

The Age-Structured Production Model for the South Coast rock lobster population extended to be sex- and area-specific, to fit to catch-at-length data, and to use Pope's approximation

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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 ($A=1,2,3$). Population equations have been modified from Baranov equations to Pope's approximation. This has reduced the number of estimable parameters, and speeded up runtime of the program.

Note that the model now includes an option for 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 fishing 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 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

\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) is allowed to vary over the time period for which catch-at-age data are available (1994-2005). 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 $y = 1994-2005$ (excluding 1999 as there are no catch-at-age data for 1999).

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 1999 is calculated as the average for 1998 and 2000, and
- $\delta_y^{m/f,A}$ for pre-1994 and 2006+ = 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:

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

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 authors have fixed the values of $l_1^{m/f,A}$ and $l_2^{m/f,A}$ at the following values after examining the length frequency distributions, to ensure that the ranges associated with these l values cover the greater part of these distributions.

m/f	A	$l_1^{m/f,A}$	$l_2^{m/f,A}$
m	1	65mm	90mm
f	1	65mm	90mm
m	2	65mm	90mm
f	2	65mm	90mm
m	3	55mm	90mm
f	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 we have

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

Now,

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

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 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:

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

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

\hat{q}^A is the catchability coefficient, estimated by its maximum likelihood value:

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

2.2 Catches-at-length (from Rademeyer 2003)

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

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

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:

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

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 length-at-age (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, and the “observed” values are as reported in Table 1.

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 for the Reference Case assessment, 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 1997 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):

$$-\ln L = -\ln L + \sum_A \sum_{y=1973}^{y=2000} \left(\frac{\epsilon_{A,y}^2}{\sigma_\epsilon^2} \right) \quad (38)$$

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, as follows:

$$-\ln L \rightarrow -\ln L + \sum_{m/f} \sum_A \sum_{y=1994}^{y=2005} \left(\frac{\delta_y^{m/f,A}}{\sigma_{sel}} \right)^2 \quad (\text{sum excludes 1999}) \quad (39)$$

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

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.

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: 80mm, 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:

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

where the values assumed for the observed growth parameters are shown in Table 1.

Mass-at-length:

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

where the values of α and β are also reported in Table (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 distribution for these parameters and other model quantities. Note that tag-recapture data were used for earlier assessments, but discarded when it became apparent that they had little impact on results. They may be reintroduced in future refinements of this approach.

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 $h = 1$.

$l_{50}^{m/f,A}$: $U[40, 140]$ mm

$\Delta^{m/f,A}$ $U[0, 100]$ 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

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
$\delta_y^{m/f,A}$	Time varying selectivity parameters	24	66
μ^A	Relative female selectivity scaling parameters	14	3
β^*	Parameter of length-at-age distribution	17	1
$L_{\infty}^{m/f,A}$	Growth parameter	16, 17	6
κ	Growth parameter	16, 17	1
t_0	Growth parameter	16, 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	84
ζ_y	Stock recruit residuals	7	24
TOTAL			202

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Table 1: Somatic growth parameters (for use in equation 36) (OLRAC, pers. commn).

α (w in gm)	0.0007
β	2.846
$l_{\infty}^{m,1}$ (mm CL)	104.55
$l_{\infty}^{f,1}$ (mm CL)	94.82
$l_{\infty}^{m,2}$ (mm CL)	109.53
$l_{\infty}^{f,2}$ (mm CL)	99.81
$l_{\infty}^{m,3}$ (mm CL)	118.07
$l_{\infty}^{f,3}$ (mm CL)	108.34
κ (year ⁻¹)	0.095
t_0 (years)	-2.0