

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

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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 ($A=1,2,3$).

1. The population model

The resource dynamics are modelled by the equations:

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

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

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

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

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

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

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)

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

$F_y^{m,A}$ is the fully selected fishing mortality in year y for male lobsters in area A ,

μ^A is the relative female selectivity scaling parameter for 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 that the proportional distribution of male and female recruitment by area remains unchanged over time, and that there is no cross-boundary movement after recruitment.

The number of recruits 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 fish 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 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 $B^{sp} = K^{sp}$):

$$\alpha = \frac{(5 - 0.2^{\gamma-1}) h R_1 (K^{sp})^{\gamma-1}}{5h - 1} \quad (9)$$

and

$$\beta = \frac{(K^{sp})^\gamma (1 - 0.2h)^{\gamma-1}}{5h - 1} \quad (10)$$

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:

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

where

$$\vec{C}_{y,a,l}^{m,A} = w_l^{m,A} \vec{N}_{y,a,l}^{m,A} \frac{S_l^{m,A} F_y^{m,A}}{Z_{y,l}^{m,A}} (1 - e^{-Z_{y,l}^{m,A}}) \quad (13)$$

$$\bar{C}_{y,a,l}^{f,A} = w_l^{f,A} \bar{N}_{y,a,l}^{f,A} \frac{S_l^{f,A} \mu^A F_y^{m,A}}{Z_{y,l}^{f,A}} (1 - e^{-Z_{y,l}^{f,A}}) \quad (14)$$

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

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

$$Z_{y,l}^{m,A} = S_l^{m,A} F_y^{m,A} + M^m \quad (16)$$

$$Z_{y,l}^{f,A} = S_l^{f,A} \mu^A F_y^{m,A} + M^m \quad (17)$$

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.:

$$l_a \sim N^* \left[l_\infty^{m/f,A} (1 - e^{-\kappa(a-t_0)}) ; \theta_a^2 \right] \quad (18)$$

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.:

$$\theta_a = \beta l_\infty^{m/f,A} (1 - e^{-\kappa(a-t_0)}) \quad (19)$$

with β a parameter estimated in the model fitting process.

Catch-at-length proportions

$$\hat{P}_{y,l}^{m,A} = \frac{\sum_a \bar{C}_{y,a,l}^{m,A}}{\sum_l \sum_{m,f} \sum_a \bar{C}_{y,a,l}^{m/f,A}} \quad (20)$$

$$\hat{P}_{y,l}^{f,A} = \frac{\sum_a \bar{C}_{y,a,l}^{f,A}}{\sum_l \sum_{m,f} \sum_a \bar{C}_{y,a,l}^{m/f,A}} \quad (21)$$

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).

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

$$\hat{B}_y^A = \hat{B}_y^{m,A} + \hat{B}_y^{f,A} \quad (22)$$

where

$$\hat{B}_y^{f,A} = \sum_a \sum_l w_{a+\frac{1}{2}}^{f,A} \mu^A S_l^{f,A} \bar{N}_{y,a,l}^{f,A} e^{-(Z_{y,l}^{f,A})/2} \quad (23)$$

$$\hat{B}_y^{m,A} = \sum_a \sum_l w_{a+\frac{1}{2}}^{m,A} S_l^{m,A} \bar{N}_{y,a,l}^{m,A} e^{-(Z_{y,l}^{m,A})/2} \quad (24)$$

and where

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

Selectivity-at-length function

Fitting to the catch-at-length data requires a selectivity-at-length function. This function is identical to that previously used for the selectivity-at-age, except that parameters refer to length not age, i.e. for the time-invariant selectivity-at-length function:

$$S_l^{m/f,A} = \frac{1}{1 + e^{(-\ln(19)(l-l_{50}^{m/f,A})/(\Delta^{m/f,A}))}} \quad (25)$$

where

$l_{50}^{m/f,A}$ is the length-at-50% selectivity for m/f lobsters in area A , which is estimated,
 $l_{95}^{m/f,A} = \Delta^{m/f,A} + l_{50}^{m/f,A}$ is the length-at-95% selectivity, where $\Delta^{m/f,A}$ is estimated.

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:

$$-\ln L = \sum_{y=y1}^{y2} \left[\frac{\zeta_y - \rho \zeta_{y-1}}{\sqrt{1-\rho^2}} \right]^2 / 2\sigma_R^2 \quad (26)$$

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. 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 ($-\ln L$) 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:

$$CPUE_y^A = q^A B_y^A e^{\varepsilon_y^A} \text{ or } \varepsilon_y^A = \ln(CPUE_y^A) - \ln(q^A B_y^A) \quad (27)$$

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:

$$-\ln L = \sum_A \sum_y \left[(\varepsilon_y^A)^2 / 2(\sigma^A)^2 + \ln(\sigma^A) \right] \quad (28)$$

where

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

$$\hat{\sigma}^A = \sqrt{1/n \sum_y (\ln CPUE_y^A - \ln \hat{q}^A \hat{B}_y^A)^2} \quad (29)$$

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:

$$\ln \hat{q}^A = 1/n \sum_y (\ln CPUE_y^A - \ln \hat{B}_y^A) \quad (30)$$

2.3 Catches-at-length (from Rademeyer 2003)

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

$$-\ell_n L^{\text{length}} = w_{len} \sum_A \sum_y \sum_l \sum_{m/f} \left[\ln(\sigma_{len}^A / \sqrt{p_{y,l}^{m/f,A}}) + p_{y,l}^{m/f,A} (\ln p_{y,l}^{m/f,A} - \ln \hat{p}_{y,l}^{m/f,A})^2 / 2(\sigma_{len}^A)^2 \right] \quad (31)$$

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:

$$\hat{\sigma}_{len}^A = \sqrt{\sum_{m/f} \sum_y \sum_l p_{y,l}^{m/f,A} (\ln p_{y,l}^{m/f,A} - \ln \hat{p}_{y,l}^{m/f,A})^2 / \sum_{m/f} \sum_y \sum_l 1} \quad (32)$$

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.

The w_{len} weighting factor may be set at a value less than 1 to down-weight the contribution of the catch-at-length data to the overall negative log-likelihood compared to that of the CPUE data. The reason that this factor is introduced is that the

$p_{y,l}^f$ data for a given year will likely show evidence of strong positive correlation, and so are not as informative as the independence assumption underlying the form of equation 31 would otherwise suggest.

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..

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, and 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:

$$w_a^{m/f,A} = \alpha \left[l_{\infty}^{m/f,A} \left(1 - e^{-\kappa(a-t_0)} \right) \right]^{\beta} \quad (33)$$

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

Mass-at-length:

$$w_l^{m/f,A} = \alpha l^{\beta} \quad (34)$$

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.

In the case of an age-structured production model, the Bayesian computations require integration over the following priors:

- K^{sp} - the pristine spawning biomass in the first year (1973)
- The ‘‘steepness’’ of the stock-recruit relationship (h), and

- Natural mortality (M_a), assumed here to independent of age and sex.

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:

$\ln K$ U[7.6, 9.9] corresponding to values for K of 1998 and 19930 tons.

h N(0.95, SD²) with SD=0.2, where the normal distribution is truncated at $h = 1$.

$M^{m/f}$ U[0.1, 0.3] yr⁻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[0,5]

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

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Table 1: Somatic growth parameters (for use in equations 33 and 34) (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