesis. University of Cape Town.

Walters, C. and D. Ludwig. 1994. Calculation of Bayes posterior probability distributions for key population parameters. *Can. J. Fish. Aquat. Sci.* 51: 713-722.